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 LUCA15 PELVRNGDEENPLKRGVAAVSGDSNHEE.....ELVERLESEEEKLADWKKMACILLCRRQFPNKKDAL 662
 DXS8237E DLPKLASDDRPSPPRGLVAAVSGESDSE.....EQERGGEREEKLTDWQKLACILLCRRQFPNKEAL 233

NY-1U-12 IKHQQLSDLPKQNLIEHRTKQSEQLAYLERRERE.GKFKGRGNDREKLQSFDSPERKKIKYSRETDS..DRKLVDKEDID 1050
 LUCA15 VRHQQLSDLEKQNDIYRRSRLESELEALELREERE.NKYDRAAERREKYGIPEPPEPKKKQFDAGTV..NYEQPTDGDID 742
 DXS8237E IRHQQLSGLHKQNLIEHRAHLESELEALELEKQNDMEQNKYDRAAERREKYGIPEPPEPKKKRYGGISTASVDPEQPTDGLG 316

NY-1U-12 TSSKGGCVQQTGWRRGTGLGYGHPGLASSEAEGRERGSPVGASGRTSKRQSNETTYRDAVRRVHFARYKELD 1123
 LUCA15 HSNIGNQLQAMGREGSGLRKQCQITAPIEAQVRLKAGLCAKGSAYGLSGADSYKDAVRKAMPARPIEME 815
 DXS8237E SDNIGSRMLQAMGKEGSGLRKQGIIVTPIEAQTRVRGSLGARGSSYGVTSYKETLHKTNTVTRFNEAQ 389

(57) Abstract

Various molecules associated with cancer are disclosed. The invention also discloses diagnostic and therapeutic methods based upon these molecules.

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CANCER ASSOCIATED NUCLEIC ACIDS AND POLYPEPTIDES

Field of the Invention

The invention relates to nucleic acids and encoded polypeptides which are cancer
5 associated antigens expressed in patients afflicted with breast cancer. The invention also relates
to agents which bind the nucleic acids or polypeptides. The nucleic acid molecules,
polypeptides coded for by such molecules and peptides derived therefrom, as well as related
antibodies and cytolytic T lymphocytes, are useful, *inter alia*, in diagnostic and therapeutic
contexts.

10

Background of the Invention

The mechanism by which T cells recognize foreign materials has been implicated in
cancer. A number of cytolytic T lymphocyte (CTL) clones directed against autologous
melanoma antigens, testicular antigens, and melanocyte differentiation antigens have been
15 described. In many instances, the antigens recognized by these clones have been
characterized.

The use of autologous CTLs for identifying tumor antigens requires that the target cells
which express the antigens can be cultured *in vitro* and that stable lines of autologous CTL
clones which recognize the antigen-expressing cells can be isolated and propagated. While this
20 approach has worked well for melanoma antigens, other tumor types, such as epithelial cancers
including breast and colon cancer, have proved refractory to the approach.

More recently another approach to the problem has been described by Sahin et al. (*Proc.
Natl. Acad. Sci. USA* 92:11810-11813, 1995). According to this approach, autologous antisera
are used to identify immunogenic protein antigens expressed in cancer cells by screening
25 expression libraries constructed from tumor cell cDNA. Antigen-encoding clones so identified
have been found to have elicited an high-titer humoral immune response in the patients from
which the antisera were obtained. Such a high-titer IgG response implies helper T cell
recognition of the detected antigen. These tumor antigens can then be screened for the presence
of MHC/HLA class I and class II motifs and reactivity with CTLs

30 The invention is elaborated upon in the disclosure which follows.

Summary of the Invention

Autologous antibody screening has now been applied to cancer using antisera from cancer patients. Numerous cancer associated antigens have been identified. The invention provides, *inter alia*, isolated nucleic acid molecules, expression vectors containing those molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and CTLs which recognize the proteins and peptides. Fragments including functional fragments and variants of the foregoing also are provided. Kits containing the foregoing molecules additionally are provided. The foregoing can be used in the diagnosis, monitoring, research, or treatment of conditions characterized by the expression of one or more cancer associated antigens.

Prior to the present invention, only a handful of cancer associated genes had been identified in the past 20 years. The invention involves the surprising discovery of many genes, some previously known and many previously unknown, which are expressed in individuals who have cancer. These individuals all have serum antibodies against the proteins (or fragments thereof) encoded by these genes. Thus, abnormally expressed genes are recognized by the host's immune system and therefore can form a basis for diagnosis, monitoring and therapy.

The invention involves the use of a single material, a plurality of different materials and even large panels and combinations of materials. For example, a single gene, a single protein encoded by a gene, a single functional fragment thereof, a single antibody thereto, etc. can be used in methods and products of the invention. Likewise, pairs, groups and even panels of these materials can be used for diagnosis, monitoring and therapy. The pairs, groups or panels can involve 2, 3, 4, 5... to as many as 25, 50, 100 or more genes, gene products, fragments thereof or agents that recognize such materials. A plurality of such materials are not only useful in monitoring, typing, characterizing and diagnosing cells abnormally expressing such genes, but a plurality of such materials can be used therapeutically. An example of the use of a plurality of such materials for the prevention, delay of onset, amelioration, etc. of cancer cells, which express or will express such genes prophylactically or acutely. Any and all combinations of the genes, gene products, and materials which recognize the genes and gene products can be tested and identified for use according to the invention. It would be far too lengthy to recite all such combinations; those skilled in the art, particularly in view of the teaching contained herein, will readily be able to determine which combinations are most appropriate for which circumstances.

As will be clear from the following discussion, the invention has *in vivo* and *in vitro* uses,

including for therapeutic, diagnostic, monitoring and research purposes. One aspect of the invention is the ability to fingerprint a cell expressing a number of the genes identified according to the invention. Such fingerprints will be characteristic, for example, of the stage of the cancer, the type of the cancer, or even the effect in animal models of a therapy on a cancer.

5 Cells also can be screened to determine whether such cells abnormally express the genes identified according to the invention.

The invention, in one aspect, is a method of diagnosing a disorder characterized by expression of a cancer associated antigen precursor coded for by a nucleic acid molecule. The method involves the steps of contacting a biological sample isolated from a subject with an
10 agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an MHC, preferably an HLA, molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and determining the interaction between the agent and the nucleic acid molecule, the expression product or fragment of the expression product as a determination of the disorder.

15 In one embodiment the agent is selected from the group consisting of (a) a nucleic acid molecule comprising NA Group 1 nucleic acid molecules or a fragment thereof, (b) a nucleic acid molecule comprising NA Group 3 nucleic acid molecules or a fragment thereof, (c) a nucleic acid molecule comprising NA Group 17 nucleic acid molecules or a fragment thereof, (d) an antibody that binds to an expression product, or a fragment thereof, of NA group 1
20 nucleic acids, (e) an antibody that binds to an expression product, or a fragment thereof, of NA group 3 nucleic acids, (f) an antibody that binds to an expression product, or a fragment thereof, of NA group 17 nucleic acids, (g) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 1 nucleic acid, (h) an agent that binds to a complex of an MHC, preferably HLA, molecule and a
25 fragment of an expression product of a NA group 3 nucleic acid, and (I) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 17 nucleic acid.

The disorder may be characterized by expression of a plurality of cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for
30 a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 such agents.

In each of the above embodiments the agent may be specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

In another aspect the invention is a method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method involves the steps of monitoring a sample, from a subject who has or is suspected of having the condition, for a parameter selected from the group consisting of (i) the protein, (ii) a peptide derived from the protein, (iii) an antibody which selectively binds the protein or peptide, and (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule, as a determination of regression, progression or onset of said condition. In one embodiment the sample is a body fluid, a body effusion or a tissue.

In another embodiment the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of (a) an antibody which selectively binds the protein of (i), or the peptide of (ii), (b) a protein or peptide which binds the antibody of (iii), and (c) a cell which presents the complex of the peptide and MHC molecule of (iv). In a preferred embodiment the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme. The sample in a preferred embodiment is assayed for the peptide.

According to another embodiment the nucleic acid molecule is one of the following: a NA Group 3 molecule, a NA Group 11 molecule, a NA Group 12 molecule, a NA Group 13 molecule, a NA Group 14 molecule, a NA Group 15 molecule, or a NA Group 16 molecule. In yet another embodiment the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

The invention in another aspect is a pharmaceutical preparation for a human subject. The pharmaceutical preparation includes an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule which comprises a NA Group 1 molecule. In one embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The agent in one embodiment comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least two, at least three, at least four or at least 5 different such agents.

5 In another embodiment the agent is selected from the group consisting of (1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof, (2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof, (3) a host cell expressing the isolated polypeptide, or functional variant thereof, and (4) isolated complexes of the polypeptide, or functional
10 variant thereof, and an HLA molecule.

The agent may be a cell expressing an isolated polypeptide. In one embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative. In another embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer
15 associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide. The cell can express one or both of the polypeptide and HLA molecule recombinantly. In another preferred embodiment the cell is nonproliferative. In yet another embodiment the agent is at least two, at least three, at least four or at least five different polypeptides, each representing a different human cancer associated antigen or
20 functional variant thereof.

The agent in one embodiment is a PP Group 2 polypeptide. In other embodiments the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

In an embodiment each of the pharmaceutical preparations described herein also includes an adjuvant.

25 According to another aspect the invention, a composition is provided of an isolated agent that binds selectively a PP Group 1 polypeptide. In separate embodiments the agent binds selectively to a polypeptide selected from the following: a PP Group 3 polypeptide, a PP Group 11 polypeptide, a PP Group 12 polypeptide, a PP Group 13 polypeptide, a PP Group 14 polypeptide, a PP Group 15 polypeptide, and a PP Group 16 polypeptide. In other
30 embodiments, the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides. In each of the above described embodiments the agent may be an antibody.

In another aspect the invention is a composition of matter composed of a conjugate of the agent of the above-described compositions of the invention and a therapeutic or diagnostic agent. Preferably the conjugate is of the agent and a therapeutic or diagnostic that is an antineoplastic.

5 The invention in another aspect is a pharmaceutical composition of an isolated nucleic acid molecule selected from the group consisting of: (1) NA Group 1 molecules, and (2) NA Group 2 molecules, and a pharmaceutically acceptable carrier. In one embodiment the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule. In another embodiment the isolated nucleic acid molecule comprises at least two isolated nucleic acid
10 molecules coding for two different polypeptides, each polypeptide comprising a different cancer associated antigen.

Preferably the pharmaceutical composition also includes an expression vector with a promoter operably linked to the isolated nucleic acid molecule. In another embodiment the pharmaceutical composition also includes a host cell recombinantly expressing the isolated
15 nucleic acid molecule.

According to another aspect of the invention a pharmaceutical composition is provided. The pharmaceutical composition includes an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier. In one embodiment the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

20 In another embodiment the isolated polypeptide comprises at least two different polypeptides, each comprising a different cancer associated antigen. In separate embodiments the isolated polypeptides are selected from the following: PP Group 11 polypeptides or HLA binding fragments thereof, PP Group 12 polypeptides or HLA binding fragments thereof, PP Group 13 polypeptides or HLA binding fragments thereof, PP Group 14 polypeptides or HLA
25 binding fragments thereof, PP Group 15 polypeptides or HLA binding fragments thereof, or PP Group 16 polypeptides or HLA binding fragments thereof.

In an embodiment each of the pharmaceutical compositions described herein also includes an adjuvant.

Another aspect the invention is an isolated nucleic acid molecule comprising a NA
30 Group 3 molecule. Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 4 molecule. In separate embodiments the isolated nucleic acid molecules are selected from the following: a Group 11 molecule or a functional fragment

thereof, a Group 12 molecule or a functional fragment thereof, a Group 13 molecule or a functional fragment thereof, a Group 14 molecule or a functional fragment thereof, a Group 15 molecule or a functional fragment thereof, or a Group 16 molecule or a functional fragment thereof.

5 ~~The invention in another aspect is an isolated nucleic acid molecule selected from the~~
group consisting of (a) a fragment of a nucleic acid selected from the group of nucleic acid
molecules consisting of SEQ ID numbered below and comprising all nucleic acid sequences
among SEQ ID NOs 1-816, of sufficient length to represent a sequence unique within the
human genome, and identifying a nucleic acid encoding a human cancer associated antigen
10 precursor, (b) complements of (a), provided that the fragment includes a sequence of
contiguous nucleotides which is not identical to any sequence selected from the sequence group
consisting of (1) sequences having the GenBank accession numbers of the sequence Group 1,
(2) complements of (1), and (3) fragments of (1) and (2).

In one embodiment the sequence of contiguous nucleotides is selected from the group
15 consisting of: (1) at least two contiguous nucleotides nonidentical to the sequence Group 1, (2)
at least three contiguous nucleotides nonidentical to the sequence Group 1, (3) at least four
contiguous nucleotides nonidentical to the sequence Group 1, (4) at least five contiguous
nucleotides nonidentical to the sequence Group 1, (5) at least six contiguous nucleotides
nonidentical to the sequence Group 1, or (6) at least seven contiguous nucleotides nonidentical
20 to the sequence Group 1.

In another embodiment the fragment has a size selected from the group consisting of at
least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18
nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30
nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, 200 nucleotides, 1000 nucleotides
25 and every integer length therebetween.

In yet another embodiment the molecule encodes a polypeptide which, or a fragment of
which, binds a human HLA receptor or a human antibody.

Another aspect of the invention is an expression vector comprising an isolated nucleic
acid molecule of the invention described above operably linked to a promoter.

30 According to one aspect the invention is an expression vector comprising a nucleic acid
operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule. In another
aspect the invention is an expression vector comprising a NA Group 1 or Group 2 molecule

and a nucleic acid encoding an MHC, preferably HLA, molecule.

In yet another aspect the invention is a host cell transformed or transfected with an expression vector of the invention described above.

In another aspect the invention is a host cell transformed or transfected with an
5 expression vector comprising an isolated nucleic acid molecule of the invention described
above operably linked to a promoter, or an expression vector comprising a nucleic acid
operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or 2 molecule and
further comprising a nucleic acid encoding HLA.

According to another aspect of the invention an isolated polypeptide encoded by the
10 isolated nucleic acid molecules the invention, described above, is provided. These include PP
Group 1-17 polypeptides. The invention also includes a fragment of the polypeptide which is
immunogenic. In one embodiment the fragment, or a portion of the fragment, binds HLA or a
human antibody.

The invention includes in another aspect an isolated fragment of a human cancer
15 associated antigen precursor which, or portion of which, binds HLA or a human antibody,
wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule.
In one embodiment the fragment is part of a complex with HLA. In another embodiment the
fragment is between 8 and 12 amino acids in length. In another embodiment the invention
includes an isolated polypeptide comprising a fragment of the polypeptide of sufficient length
20 to represent a sequence unique within the human genome and identifying a polypeptide that is
a human cancer associated antigen precursor.

According to another aspect of the invention a kit for detecting the presence of the
expression of a cancer associated antigen precursor is provided. The kit includes a pair of
isolated nucleic acid molecules each of which consists essentially of a molecule selected from
25 the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence
of any of the NA Group 1 molecules and (b) complements of ("a"), wherein the contiguous
segments are nonoverlapping. In one embodiment the pair of isolated nucleic acid molecules
is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a
NA Group 3 molecule. Preferably, the pair amplifies a human NA Group 3 molecule.

30 According to another aspect of the invention a method for treating a subject with a
disorder characterized by expression of a human cancer associated antigen precursor is
provided. The method includes the step of administering to the subject an amount of an agent,

which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of (a) a nucleic acid

5 molecule comprising NA group 1 nucleic acid molecules, (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules, (c) a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

In one embodiment the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of
10 which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

In another embodiment the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6,
15 PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

In yet another embodiment the disorder is cancer.

According to another aspect the invention is a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the
20 subject. The method includes the steps of (i) removing an immunoreactive cell containing sample from the subject, (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor, (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated
25 antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group
30 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

In one embodiment the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen. In another embodiment the host cell endogenously

expresses an HLA molecule which binds the human cancer associated antigen.

The invention includes in another aspect a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (I) identifying a nucleic acid molecule expressed by

5 the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule (ii) transfecting a host cell with a nucleic acid selected from the group consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid identified which includes a segment coding for a cancer associated antigen, (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c); (iii) culturing said transfected
10 host cells to express the transfected nucleic acid molecule, and; (iv) introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition. Preferably, the antigen is a human antigen and the subject is a human.

In one embodiment the method also includes the step of (a) identifying an MHC
15 molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

In another embodiment the method also includes the step of treating the host cells to
20 render them non-proliferative.

In yet another embodiment the immune response comprises a B-cell response or a T cell response. Preferably the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated
25 antigen.

In another embodiment the nucleic acid molecule is a NA Group 3 molecule.

Another aspect of the invention is a method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method includes the
30 step of administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

In one embodiment the antibody is a monoclonal antibody. Preferably the monoclonal antibody is a chimeric antibody or a humanized antibody.

In another aspect the invention is a method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule

5 ~~that is a NA Group 1 nucleic acid molecule. The method involves the step of administering to~~
a subject at least one of the pharmaceutical compositions of the invention described above in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject. In one embodiment the condition is cancer. In another embodiment the method includes the step of first identifying that the subject expresses in a tissue abnormal amounts of the protein.

10 The invention in another aspect is a method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the steps of (I) identifying cells from the subject which express abnormal amounts of the protein; (ii) isolating a sample of the cells; (iii) cultivating the cells, and (iv) introducing the cells to the subject in
15 an amount effective to provoke an immune response against the cells.

In one embodiment the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein. In another embodiment the method includes the step of rendering the cells non-proliferative, prior to introducing them to the subject.

20 In another aspect the invention is a method for treating a pathological cell condition characterized by abnormal expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the step of administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

25 In one embodiment the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody. In another embodiment the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein. In yet another important embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

30 The invention includes in another aspect a composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules. The composition is a plurality of peptides derived from the amino acid

sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

In one embodiment at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto. In another embodiment the composition of matter

5 includes an adjuvant. In another embodiment the adjuvant is a saponin, GM-CSF, or an interleukin.

According to another aspect the invention is an isolated antibody which selectively binds to a complex of: (I) a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and (ii) and an MHC molecule to which binds the peptide to form the
10 complex, wherein the isolated antibody does not bind to (I) or (ii) alone.

In one embodiment the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

The invention also involves the use of the genes, gene products, fragments thereof, agents which bind thereto, and so on in the preparation of medicaments. A particular medicament is for
15 treating cancer and a more particular medicament is for treating breast cancer, lung cancer, renal cancer, colon cancer, prostate cancer or gastric cancer.

Detailed Description of the Invention

In the above summary and in the ensuing description, lists of sequences are provided.
20 The lists are meant to embrace each single sequence separately, two or more sequences together where they form a part of the same gene, any combination of two or more sequences which relate to different genes, including and up to the total number on the list, as if each and every combination were separately and specifically enumerated. Likewise, when mentioning fragment size, it is intended that a range embrace the smallest fragment mentioned to the full-length of the
25 sequence (-1 so that it is a fragment), each and every fragment length intended as if specifically enumerated. Thus, if a fragment could be between 10 and 15 in length, it is explicitly meant to mean 10, 11, 12, 13, 14, or 15 in length.

The summary and the claims mention antigen precursors and antigens. As used in the summary and in the claims, a precursor is substantially the full-length protein encoded by the
30 coding region of the isolated DNA and the antigen is a peptide which complexes with MHC, preferably HLA, and which participates in the immune response as part of that complex. Such antigens are typically 9 amino acids long, although this may vary slightly.

As used herein, a subject is a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat or rodent. In all embodiments human cancer antigens and human subjects are preferred.

The present invention in one aspect involves the cloning of cDNAs encoding human cancer associated antigen precursors using autologous antisera of subjects having cancer. The

5 sequences of the clones representing genes identified according to the methods described herein are presented in the attached Sequence Listing, and the predicted amino acid sequences of some clones also are presented. Of the foregoing, it can be seen that some of the clones are considered completely novel as no nucleotide or amino acid homologies to coding regions were found in the databases searched. Other clones are novel but have some homology to sequences deposited in
10 databases (mainly EST sequences). Nevertheless, the entire gene sequence was not previously known. In some cases no function was suspected and in other cases, even if a function was suspected, it was not known that the gene was associated with cancer. In all cases, it was not known or suspected that the gene encoded a cancer antigen which reacted with antibody from autologous sera. Analysis of the clone sequences by comparison to nucleic acid and protein
15 databases determined that still other of the clones surprisingly are closely related to other previously cloned genes. The sequences of these related genes is also presented in the Sequence Listing. The nature of the foregoing genes as encoding antigens recognized by the immune systems of cancer patients is, of course, unexpected.

The invention thus involves in one aspect cancer associated antigen polypeptides, genes
20 encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as diagnostics and therapeutics relating thereto.

Homologs and alleles of the cancer associated antigen nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for cancer associated antigen precursors. Because this application
25 contains so many sequences, the following chart is provided to identify the various groups of sequences discussed in the claims and in the summary:

"Nucleic Acid Sequences"

30 NA Group 1. (a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of a nucleic acid sequence selected from the group consisting of nucleic acid sequences among SEQ ID NOs 1-816 and which code for a cancer associated antigen precursor,

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(b) deletions, additions and substitutions which code for a respective cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

5 (d) complements of (a), (b) or (c).

NA Group 2. Fragments of NA Group 1, which codes for a polypeptide which, or a portion of which, binds an MHC molecule to form a complex recognized by a an autologous antibody or lymphocyte.

10

NA Group 3. The subset of NA Group 1 where the nucleotide sequence is selected from the group consisting of:

(a) previously unknown human nucleic acids coding for a human cancer associated antigen precursor,

15 (b) deletions, additions and substitutions which code for a respective human cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

20 NA Group 4. Fragments of NA Group 3, which code for a polypeptide which, or a portion of which, binds to an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

NA Group 5. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human
25 breast cancer associated antigen precursor.

NA Group 6. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

30 NA Group 7. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

NA Group 8. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 9. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

NA Group 10. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

10 NA Group 11. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

NA Group 12. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

15

NA Group 13. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

NA Group 14. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

20

NA Group 15. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

25 NA Group 16. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

NA Group 17. A subset of NA Group 1, comprising human cancer associated antigens that react with allogenic cancer antisera.

30

Polypeptide Sequences

PP Group 1. Polypeptides encoded by NA Group 1.

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- PP Group 2. Polypeptides encoded by NA Group 2
PP Group 3. Polypeptides encoded by NA Group 3.
PP Group 4. Polypeptides encoded by NA Group 4.
PP Group 5. Polypeptides encoded by NA Group 5.
-
- 5 PP Group 6. Polypeptides encoded by NA Group 6.
PP Group 7. Polypeptides encoded by NA Group 7.
PP Group 8. Polypeptides encoded by NA Group 8.
PP Group 9. Polypeptides encoded by NA Group 9.
PP Group 10. Polypeptides encoded by NA Group 10.
10 PP Group 11. Polypeptides encoded by NA Group 11.
PP Group 12. Polypeptides encoded by NA Group 12.
PP Group 13. Polypeptides encoded by NA Group 13.
PP Group 14. Polypeptides encoded by NA Group 14.
PP Group 15. Polypeptides encoded by NA Group 15.
15 PP Group 16. Polypeptides encoded by NA Group 16.
PP Group 17. Polypeptides encoded by NA Group 17.

The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such
20 methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at
25 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5mM NaH₂PO₄(pH7), 0.5% SDS, 2mM EDTA). SSC is 0.15M sodium chloride/0.15M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed, for example, in 2 x SSC at room temperature and then at 0.1 - 0.5 x SSC/0.1 x SDS at temperatures up to 68°C.

30 There are other conditions, reagents, and so forth which can be used, which result in a similar degree of stringency. The skilled artisan will be familiar with such conditions, and thus they are not given here. It will be understood, however, that the skilled artisan will be able to

manipulate the conditions in a manner to permit the clear identification of homologs and alleles of cancer associated antigen nucleic acids of the invention (e.g., by using lower stringency conditions). The skilled artisan also is familiar with the methodology for screening cells and libraries for expression of such molecules which then are routinely isolated, followed by
5 isolation of the pertinent nucleic acid molecule and sequencing.

In general homologs and alleles typically will share at least 40% nucleotide identity and/or at least 50% amino acid identity to the sequences of breast cancer associated antigen nucleic acid and polypeptides, respectively, in some instances will share at least 50% nucleotide identity and/or at least 65% amino acid identity and in still other instances will share at least 60%
10 nucleotide identity and/or at least 75% amino acid identity. The homology can be calculated using various, publicly available software tools developed by NCBI (Bethesda, Maryland) that can be obtained through the internet (<ftp://ncbi.nlm.nih.gov/pub/>). Exemplary tools include the BLAST system available at <http://www.ncbi.nlm.nih.gov>. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyte-Doolittle hydropathic analysis can be obtained
15 using the MacVector sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

In screening for cancer associated antigen genes, a Southern blot may be performed using the foregoing conditions, together with a radioactive probe. After washing the membrane to which the DNA is finally transferred, the membrane can be placed against X-ray film to detect
20 the radioactive signal. In screening for the expression of cancer associated antigen nucleic acids, Northern blot hybridizations using the foregoing conditions (see also the Examples) can be performed on samples taken from breast cancer patients or subjects suspected of having a condition characterized by expression of breast cancer associated antigen genes. Amplification protocols such as polymerase chain reaction using primers which hybridize to the sequences
25 presented also can be used for detection of the cancer associated antigen genes or expression thereof.

The breast cancer associated genes correspond to SEQ ID NOs. 1-40 and 66. The preferred breast cancer associated antigens for the methods of diagnosis disclosed herein are those set forth in SEQ ID NOs:[31, 33 and 34], which were found to react with allogeneic breast
30 cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The colon cancer associated genes correspond to SEQ ID Nos. 544-586, even numbers

only. The preferred colon cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic colon cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The gastric cancer associated genes correspond to SEQ ID NOs 176-436 and 588-674.

5 The preferred gastric cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic gastric cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The renal cancer associated genes correspond to SEQ ID Nos. 89-169, odd numbers only, and 170, 172, and 174. The preferred renal cancer associated antigens for the methods of
10 diagnosis disclosed herein are those, which were found to react with allogeneic renal cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The lung cancer associated genes correspond to SEQ ID Nos. 689, 691, 692, 694, 696-707, 709, 711, and 712. The preferred lung cancer associated antigens for the methods of
15 diagnosis disclosed herein are those, which were found to react with allogeneic lung cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The prostate cancer associated genes correspond to SEQ ID NOs 437-543. The preferred prostate cancer associated antigens for the methods of diagnosis disclosed herein are those,
20 which were found to react with allogeneic prostate cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The invention also includes degenerate nucleic acids which include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of
25 encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, *in vitro* or *in vivo*, to incorporate a serine residue into an elongating breast cancer associated antigen polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to: CCA, CCC, CCG and CCT (proline codons); CGA,
30 CGC, CGG, CGT, AGA and AGG (arginine codons); ACA, ACC, ACG and ACT (threonine codons); AAC and AAT (asparagine codons); and ATA, ATC and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus,

the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

The invention also provides isolated unique fragments of cancer associated antigen nucleic acid sequences or complements thereof. A unique fragment is one that is a 'signature' for the larger

5 nucleic acid. It, for example, is long enough to assure that its precise sequence is not found in molecules within the human genome outside of the cancer associated antigen nucleic acids defined above (and human alleles). Those of ordinary skill in the art may apply no more than routine procedures to determine if a fragment is unique within the human genome. Unique fragments, however, exclude fragments completely composed of the nucleotide sequences of any of GenBank
10 accession numbers listed in Table 1 or other previously published sequences as of the filing date of the priority documents for sequences listed in a respective priority document or the filing date of this application for sequences listed for the first time in this application which overlap the sequences of the invention.

A fragment which is completely composed of the sequence described in the foregoing
15 GenBank deposits is one which does not include any of the nucleotides unique to the sequences of the invention. Thus, a unique fragment must contain a nucleotide sequence other than the exact sequence of those in GenBank or fragments thereof. The difference may be an addition, deletion or substitution with respect to the GenBank sequence or it may be a sequence wholly separate from the GenBank sequence.

20 Unique fragments can be used as probes in Southern and Northern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200, 250, 300 or more nucleotides are preferred for certain uses such as Southern and Northern blots, while smaller fragments will be preferred for uses such as PCR. Unique fragments also can be used to produce fusion proteins for generating
25 antibodies or determining binding of the polypeptide fragments, or for generating immunoassay components. Likewise, unique fragments can be employed to produce nonfused fragments of the cancer associated antigen polypeptides, useful, for example, in the preparation of antibodies, and in immunoassays. Unique fragments further can be used as antisense molecules to inhibit the expression of cancer associated antigen nucleic acids and polypeptides, particularly for therapeutic
30 purposes as described in greater detail below.

As will be recognized by those skilled in the art, the size of the unique fragment will depend upon its conservancy in the genetic code. Thus, some regions of cancer associated antigen sequences and complements thereof will require longer segments to be unique while others will require only short segments, typically between 12 and 32 nucleotides (e.g. 12, 13, 14, 15, 16, 17, 18,

5 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 and 32 or more bases long, up to the entire length of the disclosed sequence. As mentioned above, this disclosure intends to embrace each and every fragment of each sequence, beginning at the first nucleotide, the second nucleotide and so on, up to 8 nucleotides short of the end, and ending anywhere from nucleotide number 8, 9, 10 and so on for each sequence, up to the very last nucleotide, (provided the sequence is unique as described above).

10 Virtually any segment of the polypeptide coding region of novel cancer associated antigen nucleic acids, or complements thereof, that is 18 or more nucleotides in length will be unique. Those skilled in the art are well versed in methods for selecting such sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from other sequences in the human genome of the fragment to those on known databases typically is all
15 that is necessary, although *in vitro* confirmatory hybridization and sequencing analysis may be performed. Especially preferred include nucleic acids encoding a series of epitopes, known as "polytopes". The epitopes can be arranged in sequential or overlapping fashion (*see, e.g.,* Thomson et al., *Proc. Natl. Acad. Sci. USA* 92:5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15:1280-1284, 1997), with or without the natural flanking sequences, and can be separated by unrelated
20 linker sequences if desired. The polytope is processed to generated individual epitopes which are recognized by the immune system for generation of immune responses.

Thus, for example, peptides derived from a polypeptide having an amino acid sequence encoded by one of the nucleic acid disclosed herein, and which are presented by MHC molecules and recognized by CTL or T helper lymphocytes, can be combined with peptides from one or more
25 other cancer associated antigens (e.g. by preparation of hybrid nucleic acids or polypeptides) to form "polytopes". The two or more peptides (or nucleic acids encoding the peptides) can be selected from those described herein, or they can include one or more peptides of previously known cancer associated antigens. Exemplary cancer associated peptide antigens that can be administered to induce or enhance an immune response are derived from tumor associated genes and encoded
30 proteins including MAGE-1, MAGE-2, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MAGE-7,

MAGE-8, MAGE-9, MAGE-10, MAGE-11, GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, BAGE-1, RAGE-1, LB33/MUM-1, PRAME, NAG, MAGE-Xp2, MAGE-Xp3, MAGE-Xp4, tyrosinase, brain glycogen phosphorylase, Melan-A, and MAGE-C1. See, for example, PCT application publication no. WO96/10577. Other examples will be known to one of ordinary skill in

5 the art (for example, see Coulie, *Stem Cells* 13:393-403, 1995), and can be used in the invention in a like manner as those disclosed herein. One of ordinary skill in the art can prepare polypeptides comprising one or more peptides and one or more of the foregoing cancer associated peptides, or nucleic acids encoding such polypeptides, according to standard procedures of molecular biology.

Thus polytopes are groups of two or more potentially immunogenic or immune response
10 stimulating peptides which can be joined together in various arrangements (e.g. concatenated, overlapping). The polytope (or nucleic acid encoding the polytope) can be administered in a standard immunization protocol, e.g. to animals, to test the effectiveness of the polytope in stimulating, enhancing and/or provoking an immune response.

The peptides can be joined together directly or via the use of flanking sequences to form
15 polytopes, and the use of polytopes as vaccines is well known in the art (see, e.g., Thomson et al., *Proc. Acad. Natl. Acad. Sci USA* 92(13):5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15(12):1280-1284, 1997; Thomson et al., *J. Immunol.* 157(2):822-826, 1996; Tam et al., *J. Exp. Med.* 171(1):299-306, 1990). for example, Tam showed that polytopes consisting of both MHC class I and class II binding epitopes successfully generated antibody and protective immunity in a mouse
20 model. Tam also demonstrated that polytopes comprising "strings" of epitopes are processed to yield individual epitopes which are presented by MHC molecules and recognized by CTLs. Thus polytopes containing various numbers and combinations of epitopes can be prepared and tested for recognition by CTLs and for efficacy in increasing an immune response.

It is known that tumors express a set of tumor antigens, of which only certain subsets may be
25 expressed in the tumor of any given patient (for examples of this, see the Examples below).

Polytopes can be prepared which correspond to the different combination of epitopes representing the subset of tumor rejection antigens expressed in a particular patient. Polytopes also can be prepared to reflect a broader spectrum of tumor rejection antigens known to be expressed by a tumor type. Polytopes can be introduced to a patient in need of such treatment as polypeptide structures, or
30 via the use of nucleic acid delivery systems known in the art (see, e.g., Allsopp et al., *Eur. J.*

Immunol. 26(8):1951-1959, 1996). Adenovirus, pox virus, Ty-virus like particles, adeno-associated virus, plasmids, bacteria, etc. can be used in such delivery. One can test the polytope delivery systems in mouse models to determine efficacy of the delivery system. The systems also can be tested in human clinical trials.

5 In instances in which a human HLA class I molecule presents tumor rejection antigens derived from cancer associated nucleic acids, the expression vector may also include a nucleic acid sequence coding for the HLA molecule that presents any particular tumor rejection antigen derived from these nucleic acids and polypeptides. Alternatively, the nucleic acid sequence coding for such a HLA molecule can be contained within a separate expression vector. In a situation where the
10 vector contains both coding sequences, the single vector can be used to transfect a cell which does not normally express either one. Where the coding sequences for a cancer associated antigen precursor and the HLA molecule which presents it are contained on separate expression vectors, the expression vectors can be cotransfected. The cancer associated antigen precursor coding sequence may be used alone, when, e.g. the host cell already expresses a HLA molecule which presents a
15 cancer associated antigen derived from precursor molecules. Of course, there is no limit on the particular host cell which can be used. As the vectors which contain the two coding sequences may be used in any antigen-presenting cells if desired, and the gene for cancer associated antigen precursor can be used in host cells which do not express a HLA molecule which presents a cancer associated antigen. Further, cell-free transcription systems may be used in lieu of cells.

20 As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a cancer associated antigen polypeptide, to reduce the expression of cancer associated antigens. This is desirable in virtually any medical condition wherein a reduction of expression of cancer associated antigens is desirable, e.g., in the treatment of cancer. This is also useful for *in vitro* or *in vivo* testing of the effects of a reduction of expression of
25 one or more cancer associated antigens.

As used herein, the term "antisense oligonucleotide" or "antisense" describes an oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby,
30 inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules

are designed so as to interfere with transcription or translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise

-
- 5 that sequence. It is preferred that the antisense oligonucleotide be constructed and arranged so as to bind selectively with the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions. Based upon the sequences of nucleic acids encoding breast cancer associated antigen, or upon allelic or homologous genomic and/or cDNA sequences, one of skill in the art can easily choose and
- 10 synthesize any of a number of appropriate antisense molecules for use in accordance with the present invention. In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 10 and, more preferably, at least 15 consecutive bases which are complementary to the target, although in certain cases modified oligonucleotides as short as 7 bases in length have been used successfully as antisense oligonucleotides (Wagner et al.,
- 15 *Nature Biotechnol.* 14:840-844, 1996). Most preferably, the antisense oligonucleotides comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA transcripts, in preferred embodiments the antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted.
- 20 Targeting to mRNA splicing sites has also been used in the art but may be less preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457, 1994) and at which proteins are not expected to bind. Finally, although the listed sequences are cDNA sequences, one of ordinary skill in the art may easily derive the genomic DNA corresponding
- 25 to the cDNA of a cancer associated antigen. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to nucleic acids encoding breast cancer associated antigens. Similarly, antisense to allelic or homologous cDNAs and genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed

30 of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5' end

of one native nucleotide and the 3' end of another native nucleotide may be covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

5 In preferred embodiments, however, the antisense oligonucleotides of the invention also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which
10 (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters,
15 alkylphosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamidates, carboxymethyl esters and peptides.

The term "modified oligonucleotide" also encompasses oligonucleotides with a covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other
20 than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. The present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding
25 breast cancer associated antigen polypeptides, together with pharmaceutically acceptable carriers.

Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically effective amount of the antisense
30 oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term

- 25 -

“pharmaceutically acceptable” means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term “physiologically acceptable” refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The characteristics of the carrier will depend on the route of

5 administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art, as further described below.

As used herein, a “vector” may be any of a number of nucleic acids into which a desired sequence may be inserted by restriction and ligation for transport between different genetic
10 environments or for expression in a host cell. Vectors are typically composed of DNA although RNA vectors are also available. Vectors include, but are not limited to, plasmids, phagemids and virus genomes. A cloning vector is one which is able to replicate in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector may be cut in a determinable fashion and into which a desired DNA sequence may be ligated such that the new
15 recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence may occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication may occur actively during a lytic phase or passively during a lysogenic phase. An expression vector is one into which a desired DNA sequence may be inserted by restriction and
20 ligation such that it is operably joined to regulatory sequences and may be expressed as an RNA transcript. Vectors may further contain one or more marker sequences suitable for use in the identification of cells which have or have not been transformed or transfected with the vector. Markers include, for example, genes encoding proteins which increase or decrease either resistance or sensitivity to antibiotics or other compounds, genes which encode enzymes whose activities are
25 detectable by standard assays known in the art (e.g., β -galactosidase or alkaline phosphatase), and genes which visibly affect the phenotype of transformed or transfected cells, hosts, colonies or plaques (e.g., green fluorescent protein). Preferred vectors are those capable of autonomous replication and expression of the structural gene products present in the DNA segments to which they are operably joined.

30 As used herein, a coding sequence and regulatory sequences are said to be “operably” joined

when they are covalently linked in such a way as to place the expression or transcription of the coding sequence under the influence or control of the regulatory sequences. If it is desired that the coding sequences be translated into a functional protein, two DNA sequences are said to be operably joined if induction of a promoter in the 5' regulatory sequences results in the transcription of the

5 coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably joined to a coding sequence if the promoter region were capable of effecting transcription of that DNA
10 sequence such that the resulting transcript might be translated into the desired protein or polypeptide.

The precise nature of the regulatory sequences needed for gene expression may vary between species or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as
15 a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design of an appropriate vector is within the
20 ability and discretion of one of ordinary skill in the art.

Expression vectors containing all the necessary elements for expression are commercially available and known to those skilled in the art. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. Cells are genetically engineered by the introduction into the cells of heterologous DNA (RNA) encoding a
25 breast cancer associated antigen polypeptide or fragment or variant thereof. That heterologous DNA (RNA) is placed under operable control of transcriptional elements to permit the expression of the heterologous DNA in the host cell.

Preferred systems for mRNA expression in mammalian cells are those such as pRc/CMV (available from Invitrogen, Carlsbad, CA) that contain a selectable marker such as a gene that
30 confers G418 resistance (which facilitates the selection of stably transfected cell lines) and the

human cytomegalovirus (CMV) enhancer-promoter sequences. Additionally, suitable for expression in primate or canine cell lines is the pCEP4 vector (Invitrogen), which contains an Epstein Barr Virus (EBV) origin of replication, facilitating the maintenance of plasmid as a multicopy extrachromosomal element. Another expression vector is the pEF-BOS plasmid containing the

5 promoter of polypeptide Elongation Factor 1 α , which stimulates efficiently transcription *in vitro*. The plasmid is described by Mishizuma and Nagata (*Nuc. Acids Res.* 18:5322, 1990), and its use in transfection experiments is disclosed by, for example, Demoulin (*Mol. Cell. Biol.* 16:4710-4716, 1996). Still another preferred expression vector is an adenovirus, described by Stratford-Perricaudet, which is defective for E1 and E3 proteins (*J. Clin. Invest.* 90:626-630, 1992). The use
10 of the adenovirus as an Adeno.P1A recombinant for the expression of an antigen is disclosed by Warnier et al., in intradermal injection in mice for immunization against P1A (*Int. J. Cancer*, 67:303-310, 1996). Additional vectors for delivery of nucleic acid are provided below.

The invention also embraces so-called expression kits, which allow the artisan to prepare a desired expression vector or vectors. Such expression kits include at least separate portions of a
15 vector and one or more of the previously discussed breast cancer associated antigen nucleic acid molecules. Other components may be added, as desired, as long as the previously mentioned nucleic acid molecules, which are required, are included. The invention also includes kits for amplification of a breast cancer associated antigen nucleic acid, including at least one pair of amplification primers which hybridize to a breast cancer associated antigen nucleic acid. The
20 primers preferably are 12-32 nucleotides in length and are non-overlapping to prevent formation of "primer-dimers". One of the primers will hybridize to one strand of the breast cancer associated antigen nucleic acid and the second primer will hybridize to the complementary strand of the breast cancer associated antigen nucleic acid, in an arrangement which permits amplification of the breast cancer associated antigen nucleic acid. Selection of appropriate primer pairs is standard in the art.
25 For example, the selection can be made with assistance of a computer program designed for such a purpose, optionally followed by testing the primers for amplification specificity and efficiency.

The invention also permits the construction of cancer associated antigen gene "knock-outs" in cells and in animals, providing materials for studying certain aspects of cancer and immune system responses to cancer.

30 The invention also provides isolated polypeptides (including whole proteins and partial

proteins) encoded by the foregoing cancer associated antigen nucleic acids. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, as components of an immunoassay or diagnostic assay or as therapeutics. Cancer associated antigen polypeptides can be isolated from biological samples including tissue or cell homogenates, and can also be expressed

5 recombinantly in a variety of prokaryotic and eukaryotic expression systems by constructing an expression vector appropriate to the expression system, introducing the expression vector into the expression system, and isolating the recombinantly expressed protein. Short polypeptides, including antigenic peptides (such as are presented by MHC molecules on the surface of a cell for immune recognition) also can be synthesized chemically using well-established methods of peptide synthesis.

10 A unique fragment of a cancer associated antigen polypeptide, in general, has the features and characteristics of unique fragments as discussed above in connection with nucleic acids. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon factors such as whether the fragment constitutes a portion of a conserved protein domain. Thus, some regions of breast cancer associated antigens will require longer segments to be unique while others
15 will require only short segments, typically between 5 and 12 amino acids (e.g. 5, 6, 7, 8, 9, 10, 11 or 12 or more, including each integer up to the full length, amino acids long).

Unique fragments of a polypeptide preferably are those fragments which retain a distinct functional capability of the polypeptide. Functional capabilities which can be retained in a unique fragment of a polypeptide include interaction with antibodies, interaction with other polypeptides or
20 fragments thereof, selective binding of nucleic acids or proteins, and enzymatic activity. One important activity is the ability to act as a signature for identifying the polypeptide. Another is the ability to complex with HLA and to provoke in a human an immune response. Those skilled in the art are well versed in methods for selecting unique amino acid sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-family
25 members. A comparison of the sequence of the fragment to those on known databases typically is all that is necessary.

The invention embraces variants of the cancer associated antigen polypeptides described above. As used herein, a "variant" of a cancer associated antigen polypeptide is a polypeptide which contains one or more modifications to the primary amino acid sequence of a cancer associated
30 antigen polypeptide. Modifications which create a cancer associated antigen variant can be made to

a cancer associated antigen polypeptide 1) to reduce or eliminate an activity of a cancer associated antigen polypeptide; 2) to enhance a property of a cancer associated antigen polypeptide, such as protein stability in an expression system or the stability of protein-protein binding; 3) to provide a novel activity or property to a cancer associated antigen polypeptide, such as addition of an

5 antigenic epitope or addition of a detectable moiety; or 4) to provide equivalent or better binding to an HLA molecule. Modifications to a cancer associated antigen polypeptide are typically made to the nucleic acid which encodes the cancer associated antigen polypeptide, and can include deletions, point mutations, truncations, amino acid substitutions and additions of amino acids or non-amino acid moieties. Alternatively, modifications can be made directly to the polypeptide, such as by
10 cleavage, addition of a linker molecule, addition of a detectable moiety, such as biotin, addition of a fatty acid, and the like. Modifications also embrace fusion proteins comprising all or part of the cancer associated antigen amino acid sequence. One of skill in the art will be familiar with methods for predicting the effect on protein conformation of a change in protein sequence, and can thus "design" a variant cancer associated antigen polypeptide according to known methods. One
15 example of such a method is described by Dahiyat and Mayo in *Science* 278:82-87, 1997, whereby proteins can be designed *de novo*. The method can be applied to a known protein to vary a only a portion of the polypeptide sequence. By applying the computational methods of Dahiyat and Mayo, specific variants of a cancer associated antigen polypeptide can be proposed and tested to determine whether the variant retains a desired conformation.

20 In general, variants include cancer associated antigen polypeptides which are modified specifically to alter a feature of the polypeptide unrelated to its desired physiological activity. For example, cysteine residues can be substituted or deleted to prevent unwanted disulfide linkages. Similarly, certain amino acids can be changed to enhance expression of a breast cancer associated antigen polypeptide by eliminating proteolysis by proteases in an expression system (e.g., dibasic
25 amino acid residues in yeast expression systems in which KEX2 protease activity is present).

Mutations of a nucleic acid which encode a cancer associated antigen polypeptide preferably preserve the amino acid reading frame of the coding sequence, and preferably do not create regions in the nucleic acid which are likely to hybridize to form secondary structures, such a hairpins or loops, which can be deleterious to expression of the variant polypeptide.

30 Mutations can be made by selecting an amino acid substitution, or by random mutagenesis of

- 30 -

a selected site in a nucleic acid which encodes the polypeptide. Variant polypeptides are then expressed and tested for one or more activities to determine which mutation provides a variant polypeptide with the desired properties. Further mutations can be made to variants (or to non-variant cancer associated antigen polypeptides) which are silent as to the amino acid sequence of the

5 polypeptide, but which provide preferred codons for translation in a particular host. The preferred codons for translation of a nucleic acid in, e.g., *E. coli*, are well known to those of ordinary skill in the art. Still other mutations can be made to the noncoding sequences of a cancer associated antigen gene or cDNA clone to enhance expression of the polypeptide. The activity of variants of cancer associated antigen polypeptides can be tested by cloning the gene encoding the variant cancer
10 associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the variant cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. For example, the variant cancer associated antigen polypeptide can be tested for reaction with autologous or allogeneic sera as disclosed in the Examples. Preparation of other variant
15 polypeptides may favor testing of other activities, as will be known to one of ordinary skill in the art.

The skilled artisan will also realize that conservative amino acid substitutions may be made in cancer associated antigen polypeptides to provide functionally equivalent variants of the foregoing polypeptides, i.e., the variants retain the functional capabilities of the cancer associated antigen polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino
20 acid substitution which does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor,
25 New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants of the cancer associated antigen polypeptides include conservative amino acid substitutions of in the amino acid sequences of SEQ ID proteins disclosed herein. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c)
30 K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

For example, upon determining that a peptide derived from a cancer associated antigen polypeptide is presented by an MHC molecule and recognized by CTLs (e.g., as described in the Examples), one can make conservative amino acid substitutions to the amino acid sequence of the peptide, particularly at residues which are thought not to be direct contact points with the MHC

5 molecule. For example, methods for identifying functional variants of HLA class II binding peptides are provided in a published PCT application of Strominger and Wucherpfennig (PCT/US96/03182). Peptides bearing one or more amino acid substitutions also can be tested for concordance with known HLA/MHC motifs prior to synthesis using, e.g. the computer program described by D'Amato and Drijfhout (D'Amato et al., *Human Immunol.* 43:13-18, 1995; Drijfhout
10 et al., *Human Immunol.* 43:1-12, 1995). The substituted peptides can then be tested for binding to the MHC molecule and recognition by CTLs when bound to MHC. These variants can be tested for improved stability and are useful, *inter alia*, in vaccine compositions.

Conservative amino-acid substitutions in the amino acid sequence of cancer associated antigen polypeptides to produce functionally equivalent variants of cancer associated antigen
15 polypeptides typically are made by alteration of a nucleic acid encoding a cancer associated antigen polypeptide. Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a cancer associated antigen
20 polypeptide. Where amino acid substitutions are made to a small unique fragment of a cancer associated antigen polypeptide, such as an antigenic epitope recognized by autologous or allogeneic sera or cytolytic T lymphocytes, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of cancer associated antigen polypeptides can be tested by cloning the gene encoding the altered cancer associated antigen polypeptide into a bacterial
25 or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the altered cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. Peptides which are chemically synthesized can be tested directly for function, e.g., for binding to antisera recognizing associated antigens.

The invention as described herein has a number of uses, some of which are described
30 elsewhere herein. First, the invention permits isolation of the cancer associated antigen protein

molecules. A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated cancer associated antigen molecules. The polypeptide may be purified from cells which naturally produce the polypeptide by chromatographic means or immunological recognition. Alternatively, an expression vector may be introduced into cells to cause production of the

5 polypeptide. In another method, mRNA transcripts may be microinjected or otherwise introduced into cells to cause production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating cancer associated antigen polypeptides. These include, but are not limited to, immunochromatography, HPLC, size-exclusion
10 chromatography, ion-exchange chromatography and immune-affinity chromatography.

The isolation and identification of cancer associated antigen genes also makes it possible for the artisan to diagnose a disorder characterized by expression of cancer associated antigens. These methods involve determining expression of one or more cancer associated antigen nucleic acids, and/or encoded cancer associated antigen polypeptides and/or peptides derived therefrom. In the
15 former situation, such determinations can be carried out via any standard nucleic acid determination assay, including the polymerase chain reaction, or assaying with labeled hybridization probes. In the latter situation, such determinations can be carried out by screening patient antisera for recognition of the polypeptide.

The invention also makes it possible isolate proteins which bind to cancer associated
20 antigens as disclosed herein, including antibodies and cellular binding partners of the cancer associated antigens. Additional uses are described further herein.

The invention also provides, in certain embodiments, "dominant negative" polypeptides derived from cancer associated antigen polypeptides. A dominant negative polypeptide is an inactive variant of a protein, which, by interacting with the cellular machinery, displaces an active
25 protein from its interaction with the cellular machinery or competes with the active protein, thereby reducing the effect of the active protein. For example, a dominant negative receptor which binds a ligand but does not transmit a signal in response to binding of the ligand can reduce the biological effect of expression of the ligand. Likewise, a dominant negative catalytically-inactive kinase which interacts normally with target proteins but does not phosphorylate the target proteins can reduce
30 phosphorylation of the target proteins in response to a cellular signal. Similarly, a dominant

negative transcription factor which binds to a promoter site in the control region of a gene but does not increase gene transcription can reduce the effect of a normal transcription factor by occupying promoter binding sites without increasing transcription.

The end result of the expression of a dominant negative polypeptide in a cell is a reduction in

5 function of active proteins. One of ordinary skill in the art can assess the potential for a dominant negative variant of a protein, and using standard mutagenesis techniques to create one or more dominant negative variant polypeptides. For example, given the teachings contained herein of cancer associated antigens, especially those which are similar to known proteins which have known activities, one of ordinary skill in the art can modify the sequence of the cancer associated antigens
10 by site-specific mutagenesis, scanning mutagenesis, partial gene deletion or truncation, and the like. See, e.g., U.S. Patent No. 5,580,723 and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. The skilled artisan then can test the population of mutagenized polypeptides for diminution in a selected and/or for retention of such an activity. Other similar methods for creating and testing dominant negative variants of a
15 protein will be apparent to one of ordinary skill in the art.

The invention also involves agents such as polypeptides which bind to cancer associated antigen polypeptides. Such binding agents can be used, for example, in screening assays to detect the presence or absence of cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners and in purification protocols to isolated
20 cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners. Such agents also can be used to inhibit the native activity of the cancer associated antigen polypeptides, for example, by binding to such polypeptides.

The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to cancer associated
25 antigen polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to conventional methodology.

Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W.R. (1986) The Experimental Foundations of Modern Immunology Wiley & Sons, Inc., New York;
30 Roitt, I. (1991) Essential Immunology, 7th Ed., Blackwell Scientific Publications, Oxford). The

pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically cleaved, or which has been produced without the pFc' region, designated an F(ab')₂ fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has

5 been enzymatically cleaved, or which has been produced without the Fc region, designated an Fab fragment, retains one of the antigen binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without
10 altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

Within the antigen-binding portion of an antibody, as is well-known in the art, there are complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG
15 immunoglobulins, there are four framework regions (FR1 through FR4) separated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs, and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

It is now well-established in the art that the non-CDR regions of a mammalian antibody may
20 be replaced with similar regions of conspecific or heterospecific antibodies while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. Thus, for example, PCT International Publication Number WO 92/04381 teaches the production and use of humanized murine RSV
25 antibodies in which at least a portion of the murine FR regions have been replaced by FR regions of human origin. Such antibodies, including fragments of intact antibodies with antigen-binding ability, are often referred to as "chimeric" antibodies.

Thus, as will be apparent to one of ordinary skill in the art, the present invention also provides for F(ab')₂, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR
30 and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous

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human or non-human sequences; chimeric F(ab')₂ fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human

5 sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present invention also includes so-called single chain antibodies.

Thus, the invention involves polypeptides of numerous size and type that bind specifically to cancer associated antigen polypeptides, and complexes of both cancer associated antigen
10 polypeptides and their binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic
15 moieties.

Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select
20 phage-bearing inserts which bind to the cancer associated antigen polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the cancer associated antigen polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the cancer associated antigen polypeptide can be
25 determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the cancer associated antigen polypeptides. Thus, the cancer associated antigen polypeptides of the invention, or a fragment thereof, can be used to screen peptide libraries,
30 including phage display libraries, to identify and select peptide binding partners of the cancer

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associated antigen polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of cancer associated antigen and for other purposes that will be apparent to those of ordinary skill in the art.

As detailed herein, the foregoing antibodies and other binding molecules may be used for

5 example to identify tissues expressing protein or to purify protein. Antibodies also may be coupled to specific diagnostic labeling agents for imaging of cells and tissues that express cancer associated antigens or to therapeutically useful agents according to standard coupling procedures. Diagnostic agents include, but are not limited to, barium sulfate, iocetamic acid, iopanoic acid, ipodate calcium, diatrizoate sodium, diatrizoate meglumine, metrizamide, tyropanoate sodium and radiodiagnostics
10 including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technetium-99m, iodine-131 and indium-111, nuclides for nuclear magnetic resonance such as fluorine and gadolinium. Other diagnostic agents useful in the invention will be apparent to one of ordinary skill in the art. As used herein, "therapeutically useful agents" include any therapeutic molecule which desirably is targeted selectively to a cell expressing one of the cancer antigens
15 disclosed herein, including antineoplastic agents, radioiodinated compounds, toxins, other cytostatic or cytolytic drugs, and so forth. Antineoplastic therapeutics are well known and include: aminogluthethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabidine, dacarbazine, dactinomycin, daunorubicin, doxorubicin, taxol, etoposide, fluorouracil, interferon- α , lomustine, mercaptopurine, methotrexate,
20 mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Additional antineoplastic agents include those disclosed in Chapter 52, Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner), and the introduction thereto, 1202-1263, of Goodman and Gilman's "The Pharmacological Basis of Therapeutics", Eighth Edition, 1990, McGraw-Hill, Inc. (Health Professions Division). Toxins can be proteins such as, for example, pokeweed anti-viral protein,
25 cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin, or *Pseudomonas* exotoxin. Toxin moieties can also be high energy-emitting radionuclides such as cobalt-60.

In the foregoing methods, antibodies prepared according to the invention also preferably are specific for the cancer associated antigen/MHC complexes described herein.

When "disorder" is used herein, it refers to any pathological condition where the cancer
30 associated antigens are expressed. An example of such a disorder is cancer, breast, colon, gastric,

renal, prostate and lung cancers as particular examples.

Samples of tissue and/or cells for use in the various methods described herein can be obtained through standard methods such as tissue biopsy, including punch biopsy and cell scraping, and collection of blood or other bodily fluids by aspiration or other methods.

5 In certain embodiments of the invention, an immunoreactive cell sample is removed from a subject. By "immunoreactive cell" is meant a cell which can mature into an immune cell (such as a B cell, a helper T cell, or a cytolytic T cell) upon appropriate stimulation. Thus immunoreactive cells include CD34⁺ hematopoietic stem cells, immature T cells and immature B cells. When it is desired to produce cytolytic T cells which recognize a cancer associated antigen, the
10 immunoreactive cell is contacted with a cell which expresses a cancer associated antigen under conditions favoring production, differentiation and/or selection of cytolytic T cells; the differentiation of the T cell precursor into a cytolytic T cell upon exposure to antigen is similar to clonal selection of the immune system.

Some therapeutic approaches based upon the disclosure are premised on a response by a
15 subject's immune system, leading to lysis of antigen presenting cells, such as breast cancer cells which present one or more cancer associated antigens. One such approach is the administration of autologous CTLs specific to a cancer associated antigen/MHC complex to a subject with abnormal cells of the phenotype at issue. It is within the ability of one of ordinary skill in the art to develop such CTLs *in vitro*. An example of a method for T cell differentiation is presented in International
20 Application number PCT/US96/05607. Generally, a sample of cells taken from a subject, such as blood cells, are contacted with a cell presenting the complex and capable of provoking CTLs to proliferate. The target cell can be a transfectant, such as a COS cell of the type described herein. These transfectants present the desired complex of their surface and, when combined with a CTL of interest, stimulate its proliferation. COS cells, such as those used herein are widely available, as are
25 other suitable host cells. Specific production of a CTL clone is described herein, and is well known in the art. The clonally expanded autologous CTLs then are administered to the subject.

Another method for selecting antigen-specific CTL clones has recently been described (Altman et al., *Science* 274:94-96, 1996; Dunbar et al., *Curr. Biol.* 8:413-416, 1998), in which fluorogenic tetramers of MHC class I molecule/peptide complexes are used to detect specific CTL
30 clones. Briefly, soluble MHC class I molecules are folded *in vitro* in the presence of β_2 -

microglobulin and a peptide antigen which binds the class I molecule. After purification, the MHC/peptide complex is purified and labeled with biotin. Tetramers are formed by mixing the biotinylated peptide-MHC complex with labeled avidin (e.g. phycoerythrin) at a molar ratio of 4:1. Tetramers are then contacted with a source of CTLs such as peripheral blood or lymph node. The

5 tetramers bind CTLs which recognize the peptide antigen/MHC class I complex. Cells bound by the tetramers can be sorted by fluorescence activated cell sorting to isolate the reactive CTLs. The isolated CTLs then can be expanded *in vitro* for use as described herein.

To detail a therapeutic methodology, referred to as adoptive transfer (Greenberg, *J. Immunol.* 136(5): 1917, 1986; Riddel et al., *Science* 257: 238, 1992; Lynch et al, *Eur. J. Immunol.* 21: 1403-
10 1410, 1991; Kast et al., *Cell* 59: 603-614, 1989), cells presenting the desired complex are combined with CTLs leading to proliferation of the CTLs specific thereto. The proliferated CTLs are then administered to a subject with a cellular abnormality which is characterized by certain of the abnormal cells presenting the particular complex. The CTLs then lyse the abnormal cells, thereby achieving the desired therapeutic goal.

15 The foregoing therapy assumes that at least some of the subject's abnormal cells present the relevant HLA cancer associated antigen complex. This can be determined very easily, as the art is very familiar with methods for identifying cells which present a particular HLA molecule, as well as how to identify cells expressing DNA of the pertinent sequences, in this case a cancer associated antigen sequence. Once cells presenting the relevant complex are identified via the foregoing
20 screening methodology, they can be combined with a sample from a patient, where the sample contains CTLs. If the complex presenting cells are lysed by the mixed CTL sample, then it can be assumed that a cancer associated antigen is being presented, and the subject is an appropriate candidate for the therapeutic approaches set forth *supra*.

Adoptive transfer is not the only form of therapy that is available in accordance with the
25 invention. CTLs can also be provoked *in vivo*, using a number of approaches. One approach is the use of non-proliferative cells expressing the complex. The cells used in this approach may be those that normally express the complex, such as irradiated tumor cells or cells transfected with one or both of the genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting HLA molecule). Chen et al. (*Proc. Natl. Acad. Sci. USA* 88: 110-114, 1991) exemplifies
30 this approach, showing the use of transfected cells expressing HPVE7 peptides in a therapeutic

regime. Various cell types may be used. Similarly, vectors carrying one or both of the genes of interest may be used. Viral or bacterial vectors are especially preferred. For example, nucleic acids which encode a breast cancer associated antigen polypeptide or peptide may be operably linked to promoter and enhancer sequences which direct expression of the cancer associated antigen

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- 5 polypeptide or peptide in certain tissues or cell types. The nucleic acid may be incorporated into an expression vector. Expression vectors may be unmodified extrachromosomal nucleic acids, plasmids or viral genomes constructed or modified to enable insertion of exogenous nucleic acids, such as those encoding cancer associated antigen, as described elsewhere herein. Nucleic acids encoding a cancer associated antigen also may be inserted into a retroviral genome, thereby
- 10 facilitating integration of the nucleic acid into the genome of the target tissue or cell type. In these systems, the gene of interest is carried by a microorganism, e.g., a Vaccinia virus, retrovirus or adenovirus, and the materials de facto "infect" host cells. The cells which result present the complex of interest, and are recognized by autologous CTLs, which then proliferate.

- A similar effect can be achieved by combining the cancer associated antigen or a stimulatory
- 15 fragment thereof with an adjuvant to facilitate incorporation into antigen presenting cells *in vivo*. The breast cancer associated antigen polypeptide is processed to yield the peptide partner of the HLA molecule while a cancer associated antigen peptide may be presented without the need for further processing. Generally, subjects can receive an intradermal injection of an effective amount of the cancer associated antigen. Initial doses can be followed by booster doses, following
- 20 immunization protocols standard in the art. Preferred cancer associated antigens include those found to react with allogeneic cancer antisera, such as the nucleic acids (and encoded polypeptides and peptides) of SEQ ID NO:31,33 and 34 and others, for example, shown in the examples below.

- The invention involves the use of various materials disclosed herein to "immunize" subjects or as "vaccines". As used herein, "immunization" or "vaccination" means increasing or activating
- 25 an immune response against an antigen. It does not require elimination or eradication of a condition but rather contemplates the clinically favorable enhancement of an immune response toward an antigen. Generally accepted animal models can be used for testing of immunization against breast cancer using a cancer associated antigen nucleic acid. For example, cancer cells can be introduced into a mouse to create a tumor, and one or more cancer associated antigen nucleic acids can be
- 30 delivered by the methods described herein. The effect on the cancer cells (e.g., reduction of tumor

size) can be assessed as a measure of the effectiveness of the cancer associated antigen nucleic acid immunization. Of course, testing of the foregoing animal model using more conventional methods for immunization include the administration of one or more cancer associated antigen polypeptides or peptides derived therefrom, optionally combined with one or more adjuvants and/or cytokines to

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- 5 boost the immune response. Methods for immunization, including formulation of a vaccine composition and selection of doses, route of administration and the schedule of administration (e.g. primary and one or more booster doses), are well known in the art. The tests also can be performed in humans, where the end point is to test for the presence of enhanced levels of circulating CTLs against cells bearing the antigen, to test for levels of circulating antibodies against the antigen, to test
- 10 for the presence of cells expressing the antigen and so forth.

As part of the immunization compositions, one or more cancer associated antigens or stimulatory fragments thereof are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the

15 immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure

20 QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered mixed with a combination of DQS21/MPL. The ratio of

25 DQS21 to MPL typically will be about 1:10 to 10:1, preferably about 1:5 to 5:1 and more preferably about 1:1. Typically for human administration, DQS21 and MPL will be present in a vaccine formulation in the range of about 1 µg to about 100 µg. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well

30 known to those of skill in the art of vaccination.

Other agents which stimulate the immune response of the subject can also be administered to the subject. For example, other cytokines are also useful in vaccination protocols as a result of their lymphocyte regulatory properties. Many other cytokines useful for such purposes will be known to one of ordinary skill in the art, including interleukin-12 (IL-12) which has been shown to enhance

5 the protective effects of vaccines (*see, e.g., Science* 268: 1432-1434, 1995), GM-CSF and IL-18.

Thus cytokines can be administered in conjunction with antigens and adjuvants to increase the immune response to the antigens.

There are a number of immune response potentiating compounds that can be used in vaccination protocols. These include costimulatory molecules provided in either protein or nucleic acid form. Such costimulatory molecules include the B7-1 and B7-2 (CD80 and CD86 respectively) 10 molecules which are expressed on dendritic cells (DC) and interact with the CD28 molecule expressed on the T cell. This interaction provides costimulation (signal 2) to an antigen/MHC/TCR stimulated (signal 1) T cell, increasing T cell proliferation and effector function. B7 also interacts with CTLA4 (CD152) on T cells and studies involving CTLA4 and B7 ligands indicate that the B7- 15 CTLA4 interaction can enhance antitumor immunity and CTL proliferation, Zheng P., et al. *PNAS* 95 (11) 6284-6289 (1998).

B7 typically is not expressed on tumor cells so they are not efficient antigen presenting cells (APCs) for T cells. Induction of B7 expression would enable the tumor cells to stimulate more efficiently CTL proliferation and effector function. A combination of B7/IL-6/IL-12 costimulation 20 has been shown to induce IFN-gamma and a Th1 cytokine profile in the T cell population leading to further enhanced T cell activity, Gajewski et al., *J. Immunol*, 154:5637-5648 (1995). Tumor cell transfection with B7 has been discussed in relation to *in vitro* CTL expansion for adoptive transfer immunotherapy by Wang et al., *J Immunol*, 19:1-8 (1986). Other delivery mechanisms for the B7 molecule would include nucleic acid (naked DNA) immunization Kim J., et al. *Nat Biotechnol.*, 25 15:7:641-646 (1997) and recombinant viruses such as adeno and pox (Wendtner et al., *Gene Ther*, 4:7:726-735 (1997)). These systems are all amenable to the construction and use of expression cassettes for the coexpression of B7 with other molecules of choice such as the antigens or fragment(s) of antigens discussed herein (including polytopes) or cytokines. These delivery systems can be used for induction of the appropriate molecules *in vitro* and for *in vivo* vaccination situations.

30 The use of anti-CD28 antibodies to directly stimulate T cells *in vitro* and *in vivo* could also be

considered.

Lymphocyte function associated antigen-3 (LFA-3) is expressed on APCs and some tumor cells and interacts with CD2 expressed on T cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory

5 interaction, Parra et al., *J. Immunol.*, 158:637-642 (1997), Fenton et al., *J. Immunother*, 21:2:95-108 (1989).

Lymphocyte function associated antigen-1 (LFA-1) is expressed on leukocytes and interacts with ICAM-1 expressed on APCs and some tumor cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory
10 interaction, Fenton et al., *J. Immunothera*, 21:2:95-108 (1998). LFA-1 is thus a further example of a costimulatory molecule that could be provided in a vaccination protocol in the various ways discussed above for B7.

Complete CTL activation and effector function requires Th cell help through the interaction between the Th cell CD40L (CD40 ligand) molecule and the CD40 molecule expressed by DCS,
15 Ridge et al., *Nature*, 393:474 (1998), Bennett et al., *Nature*, 393:478 (1998), Schoenberger et al., *Nature*, 393:480 (1998). This mechanism of this costimulatory signal is likely to involve upregulation of B7 and associated IL-6/IL-12 production by the DC (APC). The CD40-CD40L interaction thus complements the signal 1 (antigen/MHC-TCR) and signal 2 (B7-CD28) interactions.

The use of anti-CD40 antibodies to stimulate DC cells directly, would be expected to
20 enhance a response to tumor antigens which are normally encountered outside of an inflammatory context or are presented by non-professional APCs (tumor cells). In these situations Th help and B7 costimulation signals are not provided. This mechanism might be used in the context of antigen pulsed DC based therapies or in situations where Th epitopes have not been defined within known TRA precursors.

25 A cancer associated antigen polypeptide, or a fragment thereof, also can be used to isolate their native binding partners. Isolation of such binding partners may be performed according to well-known methods. For example, isolated cancer associated antigen polypeptides can be attached to a substrate (e.g., chromatographic media, such as polystyrene beads, or a filter), and then a solution suspected of containing the binding partner may be applied to the substrate. If a binding
30 partner which can interact with cancer associated antigen polypeptides is present in the solution,

then it will bind to the substrate-bound cancer associated antigen polypeptide. The binding partner then may be isolated.

It will also be recognized that the invention embraces the use of the cancer associated antigen cDNA sequences in expression vectors, as well as to transfect host cells and cell lines, be these

5 prokaryotic (e.g., *E. coli*), or eukaryotic (e.g., dendritic cells, B cells, CHO cells, COS cells, yeast expression systems and recombinant baculovirus expression in insect cells). Especially useful are mammalian cells such as human, mouse, hamster, pig, goat, primate, etc. They may be of a wide variety of tissue types, and include primary cells and cell lines. Specific examples include keratinocytes, peripheral blood leukocytes, bone marrow stem cells and embryonic stem cells. The
10 expression vectors require that the pertinent sequence, i.e., those nucleic acids described *supra*, be operably linked to a promoter.

The invention also contemplates delivery of nucleic acids, polypeptides or peptides for vaccination. Delivery of polypeptides and peptides can be accomplished according to standard vaccination protocols which are well known in the art. In another embodiment, the delivery of
15 nucleic acid is accomplished by *ex vivo* methods, i.e. by removing a cell from a subject, genetically engineering the cell to include a breast cancer associated antigen, and reintroducing the engineered cell into the subject. One example of such a procedure is outlined in U.S. Patent 5,399,346 and in exhibits submitted in the file history of that patent, all of which are publicly available documents. In general, it involves introduction *in vitro* of a functional copy of a gene into a cell(s) of a subject, and
20 returning the genetically engineered cell(s) to the subject. The functional copy of the gene is under operable control of regulatory elements which permit expression of the gene in the genetically engineered cell(s). Numerous transfection and transduction techniques as well as appropriate expression vectors are well known to those of ordinary skill in the art, some of which are described in PCT application WO95/00654. *In vivo* nucleic acid delivery using vectors such as viruses and
25 targeted liposomes also is contemplated according to the invention.

In preferred embodiments, a virus vector for delivering a nucleic acid encoding a cancer associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, poxviruses including vaccinia viruses and attenuated poxviruses, Semliki Forest virus, Venezuelan equine encephalitis virus, retroviruses, Sindbis virus, and Ty virus-like particle. Examples of
30 viruses and virus-like particles which have been used to deliver exogenous nucleic acids include:

replication-defective adenoviruses (e.g., Xiang et al., *Virology* 219:220-227, 1996; Eloit et al., *J. Virol* 7:5375-5381, 1997; Chengalvala et al., *Vaccine* 15:335-339, 1997), a modified retrovirus (Townsend et al., *J. Virol.* 71:3365-3374, 1997), a nonreplicating retrovirus (Irwin et al., *J. Virol.* 68:5036-5044, 1994), a replication defective Semliki Forest virus (Zhao et al., *Proc. Natl. Acad. Sci.*

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- 5 USA 92:3009-3013, 1995), canarypox virus and highly attenuated vaccinia virus derivative (Paoletti, *Proc. Natl. Acad. Sci. USA* 93:11349-11353, 1996), non-replicative vaccinia virus (Moss, *Proc. Natl. Acad. Sci. USA* 93:11341-11348, 1996), replicative vaccinia virus (Moss, *Dev. Biol. Stand.* 82:55-63, 1994), Venezuelan equine encephalitis virus (Davis et al., *J. Virol.* 70:3781-3787, 1996), Sindbis virus (Pugachev et al., *Virology* 212:587-594, 1995), and Ty virus-like particle (Allsopp et al., *Eur J. Immunol* 26:1951-1959, 1996). In preferred embodiments, the virus vector is an
10 adenovirus.

Another preferred virus for certain applications is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus is capable of infecting a wide range of cell types and species and can be engineered to be replication-deficient. It further has advantages, such as heat
15 and lipid solvent stability, high transduction frequencies in cells of diverse lineages, including hematopoietic cells, and lack of superinfection inhibition thus allowing multiple series of transductions. The adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression. In addition, wild-type adeno-associated virus infections have been followed in
20 tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

In general, other preferred viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic viruses
25 include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Adenoviruses and retroviruses have been approved for human gene therapy trials. In general, the retroviruses are replication-deficient (i.e., capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have
30 general utility for the high-efficiency transduction of genes *in vivo*. Standard protocols for

producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., "Gene

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- 5 Transfer and Expression, A Laboratory Manual," W.H. Freeman C.O., New York (1990) and Murry, E.J. Ed. "Methods in Molecular Biology," vol. 7, Humana Press, Inc., Clifton, New Jersey (1991).

Preferably the foregoing nucleic acid delivery vectors: (1) contain exogenous genetic material that can be transcribed and translated in a mammalian cell and that can induce an immune response in a host, and (2) contain on a surface a ligand that selectively binds to a receptor on the

10 surface of a target cell, such as a mammalian cell, and thereby gains entry to the target cell.

Various techniques may be employed for introducing nucleic acids of the invention into cells, depending on whether the nucleic acids are introduced *in vitro* or *in vivo* in a host. Such techniques include transfection of nucleic acid-CaPO₄ precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the foregoing viruses including the nucleic

15 acid of interest, liposome mediated transfection, and the like. For certain uses, it is preferred to target the nucleic acid to particular cells. In such instances, a vehicle used for delivering a nucleic acid of the invention into a cell (e.g., a retrovirus, or other virus; a liposome) can have a targeting molecule attached thereto. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell can be bound to or

20 incorporated within the nucleic acid delivery vehicle. Preferred antibodies include antibodies which selectively bind a cancer associated antigen, alone or as a complex with a MHC molecule.

Especially preferred are monoclonal antibodies. Where liposomes are employed to deliver the nucleic acids of the invention, proteins which bind to a surface membrane protein associated with endocytosis may be incorporated into the liposome formulation for targeting and/or to facilitate

25 uptake. Such proteins include capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half life, and the like. Polymeric delivery systems also have been used successfully to deliver nucleic acids into cells, as is known by those skilled in the art. Such systems even permit oral delivery of nucleic acids.

30 When administered, the therapeutic compositions of the present invention can be

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administered in pharmaceutically acceptable preparations. Such preparations may routinely contain pharmaceutically acceptable concentrations of salt, buffering agents, preservatives, compatible carriers, supplementary immune potentiating agents such as adjuvants and cytokines and optionally other therapeutic agents.

5 The therapeutics of the invention can be administered by any conventional route, including injection or by gradual infusion over time. The administration may, for example, be oral, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal. When antibodies are used therapeutically, a preferred route of administration is by pulmonary aerosol. Techniques for preparing aerosol delivery systems containing antibodies are well known to those of
10 skill in the art. Generally, such systems should utilize components which will not significantly impair the biological properties of the antibodies, such as the paratope binding capacity (see, for example, Sciarra and Cutie, "Aerosols," in Remington's Pharmaceutical Sciences, 18th edition, 1990, pp 1694-1712; incorporated by reference). Those of skill in the art can readily determine the various parameters and conditions for producing antibody aerosols without resort to undue
15 experimentation. When using antisense preparations of the invention, slow intravenous administration is preferred.

 The compositions of the invention are administered in effective amounts. An "effective amount" is that amount of a cancer associated antigen composition that alone, or together with further doses, produces the desired response, e.g. increases an immune response to the cancer
20 associated antigen. In the case of treating a particular disease or condition characterized by expression of one or more cancer associated antigens, such as cancer, the desired response is inhibiting the progression of the disease. This may involve only slowing the progression of the disease temporarily, although more preferably, it involves halting the progression of the disease permanently. This can be monitored by routine methods or can be monitored according to
25 diagnostic methods of the invention discussed herein. The desired response to treatment of the disease or condition also can be delaying the onset or even preventing the onset of the disease or condition.

 Such amounts will depend, of course, on the particular condition being treated, the severity of the condition, the individual patient parameters including age, physical condition, size and
30 weight, the duration of the treatment, the nature of concurrent therapy (if any), the specific route of

administration and like factors within the knowledge and expertise of the health practitioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used, that is, the highest safe dose according to sound

5 medical judgment. It will be understood by those of ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

The pharmaceutical compositions used in the foregoing methods preferably are sterile and contain an effective amount of breast cancer associated antigen or nucleic acid encoding cancer
10 associated antigen for producing the desired response in a unit of weight or volume suitable for administration to a patient. The response can, for example, be measured by determining the immune response following administration of the cancer associated antigen composition via a reporter system as described herein, by measuring downstream effects such as gene expression, or by measuring the physiological effects of the breast cancer associated antigen composition, such as
15 regression of a tumor or decrease of disease symptoms. Other assays will be known to one of ordinary skill in the art and can be employed for measuring the level of the response.

The doses of cancer associated antigen compositions (e.g., polypeptide, peptide, antibody, cell or nucleic acid) administered to a subject can be chosen in accordance with different parameters, in particular in accordance with the mode of administration used and the state of the subject. Other
20 factors include the desired period of treatment. In the event that a response in a subject is insufficient at the initial doses applied, higher doses (or effectively higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits.

In general, for treatments for eliciting or increasing an immune response, doses of cancer associated antigen are formulated and administered in doses between 1 ng and 1 mg, and preferably
25 between 10 ng and 100 μ g, according to any standard procedure in the art. Where nucleic acids encoding cancer associated antigen or variants thereof are employed, doses of between 1 ng and 0.1 mg generally will be formulated and administered according to standard procedures. Other protocols for the administration of cancer associated antigen compositions will be known to one of ordinary skill in the art, in which the dose amount, schedule of injections, sites of injections, mode of
30 administration (e.g., intra-tumoral) and the like vary from the foregoing. Administration of cancer

associated antigen compositions to mammals other than humans, e.g. for testing purposes or veterinary therapeutic purposes, is carried out under substantially the same conditions as described above.

As part of the immunization compositions, the peptide antigens are administered with one or

5 more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants
10 include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete
15 Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

20 Where cancer associated antigen peptides are used for vaccination, modes of administration which effectively deliver the cancer associated antigen and adjuvant, such that an immune response to the antigen is increased, can be used. For administration of a cancer associated antigen peptide in adjuvant, preferred methods include intradermal, intravenous, intramuscular and subcutaneous administration. Although these are preferred embodiments, the invention is not limited by the
25 particular modes of administration disclosed herein. Standard references in the art (e.g., *Remington's Pharmaceutical Sciences*, 18th edition, 1990) provide modes of administration and formulations for delivery of immunogens with adjuvant or in a non-adjuvant carrier.

When administered, the pharmaceutical preparations of the invention are applied in pharmaceutically-acceptable amounts and in pharmaceutically-acceptable compositions. The term
30 "pharmaceutically acceptable" means a non-toxic material that does not interfere with the

effectiveness of the biological activity of the active ingredients. Such preparations may routinely contain salts, buffering agents, preservatives, compatible carriers, and optionally other therapeutic agents. When used in medicine, the salts should be pharmaceutically acceptable, but non-pharmaceutically acceptable salts may conveniently be used to prepare pharmaceutically-

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- 5 acceptable salts thereof and are not excluded from the scope of the invention. Such pharmacologically and pharmaceutically-acceptable salts include, but are not limited to, those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic, and the like. Also, pharmaceutically-acceptable salts can be prepared as alkaline metal or alkaline earth salts, such as sodium,
10 potassium or calcium salts.

- A breast cancer associated antigen composition may be combined, if desired, with a pharmaceutically-acceptable carrier. The term "pharmaceutically-acceptable carrier" as used herein means one or more compatible solid or liquid fillers, diluents or encapsulating substances which are suitable for administration into a human. The term "carrier" denotes an organic or
15 inorganic ingredient, natural or synthetic, with which the active ingredient is combined to facilitate the application. The components of the pharmaceutical compositions also are capable of being co-mingled with the molecules of the present invention, and with each other, in a manner such that there is no interaction which would substantially impair the desired pharmaceutical efficacy.

- 20 The pharmaceutical compositions may contain suitable buffering agents, including: acetic acid in a salt; citric acid in a salt; boric acid in a salt; and phosphoric acid in a salt.

The pharmaceutical compositions also may contain, optionally, suitable preservatives, such as: benzalkonium chloride; chlorobutanol; parabens and thimerosal.

- The pharmaceutical compositions may conveniently be presented in unit dosage form and
25 may be prepared by any of the methods well-known in the art of pharmacy. All methods include the step of bringing the active agent into association with a carrier which constitutes one or more accessory ingredients. In general, the compositions are prepared by uniformly and intimately bringing the active compound into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product.

- 30 Compositions suitable for oral administration may be presented as discrete units, such as

capsules, tablets, lozenges, each containing a predetermined amount of the active compound. Other compositions include suspensions in aqueous liquids or non-aqueous liquids such as a syrup, elixir or an emulsion.

Compositions suitable for parenteral administration conveniently comprise a sterile

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- 5 aqueous or non-aqueous preparation of breast cancer associated antigen polypeptides or nucleic acids, which is preferably isotonic with the blood of the recipient. This preparation may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation also may be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in
- 10 1,3-butane diol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono-or di-glycerides. In addition, fatty acids such as oleic acid may be used in the preparation of injectables. Carrier formulation suitable for oral,
- 15 subcutaneous, intravenous, intramuscular, etc. administrations can be found in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA.

Examples

Example 1: Preparation of breast cancer cDNA expression libraries

- 20 Step 1: Purification of total RNA from tumors.

Total RNA was isolated from tumor samples using the guanidium thiocyanate-phenol-chloroform extraction protocol described by Chomczynski and Sacci (*Anal. Biochem.* 162:156-159, 1987).

Step 2: Purification of mRNA.

- 25 A Dynabeads mRNA isolation kit (Dynal, Cat.No. 610.01) was used to isolate mRNA from the pool of total RNA isolated in step 1 above according to the manufacturer's instructions.

Step 3: cDNA synthesis.

- cDNA synthesis was performed using a ZAP-cDNA synthesis Kit (Stratagene, La Jolla CA; Cat. No. 200400) according to the manufacturer's protocol. A specific linker-primer which contains
- 30 a XbaI cloning site was designed and used in this protocol, to facilitate subcloning into TriplEx

vector. The sequence of the primer was:

GAGAGAGAGAGAGAGAGAGAAGTCGACTCTAGATTTTTTTTTTTTTTTTTT-Xba I site

Step 4: Ligation into the TriplEx vector arms.

- 5 The cDNAs generated in step 3 above were ligated into TriplEx vector arms (Clontech, Palo Alto, CA; Cat. No. 6162-1); the arms were predigested with EcoR I/Xba I.

Step 5: Packaging into phages with Gigapack III kit.

The ligation mix (TriplEx/cDNA) from step 4 was packed into phages using the Gigapack III Gold Cloning Kit (Stratagene, Cat. N.200450) according to the protocol supplied with the kit.

- 10 Step 6: Titering and amplification of generated libraries was performed according to the Stratagene protocols.

The foregoing protocol was used to prepare several libraries from tumor sample of different patients. Some libraries were prepared using the UNI-ZAP XR vector system (Stratagene)

- 15 according to the manufacturer's protocol, and some using the TriplEx system as described above.

Table 2

UNI-ZAP Libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
20 HBR173	1.8×10^6 pfu	Ductal Carcinoma, Grade III
HBR184	3.5×10^6 pfu	Invasive Ductal Carcinoma, Grade II
TriplEx libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
HBR173	2.3×10^6 pfu	Ductal Carcinoma, Grade III
25 HBR184	1.1×10^6 pfu	Invasive Ductal Carcinoma, Grade II
HBR257	2.5×10^6 pfu	Invasive Ductal Carcinoma, Grade II
HBR297	4.0×10^6 pfu	Ductal Carcinoma, Grade II
HBR248	1.0×10^6 pfu	Invasive Ductal Carcinoma with Vascular Permeation, Grade III

HBR271	2.5 x 10 ⁶ pfu	Medullary Carcinoma
HBR263	10.0 x 10 ⁶ pfu	Inv. Pleiomorphic Lobular Carcinoma, Grade II

All libraries were screened with the exception of HBR173 (no autologous serum). No
5 serum-positive clones were found by screening HBR271 library.

Example 2: Immunoscreening

Sera was obtained from donors undergoing routine diagnostic and therapeutic procedures. It was stored at - 70°C prior to absorption. Sera, at a dilution of 1:10 in Tris buffered saline (TBS, pH
10 7.5), was sequentially passed through Sepharose 4B columns which had been coupled to lysates from *E. coli* Y1090 and bacteriophage infected *E. coli* BNN97 (5 Prime 3 Prime, Inc. Boulder, Co.). Final serum dilutions were prepared in 0.2% non-fat dried milk/TBS (NFDm) and stored at 4°C. Library screening was performed as described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995) with following modifications. Recombinant phage at a concentration of 4 x
15 10³ per 15 cm plate were amplified for 6 hours and transferred to nitrocellulose membranes for an additional 15 hours at 37°C. Membranes were then blocked with 5% NFDm. As an alternative to generation of IgG subtracted libraries, membranes were pre-screened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific, goat anti-human IgG (Jackson Immunoresearch Laboratories Inc., West Grove, PA) for 1 hour at room temperature. Color was developed with 3,3'
20 diaminobenzidine tetrahydrochloride and IgG encoding clones were scored. Membranes were then incubated in a 1:100 dilution of absorbed autologous sera for 15 hours at room temperature. Following serum exposure, filters were incubated in a 1:3000 dilution of alkaline phosphatase conjugated, Fc fragment specific, goat anti-human IgG (Jackson Immunoresearch Laboratories Inc.) for 1 hour at room temperature and processed for 4-nitro blue tetrazolium
25 chloride/5-bromo-4-chloro- 3-indolyl-phosphate color development. Serum positive clones were subcloned and retested for serum reactivity as above except nitrocellulose transfer was decreased to 3 hours. For the determination of allogeneic serum reactivity, plates containing an equal number of serum positive clones and negative control plaques were similarly processed less the IgG prescreening steps. A minimum of 5 x 10⁵ recombinants were screened per cDNA library, a number

which approximates a point at which the likelihood of repeat isolations of previously identified clones outweigh the prospect of identifying new clones.

Example 3: DNA Sequencing

- 5 Phage cDNA clones were converted to pBKC_{CMV} phagemid forms by in vivo excision. Plasmid DNA was purified on Qiaprep spin columns (Qiagen Inc. Chatsworth, CA) and subjected to EcoRI/XbaI restriction enzyme digestion. Clones representing different cDNA inserts were sequenced at Cornell University DNA services (Ithaca, NY) using an ABI Prism (Perkin Elmer) automated DNA sequencer. The sequences of the clones were compared with sequences in
- 10 GenBank and HGI databases to detect homologous nucleic acid and/or protein sequences. The following table lists exemplary related sequences.

Table 3: Sequences Related to Breast Cancer Associated Antigen Clones

Clone	Nucleotide Homology	Clone	Nucleotide Homology	Clone	Nucleotide Homology
15 LONY-Br-1	L34543	LONY-Br-23	AA262134, U74628	LONY-Br-44	D15057
LONY-Br-2	S75417	LONY-Br-24	AA282633	LONY-Br-45	AB000815
LONY-Br-3	J05211	LONY-Br-25	M62324	LONY-Br-46	L04733
LONY-Br-4	X15187	LONY-Br-26	M99389	LONY-Br-47	X88791
LONY-Br-5	X62083	LONY-Br-27	X79389	LONY-Br-48	AF000430
20 LONY-Br-6	J04965	LONY-Br-28	D44466	LONY-Br-49	none
LONY-Br-7	D63784	LONY-Br-29	M33197	LONY-Br-50	AA226732
LONY-Br-8	U11292	LONY-Br-30	M17886	LONY-Br-51	AA046574
LONY-Br-9	HSB06D102	LONY-Br-31	L38941	LONY-Br-52	none
LONY-Br-10	none	LONY-Br-32	X17644	LONY-Br-53	AB002307
25 LONY-Br-11	none	LONY-Br-33	X75342	92	AA127328
LONY-Br-12	AA430998	LONY-Br-33	X75342	101	AA167314
LONY-Br-13	D83032	LONY-Br-34	U43368	102	AA508139
LONY-Br-14	AA034417	LONY-Br-35	X15882	107	none
LONY-Br-15	AA167070	LONY-Br-37	AA121558	109	AA220229

LONY-Br-16	none	LONY-Br-38	AA211771	110	W67775
LONY-Br-17	AA161103	LONY-Br-39	AA367417	111	AA280070
LONY-Br-19	R13835	LONY-Br-40	AA188052	112	AF004292
LONY-Br-20	HUMORF003	LONY-Br-41	THC83518	131	none
5 LONY-Br-21	S74572	LONY-Br-42	none	143	AA481578
LONY-Br-22	AA070233	LONY-Br-43	HU35246	162	AA481578

Example 4: Reverse transcriptase (RT) PCR and Rapid Amplification of cDNA Ends (RACE)

10 The mRNA expression pattern of selected cDNA clones was determined by RT-PCR using a panel of normal tissue RNA. This test panel consisted of lung, testis, small intestine, colon, breast, liver, and placenta, and was purchased from Clontech Laboratories Inc. (Palo Alto, CA). Colon tumor RNA was also included in this panel and was prepared as described above. As a control for genomic DNA contamination, all cDNA synthesis reactions were set up in duplicate with the

15 additional sample lacking reverse transcriptase. Gene specific PCR primers were designed to amplify 5' fragments of 300-400 bp and were purchased commercially (Gibco BRL, Grand Island, NY). PCR reactions were undertaken at an annealing temperature of 68°C using a Perkin Elmer thermal cycler. In certain cases, RT-PCR products were subcloned into the pCR2.1 plasmid vector (Invitrogen) and multiple clones were subjected to DNA sequencing as described. 5' and 3' RACE

20 reactions were undertaken using gene specific and adapter primers in conjunction with Marathon Ready normal colon cDNA and KlenTaq polymerase (Clontech) as per manufacturers protocol. Products were then subcloned into the pCR2.1 plasmid vector (Invitrogen) and screened by PCR with internal primers for presence of the desired insert. Multiple RACE clones were subjected to DNA sequencing as described.

25

Example 5: Northern blot analysis

Northern blots containing the transfer yields of 2 µg poly A⁺ RNA from a panel of normal tissues were obtained commercially (Clontech). Random primed ³²P labeled probes consisting of 300-600 bp PCR products from 5 prime coding sequences of serum positive cDNA clones were

30 hybridized for 1.5 hours in Expresshyb (Clontech) at 68°C and washed at high stringency (2 times,

30 min. each, 0.1X SSC/0.1% SDS at 68°C). Resultant blots were used to expose Biomax MS autoradiography film (Eastman Kodak Co., Rochester, NY).

Table 4: Breast Cancer Associated Antigen Clone mRNA sizes

5	Clone	Size (kb)	Clone	Size (kb)	Clone	Size (kb)
	LONY-Br-1	1.8	LONY-Br-17	1.0	LONY-Br-33	2.6
	LONY-Br-2	2.9	LONY-Br-19	1.5	LONY-Br-34	2.1
	LONY-Br-3	4.8	LONY-Br-20	2.4	LONY-Br-35	1.9
	LONY-Br-4	1.2	LONY-Br-21	2.4	LONY-Br-36	0.8
10	LONY-Br-5	0.9	LONY-Br-22	1.6	LONY-Br-37	1.0
	LONY-Br-6	1.4	LONY-Br-23	1.3	LONY-Br-38	2.2
	LONY-Br-7	1.3	LONY-Br-24	3.9	LONY-Br-39	1.9
	LONY-Br-8	0.9	LONY-Br-25	1.9	LONY-Br-40	3.4
	LONY-Br-9	6.0	LONY-Br-26	1.5	LONY-Br-41	3.9
15	LONY-Br-10	3.6	LONY-Br-27	1.2	LONY-Br-42	0.6
	LONY-Br-11	4.6	LONY-Br-28	0.5	LONY-Br-43	1.4
	LONY-Br-12	2.2	LONY-Br-29	0.6	LONY-Br-44	0.7
	LONY-Br-13	1.2	LONY-Br-30	0.8	LONY-Br-45	3.0
	LONY-Br-14	0.8	LONY-Br-31	0.4	LONY-Br-46	3.7
20	LONY-Br-15	0.9	LONY-Br-32	2.2	LONY-Br-47	0.5
	LONY-Br-16	2.5	LONY-Br-33	2.6	LONY-Br-48	1.6

Example 6: Isolation of gastric and prostate clones

A stomach cancer cDNA library was established, using standard techniques, then the library
 25 was screened, using the SEREX methodology described supra, and set forth by Sahin et al., *Proc. Natl. Acad. Sci. USA* 92: 11810 (1995), and by Chen et al., *Proc. Natl. Acad. Sci. USA* 94: 1914 (1997), incorporated by reference in their entirety.

To be specific, total RNA was isolated by homogenizing tumor samples in 4M guanidium thiocyanate/0.5% sodium N-lauryl sarcosine/ and 25 mM EDTA followed by centrifugation in 5.7
 30 M CsCl/25 mM sodium acetate/10 uM EDTA at 320,000 rpm. Total mRNA was removed by passing the sample over an oligo-dT cellulose column. The cDNA libraries were then constructed

by taking 5 ug of mRNA, using standard methodologies to reverse transcribe the material.

Libraries were prepared from four different stomach cancer patients, referred to as "SM", "CK" and "SS" and "KM" respectively. A total of 2.5×10^6 , 1.1×10^6 , and 1.7×10^6 cDNA clones were obtained from the "SM", "CK" and "SS" individuals. Additional libraries were prepared from

5 prostate cancer patient "OT".

The cDNA was used to construct a lambda phage library, and 500 phages were plated onto XL1-Blue MRF E. coli, and incubated for eight hours at 37°C. A nitrocellulose membrane was then placed on the plate, followed by overnight incubation. The membrane was then washed, four times, without TBS which contained 0.05% Tween, and was then immersed in TBS containing 5% non-fat
10 dried milk. After one hour, the membrane was incubated with conjugates of peroxidase-goat anti human IgG specific for Fc portions of human antibody (1:2000, diluted in TBS with 1% BSA. The incubation was carried out for one hour, at room temperature, and the membrane was then washed three times with TBS. Those clones which produced antibodies were visualized with 0.06%, 3,3'-diamino benzidine tetrachloride, and 0.015% H₂O₂, in 50 mM Tris (pH 7.5). Any clones which
15 produced immunoglobulin were marked, and then the membrane was washed, two further times, with TBS that contained 0.05% Tween, and then twice with "neat" TBS.

The membranes were then incubated in 1:100 diluted patient serum, overnight, at 4°C. The patient serum had been pretreated. Specifically, 5 ml samples were diluted to 10 ml with TBS containing 1% bovine serum albumin, and 0.02% Na₃N. The serum had been treated to remove
20 antibodies to bacteriophage, by passing it through a 5 ml Sepharose column, to which a lysate of E. coli Y1090 had been attached, followed by passage over a second column which had E. coli lysate and lysate of E. coli infected with lambda bacteriophage. The screening was carried out five times. The samples were then diluted to 50 ml, and kept at -80°C, until used as described herein.

Following the overnight incubation with the membrane, the membrane was washed twice
25 with TBS/0.05% Tween 20, and then once with TBS. A further incubation was carried out, using the protocols discussed supra, for the POD labelled antibodies.

The positive clones were then sequenced, using standard techniques. Following comparison of the sequences to information available in data banks, a total of 36 clones were resolved into known and unknown genes. In the table that follows, the "+" and "-" signs are essentially used to
30 compare signals to each other. All were positive. Table 5, which follows, summarizes some of this

work isolation and sequencing of "SM" clones. Specifically, with reference to the first page of the table, previously identified human proteins and the nucleotide sequences, set forth in SEQ ID NOS:588-626 are known. The four molecules which follow in SEQ ID NOS:627-634 (gelsolin, zinc finger protein family, variant zinc finger motif protein goliath and homeodomain proteins), have not been identified in humans previously, although there are related molecules found in other species.

Finally, with reference to Table 5, the last four moieties, i.e., prepro- α collagen, heterogeneous ribonucleoprotein D, nucleosome assembly protein 2, and NY-ESO-2/Ulsn NRP/V1 small nuclear ribonucleoprotein, are also known. Nucleotide sequences are set forth at SEQ ID NOS:635-642.

The nucleic acid molecules having the nucleotide sequences set forth at SEQ ID NOS:643-670 represent molecules for which no related sequences were found. SEQ ID NO:671 combines the sequences of SEQ ID NOS:627-630, inclusive. SEQ ID NO:672 combines SEQ ID NOS:643-656, SEQ ID NO:673 combines SEQ ID NOS:657, 659 and 662, while SEQ ID NO:674 combines SEQ ID NOS: 658, 660, 661 and 663.

SEREX analysis of clones from libraries derived from patients "CK", "SS", "KM" (all gastric cancer) and patient "OT" (prostate cancer) was carried out as described above. The nucleotide sequences of clones derived from gastric cancer patients are presented as SEQ ID NOS:176-436. The nucleotide sequences of clones derived from prostate cancer patient "OT" are presented as SEQ ID Nos:437-543.

Example 7: Isolation and analysis of colon clones

Colon tumor samples were obtained as surgical samples, and were frozen at -80°C until ready for use.

Total RNA was then isolated from the samples, using the guanidium thiocyanate method of Chirgwin, et al., *Biochemistry* 18: 5294-5299 (1979), incorporated by reference. The total RNA thus obtained was then purified to isolate all poly A⁺ RNA, using commercially available products designed for this purpose.

The poly A⁺ RNA was then converted into cDNA, and ligated into λ ZAP, a commercially available expression vector, according to the manufacturer's suggested protocol.

Three cDNA libraries were constructed in this way, using colorectal carcinoma samples.

A fourth library, also from colorectal carcinoma, was prepared, albeit in a different way. The

fourth library was an IgG subtraction library, prepared by using a subtraction partner, generated by PCR amplification of a cDNA clone which encoded an IgG molecule. *See, e.g., Ace et al, Endocrinology* 134: 1305-1309 (1994), and incorporated by reference in its entirety. IgG subtraction is done to eliminate any false, positive signals resulting from interaction of cDNA clones

5 which encode IgG, with the IgG then interacting with the anti-human IgG used in the SEREX assay, as described herein. PCR products were biotinylated, and hybridized with denatured second strand cDNA, at 68°C for 18 hours. Biotinylated hybrid molecules were coupled to streptavidin, and then removed by phenol chloroform extraction. Any remaining cDNA was also ligated into λ ZAP. All libraries were amplified, prior to immunoscreening.

10 Immunoscreening was carried out using sera obtained from patients undergoing routine diagnostic and therapeutic procedures. The sera were stored at -70°C prior to use. Upon thawing, the sera were diluted at 1:10 in Tris buffered saline (pH 7.5), and were then passed through Sepharose 4B columns. First, the sera were passed through columns which had *E. coli* Y1090 lysates coupled thereto, and then lysates from bacteriophage infected *E. coli* BNN97 lysates. Final
15 serum dilutions were then prepared in 0.2% non-fat dried milk/Tris buffered saline.

The method of Sahin et al., *Proc. Natl. Acad. Sci. USA* 92:11810-11813 (1995), and U.S. Patent No. 5,698,396, both of which are incorporated by reference, was used, with some modifications. Specifically, recombinant phages at a concentration of 4×10^3 phages per 15 cm plate (pfus), were amplified for six hours, after which they were transferred to nitrocellulose membranes
20 for 15 hours. The membranes then were blocked with 5% nonfat dried milk.

As an alternative to the IgG subtraction procedure discussed above, membranes were prescreened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific goat anti-human IgG, for one hour, at room temperature. Color was developed using 3,3'-diaminobenzidine tetrahydrochloride, which permitted scoring of IgG encoding clones.

25 Membranes were then incubated in 1:100 dilutions of autologous sera, which had been pretreated with the Sepharose 4B columns, as described *supra*. The filters were then incubated, in a 1:3000 dilution of alkaline phosphatase conjugated Fc fragment specific, goat anti-human IgG, for one hour, at room temperature. The indicator system 4-nitroblue tetrazolium chloride/5-bromo-4-chloro-3-indolyl-phosphate was then added, and color development assessed. Any positive clones
30 were subcloned, and retested, except the time on the nitrocellulose membrane was reduced to three

hours.

Positive clones were isolated and sequenced according to standard procedures. The nucleotide sequences of the clones are set forth in the even numbered sequences from SEQ ID Nos:544-586. The odd numbered sequences from SEQ ID Nos:545-587 represent the translated

5 amino acid sequences of the colon nucleic acid clones. Analysis of probes for SEQ ID NOS:544 and 546 confirmed their universal expression.

The foregoing results reflect SEREX isolation of colon cancer clones using autologous serum. The positive clones were then rescreened, using allogeneic serum, following the same method discussed supra, in example 2, except IgG prescreening was omitted. The allogeneic sera
10 was obtained from sixteen normal blood donors, and twenty nine patients who had been diagnosed with colorectal cancer.

The analysis with the two types of serum revealed that fourteen reacted with a subset of sera from normal and cancer patients, twenty-eight only with autologous sera, and six with both allogeneic and autologous sera. Over 60% of the allogeneic serum samples tested reacted with at
15 least one of these positive clones. About 20% reacted with two or more.

In view of the results described above, further experiments were carried out using serum samples from patients with other forms of cancer, i.e., renal cancer (13 samples), lung cancer (23 samples), and breast cancer (10 samples). The results are set forth in Table 6 which follows:

20 Table 6: Allogeneic serotyping using colon cancer clones

Clone Number	Normal Sera	Colon Cancer	Renal Cancer	Lung Cancer	Breast Cancer
25 NY-Co-8	0/16	8/29	1/13	0/23	0/10
NY-Co-9	0/16	5/29	1/13	1/23	0/10
NY-Co-13	0/16	5/29	0/13	0/23	0/10
NY-Co-16	0/16	3/29	0/13	0/23	0/10
NY-Co-20	0/16	4/29	0/13	0/23	0/10
30 NY-Co-38	0/16	4/29	3/13	0/23	1/10

Of the six clones which were identified as being reactive with autologous and allogeneic

cancer serum, and not with normal serum, two were found to be identical to previously identified molecules (NY-Co-. Four others were found to have little or no homology to known sequences and thus are preferred allogeneic-reactive colon cancer clones. These nucleic acids and their polypeptide translations are presented as SEQ ID NOS: 544-551: SEQ ID NO: 544/545 (NY-CO-

5 8), SEQ ID NO: 546/547 (NY-CO-9), SEQ ID NO: 548/549 (NY-CO-16) and SEQ ID NO: 550/551 (NY-CO-38). . Of twenty seven allogeneic colon cancer serum samples tested, 67% reacted with at least one of these antigens.

The expression pattern of mRNA corresponding to SEQ ID NOS:544, 546 and 550, as well as other sequences identified via the preceding examples was determined. To do this, RT-
10 PCR was carried out on a panel of RNA samples, taken from normal tissue. The panel contained RNA of lung, testis, small intestine, colon, breast, liver and placenta tissues. The RNA was purchased from a commercial source. RNA from a colon tumor sample was also included. All samples were set up for duplicate runs, so that genomic DNA contamination could be accounted for. In the controls, no reverse transcriptase was used.

15 Primers were designed which were specific for the cDNA, which would amplify 5'-fragments, from 300-400 base pairs in length. The PCR reactions were undertaken at an annealing temperature of 68°C. Where appropriate, 5' and 3'-RACE reactions were undertaken, using gene specific primers, and adapter primers, together with commercially available reagents. Specifically, SEQ ID NOS: 546 and 550 were tested using RACE. The resulting products were
20 subcloned into vector pCR 2.1, screened via PCR using internal primers, and then sequenced.

SEQ ID NOS:544 and 546 were found to be amplified in all tissues tested. SEQ ID NO:550 was found in colon tumor, colon metastasis, gastric cancer, renal cancer and colon cancer cell lines Colo 204 and HT29, as well as in normal colon, small intestine, brain, stomach, testis, pancreas, liver, lung, heart, fetal brain, mammary gland, bladder, adrenal gland tissues. It
25 is was not found in normal uterine, skeletal muscle, peripheral blood lymphocytes, placental, spleen thymus, or esophagus tissue, nor in lung cancer.

The analysis also identified differential expression of a splice variant of SEQ ID NO:550, i.e., SEQ ID NO:552. When the two sequences were compared, it was found that SEQ ID NO:550 encodes a putative protein of 652 amino acids (SEQ ID NO:551), and molecular weight
30 of 73,337 daltons. SEQ ID NO:552, in contrast, lacks an internal 74 base pairs, corresponding to

nucleotides 1307-1380 of SEQ ID NO:550. The deletion results in formation of a stop codon at the splice function, and a putative protein of 403 amino acids (SEQ ID NO:553), and molecular weight 45,839. The missing segment results in the putative protein lacking a PEST protein degradation sequence, thereby suggesting a longer half life for this protein.

5 In additional experiments, primers designed not to differentiate between SEQ ID NOS: 550 and 552 resulted in almost universal amplification (placenta being the only exception). In contrast, when primers specific for SEQ ID NO:552 were used differences were seen in normal pancreatic, liver, lung, heart, fetal brain, mammary gland, bladder, and adrenal gland tissue, where there was no expression of SEQ ID NO:552 found.

10 Northern blotting was also carried out for SEQ ID NOS: 544, 546, 550 and 552. These experiments employed the same commercially available RNA libraries discussed above were used.

Samples (2 ug) of polyA⁺ RNA were analyzed from these samples, using random, ³²P labelled probes 300-360 nucleotides in length, obtained from PCR products. These probes were hybridized to the RNA, for 1.5 hours, at 68°C, followed by two washes at 0.1xSSC, 0.1% SDS, 15 68°C, for 30 minutes each time.

SEQ ID NOS:544 and 546 were again found to be universally expressed.

Further screening identified additional isoforms of SEQ ID NOS:544 and 550. These are set forth as SEQ ID NOS: 554, 556, 558 and 560. The isoform represented by SEQ ID NO:554 (translated as SEQ ID NO:555) is a naturally occurring splice variant of SEQ ID NO:544, found 20 in normal colon. SEQ ID NO:556 (translated as SEQ ID NO:557), which is an isoform of SEQ ID NO:550 (translated as SEQ ID NO:551), was found in brain tissue, primarily spinal chord and medulla. SEQ ID NO:558 (translated as SEQ ID NO:559), was found in normal kidney and in colon tumors, metastasized colon cancer, renal cancer, gastric cancer, and in colon cancer cell line Colo 205. It was not found in any normal tissue other than kidney.

25 The nucleic acid molecule whose nucleotide sequence set forth as SEQ ID NO:560 (translated as SEQ ID NO:561), is a further isoform of SEQ ID NO:552. It is similar to SEQ ID NO:558, except it contains a long nucleotide insert encoding a longer COOH terminus. It was expressed in normal bladder and kidney cells, and renal cancer cells. It was not expressed in colon cancer cells.

30 It is reported above that fourteen clones reacted with subsets of serum from both normal

and cancer patients, while twenty eight reacted with autologous sera only. These clones were sequenced, in accordance with standard, art recognized methods. Of the clones which reacted only with autologous sera, nine appear to be previously unidentified sequences. These are set forth as SEQ ID NOS: 562, 564, 566, 568, 570, 572, 574, 576 and 578. SEQ ID NO:562

5 (translated as SEQ ID NO:563) is 1445 nucleotides long, and shows some similarity to known sequences for myosin and tropomyosin. SEQ ID NO:564 (translated as SEQ ID NO:565), which is 1226 nucleotides long, contains a TPR motif. The sequence set forth in SEQ ID NO:566 (translated as SEQ ID NO:567) is 1857 nucleotides long, and shows similarity to cyclophilins. The nucleotide sequence set forth in SEQ ID NO:568 (translated as SEQ ID NO:569) is 1537
10 nucleotides long, and shows similarity to murine gene 22A3, which has unknown function, but resembles an unconventional form of myosin, as well as an EST for heat shock inducible mRNA. As for the molecule set forth in SEQ ID NO:570 (translated as SEQ ID NO:571), it appears to resemble a nucleic targeting signal protein. SEQ ID NO: 572 (translated as SEQ ID NO:573) is 604 nucleotides long, and may encode a lysosomal protein. The molecule set forth in SEQ ID
15 NO:574 (translated as SEQ ID NO:575) is 742 nucleotides long, and encodes a protein with an SH3 domain and which shows some similarity to GRB2 and human neutrophil oxidase factor. The molecule set forth in SEQ ID NO:576 (translated as SEQ ID NO:577) is 1087 nucleotides long, and encodes a protein which contains coiled core domains. The molecule set forth in SEQ ID NO:578 (translated as SEQ ID NO:579) is 2569 nucleotides long, shows some similarity with
20 Drosophila homeotic material tudor protein, and has a DY(F)GN repeat.

Additional sequences were identified which were expressed in both normal sera and cancer cells. The sequence set forth in SEQ ID NO:580 (translated as SEQ ID NO:581), e.g., is 2077 nucleotides long, and was expressed by both colorectal cancer and normal cells. Analysis of the sequence showed that it possesses a nuclear targeting sequence. The molecule set forth in SEQ
25 ID NO:582 (translated as SEQ ID NO:583) is 3309 nucleotides long, was expressed by colorectal cancer and normal cells, and is similar to heat shock protein 110 family members. The molecule presented in SEQ ID NO:584 (translated as SEQ ID NO:585) was expressed in a colon to lung metastasis, as well as by normal tissue. It is 2918 nucleotides in length. Analysis shows that it contains 2 zinc finger domains. The nucleotide sequence of SEQ ID NO:586 (translated as SEQ
30 ID NO:587) was also expressed in a colon to lung metastasis, is 1898 nucleotides long, and is

also expressed by normal tissue. Specifically, the reactivity of the molecules was as follows:

Table 7

5	SEQ ID NO:	Normal Sera	Tumor Sera
		Reactivity	Reactivity
	580	2/16	2/16
	582	2/16	3/16
10	584	2/16	2/16
	586	2/8	1/16

A more extensive set of RT-PCR experiments were carried out to study the expression pattern of SEQ ID NOS: 550, 552, 558 and 560. The results follow.

15

Table 8: RT-PCR analysis of colon SEREX clones

	<u>normal tissue</u>	<u>SEQ ID NO.:550</u>	<u>SEQ ID NO.:552</u>	<u>SEQ ID NO.:558</u>	<u>SEQ ID NO.:560</u>
20	kidney	+	Negative	Negative	Negative
	colon	+	Negative	Negative	Negative
	small		Negative	Negative	Negative
	intest.	+	Negative	Negative	Negative
	brain	+	Negative	Negative	Negative
25	stomach	+	Negative	Negative	Negative
	testis	+	Negative	Negative	Negative
	pancreas	+	Negative	Negative	Negative
	lung	+	Negative	Negative	Negative
	liver	+	Negative	Negative	Negative
30	heart	+	Negative	Negative	Negative
	fetal		Negative	Negative	Negative
	brain	+	Negative	Negative	Negative
	mammary		Negative	Negative	Negative
	gland	+	Negative	Negative	Negative
35	bladder	+	Negative	Negative	Negative
	adrenal		Negative	Negative	Negative
	gland	+	Negative	Negative	Negative
	uterus	Negative	Negative	Negative	Negative
	skeletal		Negative	Negative	Negative
40	muscle	Negative	Negative	Negative	Negative
	PBL	Negative	Negative	Negative	Negative
	placenta	Negative	Negative	Negative	Negative

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	spleen	Negative	Negative	Negative	Negative
	thymus	Negative	Negative	Negative	Negative
	esophagus	Negative	Negative	Negative	Negative
	<u>Tumor Tissue</u>				
5	renal cancer (4)	+ (2/4)	+ (2/4)	+ (2/4)	+ (2/4)
	colon primary tumors (10)	+ (10/10)	+ (10/10)	+ (10/10)	Negative
10	colon mets (4)	+ (4/4)	+ (4/4)	+ (4/4)	Negative
	breast cancer (6)	+ (3/6)	Negative	Negative	Negative
	lung cancer (6)	+ (6/6)	Negative	Negative	Negative
15	gastric cancer (1)	+	+	+	Not tested
	<u>colon cancer cell lines</u>				
	colo 205	+	+	+	Negative
	HT29	+	+	Negative	Negative
20	HCT15	Negative	Negative	Negative	Negative

Example 8: Isolation and analysis of additional clones

For the establishment of a cDNA library from human tissue total RNA was obtained from

25 0.5 g of a renal clear cell carcinoma and established according to the method of Chomzynski as described above. The mRNA was extracted from total RNA with oligo-dT-cellulose. The synthesis of the first strand cDNA was accomplished by the method described by Gubler and Hoffmann, *Gene* 25: 263 (1983) using RNase H and DNA polymerase I. For adaptation of the cDNA Klenow enzyme, adaptors with EcoRI restriction enzyme sites were ligated to the cDNA ends using T4 DNA

30 ligase (Ferretti L and Sgamerella V, *Nucl. Acids Res.* 9: 3695 (1981)). Following restriction enzymatic digestion with the enzyme XhoI, cDNA molecules of different length were separated using Sephacryl 400 and transfected into λ ZAPII phage vectors (Short JM et al., *Nucleic Acids Res.* 16: 7583 (1988)). The recombinant phage DNA was packaged into phages after ligation with packaging extracts and used for the transfection of *E. coli* bacteria. The titration of the library

35 resulted in 1.8×10^6 recombinant primary clones. The total cDNA library was transfected in *E. coli* and amplified. The titer of the cDNA library after amplification was 10^{11} plaque forming units per ml (pfu/ml). These transfected cells were used in experiments which follow.

In accordance with the invention as described above, identification of immunogenic material was achieved by using human sera which has been completely depleted of antibodies directed against antigens derived from native and lytic λ phage-transfected *E. coli* bacteria. To this end, the serum was absorbed, as follows.

5 *E. coli* bacteria of the strain XL1-blue were cultured in 50 ml LB medium overnight. After achieving an optical density of $OD_{600} = 1.0$, the bacteria were pelleted by centrifugation, resuspended in 5 ml phosphate buffered saline (PBS), and lysed by sonication. The bacterial lysate was bound onto a matrix of activated Sepharose, which was then put into a column and used for the absorption of the human serum. The serum was run over this column 10 times.

10 A culture of *E. coli* XL1 blue bacteria in the exponential growth phase was pelleted by centrifugation, transfected in 0.01 M magnesium sulfate with 10^6 λ ZAPII phages without a recombinant insert and incubated in 5 ml LB medium for four hours. The lysate of the transfected bacteria was used in the same manner as the untransfected bacteria, with the human serum described supra being passed through the column an addition ten times.

15 To complete the depletion of the serum, interfering antibodies from lytically transfected *E. coli* bacteria were cultured on agar plates and their proteins were blotted onto nitrocellulose membranes after 10 hours of culture at 37°C. Following this, the serum which had been preabsorbed according to the above steps was transferred to the blotted nitrocellulose membrane, and the absorption procedure was repeated five times. The serum, which was processed in
20 accordance with the invention, was totally depleted of antibodies directed against antigens derived from *E. coli* and phages.

In this, a renal cancer-specific antigen was identified via the following steps. Bacteria of the strain XL1 blue were transfected with recombinant phages derived from the described cDNA library and plated at a density of $4-5 \times 10^3$ plaque forming units (pfu) per plate in LB-medium with
25 isopropylthiogalactopyranoside ("IPTG"). After 12 hours of incubation at 37°C, nitrocellulose membranes were put on top of the cultures and culture plates were incubated for another four hours. This was followed by incubation of the nitrocellulose membrane for one hour in Tris-buffered saline (PBS) with 5% milk powder. After washing the nitrocellulose membranes three times in TBS, the stripped human serum secured following Example 2 was diluted 1:1000 in TBS/0.5% (w/v) milk
30 power and incubated overnight with gentle shaking. After the incubation with the nitrocellulose

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membrane the serum was removed and kept for additional testing. Following incubation with serum, the nitrocellulose membranes were washed three times in TBS, and incubated with a polyclonal alkaline phosphatase-conjugated goat anti-human IgG serum for one hour. Following this, the nitrocellulose membranes were washed repeatedly with TBS/0.01% (v/v Tween 20). The

5 reaction was developed using nitroblue tetrazolium chloride and bromochloro-indoyl-phosphate in TBS. The binding of human antibodies to the expressed protein became visible by a blue ring-formed color deposit on the nitro-cellulose membrane. The efficient preabsorption of the serum made it possible to develop the membrane at 37°C over several hours without compromising the quality of the test because of background reactivity caused by antibodies against *E. coli* and phage
10 antigens.

Positive clones were localized on the agar plates, transferred into transfection buffer, and used for a second round of transfection and subcloning. A total of 1.8×10^6 recombinant clones were subjected to screening and five different positive-reacting clones were identified.

Positive clones, i.e., those which had bound antibodies derived from the processed human
15 serum, were subcloned to monoclonality by repeated rounds of transfection and testing of reactivity with the processed human serum. P-bluescript phagemids with the respective cDNA inserts were cloned by *in vivo* excision (Hay B and Short JM, *Strategies* 5: 16-19, 1992) from the λ ZAPII phage vectors and used for the transfection of *E. coli* SOLR bacteria. Plasmids were isolated from the bacteria after alkaline lysis with NaOH in a modification of the method of Birnboim HC and Doly J.
20 *J. Nucl. Acids Res.* 7: 1513 (1979). The recombinant plasmid DNA was sequenced according to standard methods using M13-forward and M13-reverse oligonucleotides. The DNA sequence obtained and the resulting amino acid sequence were compared with nucleic acid and protein data banks (Gene Bank, EMBL, Swiss Prot). The sequencing of the cDNA inserts was continued using internal oligonucleotides. Analysis showed no homology with any sequences deposited in the data
25 banks. The full length cDNA clone, referred to as SK313, was cloned with the RACE method (Frohman MA, Dush MK, Martin GR, *Proc. Natl. Acad Sci. USA* 85: 8998 (1988)), and had a carbonic anhydrase domain at the 5' end.

As a continuation of these experiments, RNA was isolated from a spectrum of malignant and normal human tissues and Northern blots were performed with labeled SK313 (also referred to as
30 clone HOM-RCC-313). The Northern blot analysis demonstrated that the mRNA of clone HOM-

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RCC-313 was overexpressed in 4 out of 19 renal cell carcinomas compared to normal kidneys. Very weak expression was found only in colonic mucosal tissue and in normal kidney. Expression in other tissues was not observed.

To determine the incidence of antibodies against antigens which are identified above,

5 allogeneic sera from healthy individuals and tumor patients were analyzed. To this end, the sera were processed as described above and depleted from antibodies against antigens derived from *E. coli* and phages. For the detection of antigen-specific antibodies, phages derived from reactive clones were mixed with non-reactive phages derived from the same cDNA library at a ratio of 1:10 and tested as described above for reactivity with antibodies in the human test serum. The serum
10 which had been used for the identification of the antigen was used as a positive control. The non-reactive phages served as a negative control. A serum sample was positive for antigen reactive antibodies, if the expected percentage of the phage plaques showed a positive reaction. In the case of the renal cell carcinoma antigen represented by clone HOM-RCC-313, the analysis of a spectrum of human sera showed that only sera from renal cell carcinoma patients contained reactive
15 antibodies. Sera from healthy controls and patients with other tumors did not contain such antibodies.

The cDNA for clone HOM-RCC-313 was excised from the plasmid DNA by digestion with the restriction enzyme EcoR1, was separated by agarose gel electrophoresis, followed by extraction from the gel. This was then used to create a vector which expresses a fusion protein with the
20 bacterial protein anthranilate synthetase. A relevant fragment in the exact open reading frame was cloned into pATH plasmid vectors (Koerner et al., *Meth. Enzymol.* 194: 477 (1991)). Induction of protein expression was obtained after transformation of the plasmids into *E. coli* of strain BL21 as described (Spindler et al., *J. Virol.* 49: 132 (1984)). Expressed fusion proteins were separated by SDS gel electrophoresis, excised from the gel, eluted and freeze dried. Rabbits were immunized by
25 subcutaneous injection with 100 µg of the lyophilisate combined with Freund's adjuvant according to standard procedures. Immunization was repeated three times at two-week intervals using incomplete Freund's adjuvant. The rabbit was bled and antiserum was obtained. The obtained antiserum was depleted from antibodies reactive with *E. coli* and phages as described above and tested for reactivity against the renal carcinoma antigen as described for the human serum.
30 Reactivity was detected at dilutions of 1: >100,000.

Additional clones were identified from pancreatic cancer tumor specimen using the SEREX method of Sahin et al., (1995). A cDNA library was prepared and reacted with high titer IgG in sera of pancreatic carcinoma patients. A total of 8×10^5 clones were screened with autologous serum, and 4.5×10^3 clones were screened with three different allogeneic sera. Twenty three clones, representing

5 seven different transcripts were found. Four were previously unknown, unisolated genes. Of the remaining three, glycolytic enzyme aldolase A was found (SEQ ID Nos:799 and 800). Another molecule was "known" in that it was homologous to the rat eIF-5 gene (SEQ ID Nos:801 and 802), which is a eukaryotic translation initiation factor. The human eIF-5 gene was not previously known.

When hepatocellular carcinoma libraries were studied in the same way, a total of 1.5×10^6 clones were screened, and 98 positives were found. A total of 59 of these were sequenced, and corresponded to at least 20 different transcripts. Nine of these were assayed with allogeneic sera from hepatocellular cancer (HCC) patients and normal patients. High titered antibody was restricted to HCC patients. The majority of isolated sequences did not correspond to known molecules. Three which did were human albumin (SEQ ID Nos:803 and 804), senescence marker protein SMP30
15 (SEQ ID NOs:805 and 806), and C3VS (SEQ ID NOs:807 and 808). The latter was overexpressed in 2 of 4 hepatocarcinoma tissues, as compared to normal. Expression of SMP30 was found to vary highly.

The methodology was combined with subtractive cDNA techniques when assaying leukemia cells (T-ALL). An antigen was found which was identical to a broadly expressed, DNA repair
20 enzyme.

Further assays identified the known molecule galectin-9 (SEQ ID NOs:809 and 810), as being highly expressed on human macrophages and dendritic cells. Expression is upregulated during differentiation of monocytes to macrophages. Highest levels were found on monocyte derived, dendritic cells.

25 Fusion proteins "LD1-mFc" and "LD2-mFc" were constructed to help analyze galectin-9. These consist of murine IgG heavy chain fragments, and a lectin domain (LD1, or LD2), as the N-terminus. Analysis indicated that the C-terminal lectin domain binds to the surface ligands, while the cell surface ligands recognized by the C-terminal lectin domain of galectin-9 was expressed only in a small, subpopulation of dendritic cells.

30 Further analysis of ovarian cancer cells (500,000 clones, using the SEREX method described

above), identified previously known antigens MAGE-4 (SEQ ID Nos:811 and 812) and restin (SEQ ID Nos:813 and 814), and six other newly identified molecules.

Further experiments were carried out which involved restin. A variation of restin is known, i.e., "CLIP170", which was reported to mediate binding of endosomes to microlubules. It was found

5 that both resin and CLIP 170 are highly expressed in dendritic cells, and are involved in the formation and transport of macropinosomes, a feature of professional antigen presenting cells. Expression of restin was induced after 48 hours of culture of monocytes in GM-CSF/IL-4 supplemented medium. Highest levels were found in immature dendritic cells. When microlubile systems, which are essential for the activity of restin/CLIP-170 were disrupted, macropinocytosis
10 was lost completely.

Further work with the methodology disclosed herein on glioma identified a clone encoding nm23-H2 protein (SEQ ID Nos:815 and 816). This clone corresponds to subunit B of nucleoside diphosphate kinase, which is implicated in tumor metastasis control. It is also known as PuF, a transcriptional factor, for c-myc proto-oncogenes. Antibodies against the protein were found in 1 of
15 18 sera of brain malignancy patients, 3 of 20 melanoma patients, and 2 of 20 sera from healthy patients. When expression studies were carried out using RT-PCR, 25 of 28 brain tumor, and 4 or 5 meningioma tumor samples were found to express the gene.

Example 9: Isolation and analysis of lung cancer clones

20 A cDNA library was constructed from a case of moderately differentiated adenocarcinoma of the lung, obtained from the Department of Pathology at The New York Hospital. The library was constructed in a λ ZAP Express vector using a cDNA library kit (Stratagene, La Jolla, CA).

The cDNA library was screened with autologous patient's serum as described previously [Sahin, U. et al., *Proc Natl Acad Sci USA* 92:11810-3 (1995); Chen, Y.T. et al. *Proc Natl Acad Sci*
25 *USA*. 94:1914-8 (1997)]. Briefly, the serum was diluted 1:10, pre-absorbed with transfected *E. coli* lysate, and a 1:10 dilution of the absorbed serum (final dilution of serum 1:100) was incubated overnight at room temperature with the nitrocellulose membranes containing the phage plaques. After washing, the filters were incubated with alkaline phosphatase-conjugated goat anti-human Fc γ secondary antibodies and the reactive phage plaques were visualized by incubating with 5-bromo-
30 4-chloro-3-indolyl-phosphate and nitroblue tetrazolium. Phagemid clones encoding human

immunoglobulin sequences were subsequently eliminated during the secondary screening.

The reactive clones were subcloned, purified, and *in vitro* excised to pBK-CMV plasmid forms (Stratagene). Plasmid DNA was prepared using Wizard Miniprep DNA Purification System (Promega, Madison, WI). The inserted DNA was evaluated by EcoRI-XbaI restriction mapping, and clones representing different cDNA inserts were sequenced. The sequencing reactions were performed by DNA Services at Cornell University (Ithaca, NY) using ABI PRISM (Perkin Elmer) automated sequencers.

To evaluate the mRNA expression pattern of the cloned cDNA in normal and malignant tissues, gene-specific oligonucleotide primers for PCR were designed to amplify cDNA segments of 300-400bp in length, with the estimated primer melting temperature in the range of 65-70°C. All primers were commercially synthesized (Operon Technologies, Alameda, CA). RT-PCR were performed using 35 amplification cycles in a thermal cycler (Perkin Elmer) at an annealing temperature of 60°C.

Genomic DNA were extracted from cell lines and frozen tumor tissue. Following restriction enzyme digestion, the DNA was separated on a 0.7% agarose gel, blotted onto nitrocellulose filters, and hybridized to an a ³²P-labeled DNA probe at high stringency (65°C, aqueous buffer). Washing of the blot was also under high stringency conditions, with a final wash in 0.2XSSC with 0.2% SDS at 65°C.

To identify the 5'end of the mRNA transcripts, RACE (rapid amplification of cDNA ends) methodology was utilized using the Marathon cDNA amplification kit (Clontech) and adaptor-ligated testicular cDNA as the substrate. The PCR products, after separation by agarose gel electrophoresis, were cloned into the direct PCR cloning vector pGEM-T (Promega).

Single-strand conformation polymorphism (SSCP) analysis was performed to analyze cDNA from various tissues, using previously described protocols [Drapopoli, C.D. et al., New York: John Wiley and Sons, Inc. (1997)]. Briefly, PCR was performed with 5 µl RT product in a final volume of 25 µl, with 2µCi of α³²P-dCTP (~3000 Ci/mmol, New England Nuclear) per reaction. The PCR conditions was as described for RT-PCR above. After the PCR, 1 µl of the mixture was diluted with 5 µl of denaturing buffer (95% formamide, 20 mM EDTA, 0.05% bromophenol blue, 0.05% xylene cyanol), heat-denatured at 98°C for 2 min, and electrophoresed through an 8% polyacrylamide gel with 10% glycerol. As controls, aliquots of the same samples were diluted with a standard non-

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denaturing DNA loading dye and electrophoresed in parallel. The electrophoresis was performed at room temperature at a constant power of 10-12 watts. The gel was then dried and autoradiography performed for 15-24 hours with an intensifying screen.

5 Identification of Immunoreactive cDNA clones

A cDNA expression library of 1.42×10^7 primary clones was prepared from Lu15, a specimen of moderately differentiated adenocarcinoma of the lung and 8×10^5 phage plaques were immunoscreened with absorbed autologous patient serum at 1:100 dilution. Excluding false-positive clones encoding immunoglobulin gene fragments, 20 positive clones were identified. These clones
10 were purified and sequence analyzed. Comparisons of the sequences showed that these clones represented cDNAs from 12 distinct genes, designated NY-LU-1 through NY-LU-12 (Table 9). A homology search through the GenBank/EMBO databases revealed that 4 of the 12 genes corresponded to previously known molecules, and 8 others were unknown genes, with sequence identity limited only to short segments of known genes or to expressed sequence tags (ESTs).

15

Table 9: NY-LU clones

Gene Designation	Gene/Sequence Identity [Accession Number]	cDNA	Comments
NY-LU-1	Aldolase A (N and H type) [X06352]	Lu-15/24, 72, 83, 158, 219, 241	Human fructose, 1,6 diphosphate aldolase A. Expressed in muscle (M type), but also in most other tissues (N and H types). Levels increased in most lung cancers; released into blood upon trauma and in several cancers.
20 NY-LU-2	hASNA-1 [U60276]	Lu-15/26, 66	Human homolog of the ATP-binding ars A component of the bacterial arsenite transporter. Previously cloned by SEREX from a testicular library (Chen et al., unpublished). Ubiquitously expressed.
NY-LU-3	Annexin 1X [L19605]	LU-15/64	Homosapiens 56K autoantigen. Antibodies to Annexin 1X are found in multiple autoimmune diseases. ubiquitously expressed.

	NY-LU-4	Rip-1 [U55766]	Lu-15/65	Human HIV Rev-interacting protein. Expressed in B cells, monocytes and rhabdomyoma cells.
	NY-LU-5	Unknown [W61291, W92962, etc.]	Lu-15/80	Expressed ubiquitously (by RT-PCR).
	NY-LU-6	Unknown [none]	Lu-15/85	Sequence contains no ORF, expressed ubiquitously (by RT-PCR).
	NY-LU-7	Unknown [W23466, AA167732, etc.]	Lu-15/135,217	Expressed in neuron, pregnant uterus, lung ca., parathyroid tumors, etc.
5	NY-LU-8	Unknown [Z78323, N39225, etc.]	Lu-15/139	Expressed in fetal heart, retin, multiple sclerosis, etc.
	NY-LU-9	Unknown [W26569, AA036884, etc.]	Lu-15/145	Expressed in retina, pregnant uterus, fetal liver-spleen, etc.
	NY-LU-10	Unknown [M29204, etc.]	Lu-15/154	Expressed in colon, pancreas, pregnant uterus, fibroblasts, etc.
	NY-LU-11	Unknown [W23466, AA057400, etc.]	Lu-15/270	Expressed in retina, pregnant uterus, fetal heart, fetal liver-spleen, parathyroid tumors, etc.
	NY-LU-12	g16	Lu-15/251	Located at the 3p21 TSG locus (see text)

10

Of the 4 known genes, aldolase A (NY-LU-1; SEQ ID NOs:689 and 690) was most frequently isolated, representing 6 of 20 primary positive clones in the entire screening. NY-LU-2 (SEQ ID NO:691), represented by two isolates, was the human homolog of the ATP-binding arsA component of the bacterial arsenite transporter, a gene which has been shown to be ubiquitously expressed in various tissues [Kurdi-Haidar, B. et al., *Genomics* 36:486-91 (1996)]. NY-LU-3 (SEQ ID Nos:692 and 693) encodes annexin XI, which is a 56KD ubiquitously expressed antigen to which autoantibodies have been described in sera from patients with various autoimmune diseases [Misaki, Y. et al., *J Biol Chem* 269:4240-6 (1994); Misaki, Y. et al., *J Rheumatol.* 22:97-102 (1995)]. The last gene in this group, NY-LU-4 (SEQ ID NOs:694 and 695), codes for the human HIV Rev interacting protein Rip-1, which has been shown to be expressed in the monocyte cell line U937, the rhabdomyoma cell line RD, as well as in adherent monocytes and primary lymphocytes [Refaeli, Y.

20

et al., *Proc Natl Acad Sci USA* 92:3621-5 (1995)].

Of the eight unknown genes, 6 (NY-LU-5, 7, 8, 9, 10, 11; SEQ ID Nos:696, 698, 699, 700, 701 and 702/703, respectively) shared sequence identity with reported expressed sequence tags (EST), likely representing cDNA products derived from the same genes. These ESTs were derived

5 from various somatic tissues unrelated to lung, e.g., neuron, pregnant uterus, colon, endothelial cells, etc., suggesting that these genes are widely expressed in human tissues (Table 9), making them unlikely candidates for vaccine-based tumor immunotherapy. These clones were not further investigated. The only novel gene in this group, NY-LU-6 (SEQ ID NO:697), showed no sequence identity to deposited sequences in the public databases. The tissue expression pattern of this gene
10 was evaluated by RT-PCR analysis using gene-specific primers and a normal tissue RNA panel consisting of lung, colon, kidney, liver, brain and testis. Results showed universal expression in these tissues, and this clone was not further analyzed.

NY-LU-12 is on TSG locus of chromosome 3p21.

15 The last gene in the unknown gene group, NY-LU-12, was represented by the immunoreactive clone Lu15-251. This clone, 1081bp in length, contained an uninterrupted open reading frame (ORF) of 952 bp, followed by a 129bp 3'untranslated region. No translation initiation codon was identified, indicating that this was a partial cDNA clone.

A sequence homology search revealed that this gene shared up to 30% homology with two
20 different human proteins at its C-terminus (Fig. 1), LUCA15 and DXS8237E (GenBank accession numbers U23946, and P98175) and also shared homology to S1-1, the rat counterpart of DXS8237E [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)]. LUCA15 was subsequently proven to be a gene immediately centromeric to NY-LU-12 on the TSG locus on chromosome 3p21 (see below and [Wei, M.H. et al., *Cancer Res.* 56: 2487-92 (1996)]). Our analysis of LUCA15 revealed the
25 presence of a nuclear localization signal in the putative LUCA15 protein. DXS8237E, was located on chromosome Xp11.23 [Coleman, M.P. et al., *Genomics* 31:135-8 (1996)] and its rat homolog, S1-1, has been shown to be an RNA-binding protein [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)].

Of particular interest, however, was that a short segment (92bp) at the 5' end of NY-LU-12
30 was identical to a previously identified gene, g16 (GenBank accession number U50839), which was

mapped to chromosome 3p21.3 and was interrupted in the small cell lung cancer line NCI-H740.

To compare NY-LU-12 with g16, the full-length NY-LU-12 cDNA sequence was obtained from normal testicular mRNA through a combination of 5'RACE and direct PCR cloning strategies. The predominant cDNA form (SEQ ID No:707), excluding the poly A tail, is of 3591bp in length.

5 An open-reading-frame of 1123 amino acid residues (SEQ ID No:708) was identified (nt. 102-3470), with 101bp of 5' untranslated and 129bp of the 3' untranslated region. The nucleotide and amino acid sequences are shown in Fig. 2.

Comparison with the g16 sequence verified that these two are identical genes and mapped NY-LU-12 to *TSG* locus on 3p21. However, the reported g16 sequence, 2433 bp in length, lacks the
10 5' end 110 bases which include the translational initiation codon at nucleotide 102, and also the 3' end 980 nucleotides of NY-LU-12. In addition, 74bp DNA segment (nt. 1587-1659 of NY-LU-12) was absent in the reported g16 sequence. Oligonucleotide primers flanking this 74 bp region were designed and used to amplify RNA from 1 normal lung, 5 lung cancer cell lines, and 6 lung cancer specimens. Two RT-PCR products were seen in every specimen, corresponding to the sizes of the
15 two cDNA variants. It was thus concluded that this variation represents an alternate splicing event which occurs in both normal and cancerous lung tissues. Of interest, however, was the difference in the putative translational products resulting from this additional 74bp exon. In the absence of this exon, the open-reading-frame of NY-LU-12 would end in the termination codon at nt.1736, as reported for g16, with a total length of 520 amino acid residues (in contrast to 1123 residues in the
20 longer transcript). Moreover, this shorter form would not encode the C-terminal portion of the NY-LU-12 protein, the segment responsible for the immunoreactivity of Lu15-251 to the autologous patient serum.

Additional cDNA variants of NY-LU-12

25 In the process of 5'RACE cloning of the full-length NY-LU-12, three minor forms of cDNA products were identified which varied in their transcriptional initiation site and in their exon usage in the 5' segment of this gene. These variants will be described as transcripts B, C, and D (SEQ ID Nos:709, 711 and 712). Fig. 3 shows the comparison of these transcripts to the predominant cDNA form (transcript A, see Fig. 2).

30 Transcript B (Fig. 3A, bottom) contains an additional exon of 208 base pairs, inserted at

nucleotide 145 of the NY-LU-12 sequence. The original ORF of NY-LU-12 is disrupted due to this inserted sequence, and the AUG initiation codon used by transcript A is thus unlikely to be used by this transcript. A new potential translational initiation site, however, is found within this new exon and would continue the translation into the ORF of transcript A. The final product would be a

5 protein of 1177 amino acids (SEQ ID NO:710), with the 69 residues at the N-terminus different from transcript A. Interestingly, this new exon encodes for a signal peptide not present in the transcript A (Fig. 3A, bottom), and it is possible that these two products are localized to different subcellular compartments.

Similar to transcript B, transcripts C and D both contained additional exon(s) not present in
10 transcript A. Transcript C contained two extra exons in tandem and a length of 364bp, only one of which (137bp) was present in transcript D, Figure 3B. These extra exon(s), inserted at the same alternate splicing site as transcript B, disrupted the original ORF, and the only long ORF would initiate at nucleotide position 498 of NY-LU-12 (959 of transcript C, 635 of transcript D). Considering the long untranslated region at the 5' end, it is doubtful whether transcripts C and D are
15 indeed translated *in vivo*.

Correlating with this variation of NY-LU-12 mRNA, Northern blot analysis showed several RNA species in normal tissues, ranging approximately from 3 to 4.4 Kb. The intensity of individual bands also appear to vary among different tissues, suggesting post-transcriptional tissue specific regulation of NY-LU-12 mRNA.

20

Features of NY-LU-12 and its putative gene product

Analysis of the NY-LU-12 amino acid sequence showed 20 inexact 6 amino acid repeats with a consensus sequence of D(F/Y)RGR(D/E) close to the N-terminus (Fig. 2). These repeats were separated by 4 to 6 amino acid intervals, which showed no apparent sequence homology
25 among each other. This feature in primary sequence is distinctive among known proteins. Hydrophilicity plot revealed that this region, although hydrophilic in general, has regular hydrophobic turns, and these cycles of hydrophilicity changes correspond to the hexapeptide repeats. Although the significance of this characteristic is unclear at present, this segment of sequence is highly rich in arginine and aspartic acid, a feature shared by RNA binding proteins. Similar motifs,
30 rich in arginine and aspartic acid residues, were found in other RNA-binding proteins [Witte, M.M.

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et al., *Proc Natl Acad Sci USA* 94: 1212-7 (1997); Wilson, R. et al., *Nature* 368:32-8 (1994); Seraphin, B. et al., *Nature* 337:84-7 (1989); Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], e.g., RNA [Seraphin, B. et al., *Nature* 337:84-7 (1989)] hnRNA 3' end cleavage stimulation factor [Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], etc., indicating that NY-LU-

12 is likely to be an RNA-binding protein. Consistent with this, PROSITE analysis of the putative NY-LU-12 protein identified a bipartite nuclear localization signal between amino acids 1016-1032 and a 4-residue nuclear localization pattern (PRKR) at amino acid 604-607 (Fig. 2), suggesting that NY-LU-12 is a nuclear protein. Analysis for post-translational modification sites showed potential sites for tyrosine sulfation, amidation, as well as phosphorylation sites for protein kinase A, C, casein kinase II, and tyrosine kinase. A PEST region, peptide sequences consistently found among unstable proteins with short half lives, was identified at amino acids 897-928 (Fig. 2), implying NY-LU-12 as an unstable protein.

Southern blot analysis of NY-LU-12 in normal and tumor tissues

To investigate the status of NY-LU-12 in normal and tumor cells, Southern blot analysis was performed on 9 lung cancer cell lines (3 adenocarcinoma, 2 squamous, and 3 large cell anaplastic), Lu15 tumor DNA, and a colon cancer cell line HT29 (Fig. 4). (HT29 was included due to the finding of an EST identified in the GenBank, accession number AA079461, which appeared to be a fusion sequence between semaphorin IV gene and NY-LU-12.) Using a 1.1Kb cDNA probe (nucleotide 1095-2140) and HindIII digested DNA, the results showed that one of the two hybridizing bands was absent in NCI-H740, confirming that NY-LU-12 was partially deleted in this cell line. The breakpoint of this deletion, by using primers from different regions, was further defined to be between nucleotides 1433 and 1777 of NY-LU-12, with the 3' sequences homozygously deleted. Besides NCI-H740, however, no evidence of homozygous deletion was seen in any other tumor cell line sample or in LU15. The similar band intensities and identical sizes of the DNA signals in all specimens also argued against the possibility of a heterozygous deletion or translocation of this gene, at least in the region analyzed. No change was found in HT29, suggesting that the semaphorin IV/NY-LU-12 fusion sequence in the GenBank probably represents a cloning artifact.

SSCP and sequence analysis of NY-LU-12 in Lu15 tumor DNA.

The mapping of NY-LU-12 to the lung cancer *TSG* locus raised the possibility that an altered protein product due to mutational event may be the basis for the autologous immune recognition. This possibility was explored using DNA sequencing and single-strand confirmational

5 polymorphism (SSCP) analysis.

The DNA sequence contained in the immunoreactive clone Lu15-251 (nucleotide 2518-3599 of NY-LU-12) was obtained from the normal counterpart by RT-PCR cloning using autologous normal lung tissue, and no mutations were found when compared to Lu15-251.

RT-PCR SSCP was then used to analyze the entire NY-LU-12 gene, comparing Lu15 tumor
10 tissue and autologous normal lung tissue. To encompass the whole sequence, 10 sets of primer pairs were designed, each amplifying a range of 205 to 603 bps. For products >400bps, a restriction enzyme digestion step was added prior to the electrophoresis step to further reduce the fragment sizes and increase the assay sensitivity. Results showed no reproducible changes between normal and tumor tissues, and thus no evidence of mutation in Lu15 tumor cDNA. A representative set of
15 SSCP analysis is shown in Fig. 5.

Serological response to NY-LU-12 in lung cancer patient

The frequency of anti-NY-LU-12 response was examined among normal adult and patient sera using the phage plaque assay identical to the original immunoscreening procedure. Of 21
20 absorbed sera from allogeneic lung cancer patients, one (Lu22) reacted strongly with the Lu15-251 plaque at 1:1000 dilution, and another (Lu7) also reacted at 1:1000, but only weakly. Nineteen other lung cancer patient sera were non-reactive, nor were the sera from 16 healthy donors, 15 colon cancer, 5 breast cancer, 1 renal cancer, 1 prostate cancer, 1 esophageal cancer, and 1 melanoma patients.

25

Example 10: Expression analysis of additional cancer associated nucleic acids

The clone RING 3 was isolated from breast SEREX analysis as LONY-Br-5 (see above). The gene was identified as homologous to the "bromodomain testis" gene (BRDT; GenBank accession number AF019085). Analysis of related genes identified BRDT as a gene expressed only
30 in testis, which was then investigated by RT-PCR analysis as described above.

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The primers used to perform RT-PCR had the following sequences:

BRDT F1: CAAGAAAGGCACTCAACAG (bp 543-563 of BRDT)

BRDT R1: TTCACTACTTGCTTTAACTGC (bp 776-797 of BRDT)

The meiotic protein H1T (Histone 1 Testis; GenBank accession number M60094) was

5 identified through a literature search for meiotic proteins (testis specific expression).

The primers used to perform RT-PCR had the following sequences:

H1F1: TGCCGAACCTCTCTGTGTC (bp 116-135 of H1T)

H1R1: GCTTCGTGTAGATTAGGAATC (bp 344-366 of H1T)

10 Table 10: RT-PCR analysis

	<u>Normal Tissue</u>	<u>BRDT</u>	<u>H1T</u>
	mammary gland	-	-
	liver	-	-
15	small intestine	-	-
	brain	-	+/- (very weak)
	lung	-	-
	fetal brain	-	-
	placenta	+	+
20	kidney	-	-
	skeletal muscle	-	-
	pancreas	-	-
	adrenal gland	-	-
	heart	-	-
25	thymus	-	-
	uterus	-	-
	prostate	-	+/- (very weak)
	spleen	-	-
	Testis	+	+

30

	<u>Tumor Tissue</u>	<u>BRDT</u>	<u>H1T</u>
	Colon	0/6	0/6
35	Breast	0/6	6/6+
	Melanoma	0/12	3/12+
	Lung	8/26+	4/26+
	Renal	0/2	0/2
	Ovary	0/2	0/2
40	Esophageal	0/1	0/1

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Gastric	0/1	0/1
Bladder	0/2	0/2

Lung cancer specific expression of BRDT was observed (see table above). BRDT was
 5 expressed only in normal testis and possibly in placenta. The expression analysis of H1T revealed
 that all breast tumor samples (6 of 6) and ~30% lung cancers and melanoma tissue samples
 expressed H1T. H1T was expressed in normal testis and possibly in placenta and brain.

Example 11: allogeneic serotyping

10 To confirm the cancer associated expression of SEREX clones, allogenic sera screening of
 gastric cancer patients' sera was conducted. Sera from normal patients (gastritis) was used as a
 control for expression of the clones in non-gastric cancer. The screening procedure used was as
 described above for the SEREX screening, except for the absorption of anti-bacterial and
 anti-bacteriophage antibodies. The modifications were as follows.

15 Serum from a stomach cancer patient or a normal individual was diluted to 1:10 in TBS (Tris
 buffered saline; final volume 5 ml) and passed through a column (BIO-RAD Poly-Prep
 Chromatography Column, Hercules, CA, USA) containing 0.5 ml Sepharose-4B cross linked to E.
 coli Y1090 lysate and 0.5 ml Sepharose-4B cross linked to E. coli BNN97 (5 Prime 3 Prime, Inc,
 Boulder, CO, USA). After repeating the column chromatography 10 times, serum was then diluted
 20 to 1:100 in TBS containing 1% BSA and 0.02% sodium azide. To remove antibodies to bacteria and
 bacteriophages further, 10 ml absorbed serum was incubated overnight with a 82 mm nitrocellulose
 membrane on which XL-1 Blue MRF' bacteria and lambda ZAP Express phages (Stratagene, La
 Jolla, CA USA) were immobilized. The serum was stored at - 80°C until use. For allogeneic
 typing, an equal numbers of positive phage and negative phage were mixed and plated and processed
 25 by the standard SEREX screening procedure.

The results of the allogenic screening experiments follow:

Table 11: Allogenic Sera Screening of SEREX Sequences from Gastric Patients

	Sequence		Isolated in Serex Patients	Allogenic Serotyping Gastric Cancer Sera	Allogenic Serotyping Normal Sera
	Gene/Clone	Number			
	RPB-J H-2K binding factor		SM1	6/12	6/16
5	Telomeric repeat binding protein		SM1	1/12	0/16
	Ser/Thr protein kinase		SM1	1/12	0/16
	SRY interacting protein-1		SM1	2/12	1/16
	Sterol carrier protein X		SM1	2/12	0/16
10	Archain		SM1	1/12	1/16
	HEM-1		SM1	2/12	1/16
	Id-1 helix-loop-helix protein		SM1	1/12	0/16
15	helix-loop-helix transcription factor		SM1	1/12	0/16
	Follistatin related precursor protein		SM1,CK, KM	6/12	0/16
	Translation initiation factor eIF-4gamma		SM1,SS1, KM	5/12	2/16
20	M phase phosphoprotein I		SM1,SS1	8/12	5/16
	Lysal tRNA synthase		SM1	1/12	0/16
	Gelsolin		SM1	4/12	0/16
	Zinc finger protein		SM1	1/12	1/16
	Goliath		SM1	2/12	1/16
25	zhx-1		SM1	1/12	1/16
	SG24		SM1,SS1, KM	5/12	0/16
	SG132		SM1	3/12	0/16
	S553		SM1	7/12	7/16
	S134		SM1	3/12	0/16
30	S328		SM1	2/12	1/16
	S365		SM1, KM	2/12	0/16

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	FKBP25		KM, SS1	5/12	0/16
	Pros-27		KM, CK	3/12	1/16
	BS4		KM	1/12	1/16
	GnRH-II		KM	1/12	0/16
5	CTBP		KM	1/12	0/16
	ETF		KM	3/12	1/16
	KIAA0438		KM	1/12	5/16
	KIAA0367		KM	4/12	3/16
	APK1		KM	2/12	0/16
10	IPP		KM	1/12	0/16
	Tropomyosin		KM	1/12	0/16
	p63		KM	1/12	0/16
	KIAA0181		KM	1/12	0/16
	KIAA0349		KM	1/12	0/16
15	RPB1		KM	5/12	9/15
	PPIM		KM	1/12	-
	EB virus		KM	3/12	-
	G.KM073		KM	6/12	-
	G.KM403		KM	1/12	-
20	KM192		KM	1/12	-
	KM294		KM	1/12	-
	KM362		KM	1/12	-
	KM031		KM	1/12	-
	KM081		KM	3/12	-
25	KM201		KM	1/12	-
	KM1496		KM	1/12	-
	KM334		KM	1/12	-
	KM313		KM	1/12	-
	E-cad/Y		CK	1/12	0/16
30	IPBP		SS1	1/4	-
	OS-9		SS1	1/4	-

Kinesin light chain		SS1	1/4	-
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The screening results shown above confirm the association of the SEREX clones with cancer. There is a higher correlation of cancer and the expression of certain clones, in particular, follistatin related precursor protein, the translation initiation factor eIF-4gamma, the unknown sequence SG24, the FK506-binding protein 25, and the unknown sequence G.KM073. These clones are well suited to serve as diagnostic indicators of disease and as targets for therapeutics (e.g., vaccine compositions) development.

10 **Example 12: Preparation of recombinant cancer associated antigens**

To facilitate screening of patients' sera for antibodies reactive with cancer associated antigens, for example by ELISA, recombinant proteins are prepared according to standard procedures. In one method, the clones encoding cancer associated antigens are subcloned into a baculovirus expression vector, and the recombinant expression vectors are introduced into appropriate insect cells. Baculovirus/insect cloning systems are preferred because post-translational modifications are carried out in the insect cells. Another preferred eukaryotic system is the *Drosophila* Expression System from Invitrogen. Clones which express high amounts of the recombinant protein are selected and used to produce the recombinant proteins. The recombinant proteins are tested for antibody recognition using serum from the patient which was used to isolated the particular clone, or in the case of cancer associated antigens recognized by allogeneic sera, e.g. certain breast cancer and gastric cancer associated antigens, by the sera from any of the patients used to isolate the clones or sera which recognize the clones' gene products.

Alternatively, the cancer associated antigen clones are inserted into a prokaryotic expression vector for production of recombinant proteins in bacteria. Other systems, including yeast expression systems and mammalian cell culture systems also can be used.

Example 13: Preparation of antibodies to cancer associated antigens

The recombinant cancer associated antigens produced as in Example 12 above are used to generate polyclonal antisera and monoclonal antibodies according to standard procedures. The antisera and antibodies so produced are tested for correct recognition of the cancer associated

antigens by using the antisera/antibodies in assays of cell extracts of patients known to express the particular cancer associated antigen (e.g. an ELISA assay). These antibodies can be used for experimental purposes (e.g. localization of the cancer associated antigens, immunoprecipitations, Western blots, etc.) as well as diagnostic purposes (e.g., testing extracts of tissue biopsies, testing for the presence of cancer associated antigens).

Example 14: Expression of cancer associated antigens in cancers of similar and different origin.

The expression of one or more of the cancer associated antigens is tested in a range of tumor samples to determine which, if any, other malignancies should be diagnosed and/or treated by the methods described herein. Tumor cell lines and tumor samples are tested for cancer associated antigen expression, preferably by RT-PCR according to standard procedures. Northern blots also are used to test the expression of the cancer associated antigens. Antibody based assays, such as ELISA and western blot, also can be used to determine protein expression. A preferred method of testing expression of cancer associated antigens (in other cancers and in additional same type cancer patients) is allogeneic serotyping using a modified SEREX protocol (as described above for gastric clones).

In all of the foregoing, extracts from the tumors of patients who provided sera for the initial isolation of the cancer associated antigens are used as positive controls. The cells containing recombinant expression vectors described in the Examples above also can be used as positive controls.

The results generated from the foregoing experiments provide panels of multiple cancer associated nucleic acids and/or polypeptides for use in diagnostic (e.g. determining the existence of cancer, determining the prognosis of a patient undergoing therapy, etc.) and therapeutic methods (e.g., vaccine composition, etc.).

Example 15: HLA typing of patients positive for cancer associated antigen

To determine which HLA molecules present peptides derived from the cancer associated antigens, cells of the patients which express the cancer associated antigens are HLA typed. Peripheral blood lymphocytes are taken from the patient and typed for HLA class I or class II, as

well as for the particular subtype of class I or class II. Tumor biopsy samples also can be used for typing. HLA typing can be carried out by any of the standard methods in the art of clinical immunology, such as by recognition by specific monoclonal antibodies, or by HLA allele-specific PCR (e.g. as described in WO97/31126).

Example 16: Characterization of breast cancer associated antigen peptides presented by MHC class I and class II molecules.

Antigens which provoke an antibody response in a subject may also provoke a cell-mediated immune response. Cells process proteins into peptides for presentation on MHC class I or class II molecules on the cell surface for immune surveillance. Peptides presented by certain MHC/HLA molecules generally conform to motifs. These motifs are known in some cases, and can be used to screen the breast cancer associated antigens for the presence of potential class I and/or class II peptides. Summaries of class I and class II motifs have been published (e.g., Rammensee et al., *Immunogenetics* 41:178-228, 1995). Based on the results of experiments such as those described in Example 15, the HLA types which present the individual breast cancer associated antigens are known. Motifs of peptides presented by these HLA molecules thus are preferentially searched.

One also can search for class I and class II motifs using computer algorithms. For example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (see, e.g., Parker et al., *J. Immunol.* 152:163, 1994; D'Amato et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health World Wide Web site at URL <http://bimas.dcrt.nih.gov>. Methods for determining HLA class II peptides and making substitutions thereto are also known (e.g. Strominger and Wucherpfennig (PCT/US96/03182)).

The lung cancer SEREX clone polypeptides NY-LU-12 and NY-LU-12B (variant B), SEQ ID NOs: 708 and 710, were subjected to the HLA binding peptide analysis described above, using the NIH website, to identify HLA binding peptides for several common HLA molecules (HLA-A1, A2, A3, A24, B7, B44, and B52). The results are listed below in Table 12.

Table 12: Identification of HLA binding peptides in lung SEREX clones

- 85 -

		amino acids of	
HLA	peptide	NY-LU-12 protein	SEQ ID NO
5	A1 NVEE-HSFSY	67 - 75	713
	PVDP-NILDY	287 - 295	714
	DTDY-RSMEY	398 - 406	715
10	A2 SLLE-DAIGC	506 - 514	716
	TLMI-QDKEV	521 - 529	717
	YVSSLDFWYC	533 - 542	718
	VIVEVLEPYV	671 - 680	719
	KLTD-WNKLA	948 - 956	720
	QLSDLHKQNL	975 - 984	721
	KQSEQELAYL	991 - 1000	722
	KLVDKEDIDT	1042 - 1051	723
15	VMFA-RYKEL	1114 - 1122	724
20	A3 QMFG-YGQSK	417 - 425	725
	GMPVKNLQLK	481 - 490	726
	GLPE-EEEEIK	823 - 831	727
	LLCRRQFPNK	958 - 967	728
25	A24 EYRD-VDHRL	405 - 413	729
	GYVC-VEFSL	499 - 507	730
	DYGY-VCVEF	497 - 505	731
	WYCKRCKANI	540 - 549	732
	TYPQPQKTSI	574 - 583	733
	IYRSTPPEVI	663 - 672	734
	HYYQ-GKKYF	754 - 762	735
30	VYVP-QDPGL	816 - 824	736
	B7 WNRDYPPPPPL	26 - 35	737
	MPPV-DPNIL	285 - 293	738
	TARD-AQRDL	432 - 440	739
35	GPSEEKPSRL	448 - 457	740
	TPPEVIVEVL	667 - 676	741
	RVMFARYKEL	1113 - 1122	742
40	B44 REMG-SCMEF	272 - 280	743
	EEQSSDAGLF	376 - 385	744
	KEYN-TGYDY	490 - 498	745
	TEAQELITY	566 - 575	746
	VEALRVVKIL	710 - 719	747
	GEYG-GSDSY	906 - 914	748
	LERREREGKF	1000 - 1009	749

- 86 -

B52	RQDGESKTIM	650 - 659	750
	TPPEVIVEVL	667 - 676	751
	YGFIDLDSHV	701 - 710	752
	RQFP-NKEVL	962 - 970	753

5

NY-LU-12B (variant B)

A1	NVEE-HSFSY	121 - 129	754
10	PVDP-NILDY	341 - 349	755
	DTDY-RSMEY	452 - 460	756
A2	WQSA-RFYYL	41 - 49	757
	SLLE-DAIGC	560 - 568	758
15	TLMI-QDKEV	575 - 583	759
	YVSSLDWFYC	587 - 596	760
	VIVEVLEPYV	725 - 734	761
	KLTD-WNKLA	1002 - 1010	762
	QLSDLHKQNL	1029 - 1038	763
20	KQSEQELAYL	1045 - 1054	764
	KLVDKEDIDT	1096 - 1105	765
	VMFA-RYKEL	1168 - 1176	766
A3	QMFG-YGQSK	471 - 479	767
25	GMPVKNLQLK	535 - 544	768
	GLPE-EEEIK	877 - 885	769
	LLCRRQFPNK	1012 - 1021	770
A24	YYLN-ATDVL	47 - 55	771
30	FYYLNATDVL	46 - 55	772
	EYRD-VDHRL	459 - 467	773
	GYVC-VEFSL	553 - 561	774
	DYGY-VCVEF	551 - 559	775
	WYCKRCKANI	594 - 603	776
35	TYPQPQKTSI	628 - 637	777
	IYRSTPPEVI	717 - 726	778
	HYYQ-GKKYF	808 - 816	779
	VYVP-QDPGL	870 - 878	780
40	B7 WNRDYPPPPL	80 - 89	781
	MPPV-DPNIL	339 - 347	782
	TARD-AQRDL	486 - 494	783
	GPSEEKPSRL	502 - 511	784
	TPPEVIVEVL	721 - 730	785
45	RVMFARYKEL	1167 - 1176	786

- 87 -

5	B44	SEAWSSNEKF	59 - 68	787
		REMG-SCMEF	326 - 334	788
		EEQSSDAGLF	430 - 439	789
		KEYN-TGYDY	544 - 552	790
		TEAKQELITY	620 - 629	791
		VEALRVVKIL	764 - 773	792
		GEYG-GDSY	960 - 968	793
10	B52	LERREREGKF	1054 - 1063	794
		RQDGESKTIM	704 - 713	795
		TPPEVIVEVL	721 - 730	796
		YGFIDLSHV	755 - 764	797
		RQFP-NKEVL	1016 - 1024	798

- 15 Likewise, other clones identified herein can be analyzed for the presence of candidate HLA binding peptides using no more than routine experimentation.

Example 17: Identification of the portion of a cancer associated polypeptide encoding an antigen

- 20 To determine if the cancer associated antigens isolated as described above can provoke a cytolytic T lymphocyte response, the following method is performed. CTL clones are generated by stimulating the peripheral blood lymphocytes (PBLs) of a patient with autologous normal cells transfected with one of the clones encoding a cancer associated antigen polypeptide or with irradiated PBLs loaded with synthetic peptides corresponding to the putative protein and matching
- 25 the consensus for the appropriate HLA class I molecule (as described above) to localize an antigenic peptide within the cancer associated antigen clone (*see, e.g., Knuth et al., Proc. Natl. Acad. Sci. USA* 81:3511-3515, 1984; van der Bruggen et al., *Eur. J. Immunol.* 24:3038-3043, 1994). These CTL clones are screened for specificity against COS cells transfected with the cancer associated antigen clone and autologous HLA alleles as described by Brichard et al. (*Eur. J. Immunol.* 26:224-230,
- 30 1996). CTL recognition of a cancer associated antigen is determined by measuring release of TNF from the cytolytic T lymphocyte or by ⁵¹Cr release assay (Herin et al., *Int. J. Cancer* 39:390-396, 1987). If a CTL clone specifically recognizes a transfected COS cell, then shorter fragments of the cancer associated antigen clone transfected in that COS cell are tested to identify the region of the gene that encodes the peptide. Fragments of the cancer associated antigen clone are prepared by

exonuclease III digestion or other standard molecular biology methods. Synthetic peptides are prepared to confirm the exact sequence of the antigen.

Optionally, shorter fragments of cancer associated antigen cDNAs are generated by PCR. Shorter fragments are used to provoke TNF release or ^{51}Cr release as above.

5 Synthetic peptides corresponding to portions of the shortest fragment of the cancer associated antigen clone which provokes TNF release are prepared. Progressively shorter peptides are synthesized to determine the optimal cancer associated antigen tumor rejection antigen peptides for a given HLA molecule.

10 A similar method is performed to determine if the cancer associated antigen contains one or more HLA class II peptides recognized by CTLs. One can search the sequence of the cancer associated antigen polypeptides for HLA class II motifs as described above. In contrast to class I peptides, class II peptides are presented by a limited number of cell types. Thus for these experiments, dendritic cells or B cell clones which express HLA class II molecules preferably are used.

15

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

20 All references disclosed herein are incorporated by reference in their entirety.

We claim:

AA683066, AA446279, AA332363, T09328, R80982, AA069486, AA410842, C18527,
AA293033, H12730, AA287344, AA029631, R83063, AA061290, AA185993, AA880204,
AA499308, AA183172, AA242360, AA792388, AA175587, AA277140, AA880395,
AA899046, AA859550, C35363, C35702, C32682, F14140, T18049, C83149, T45787,
5 AA924623, D47525, Z30723, AA897884, AA042465, AI009871, AA875198, C83016.

SEQ ID NO. 7:

10 X74116, AL022148, AC004548, AC000352, Z11664, Z78065, Z74028, AE000163, AE000750,
X74229, D90700, R59414, AA176708, W02568, AA354664, R43017, AA973553, F10008,
D61827, AA826300, Z41398, T77572, R40189, H85823, W86541, T17276, AA679337,
X83357, AA184845, AA416260, AA475603, AA388692, AA764445, AA388689, AA219880,
AA290020, AA388507, AA387267, C86741, AA414436, AA451259, AA413796, AA930916,
15 AA793690, AA619447, AA062257, AA522026, AA816247, AA892032, AA817702, H33461,
AA925507, AA849449, AI029236, AA247069, AA697975, AA882508, AA893258, AA698410,
AA891755, AA698227, AA892782, AA899328, T04373, AA567522, AA698408, AA202615,
AA141016, AA697974, AA697998, C61176, D69691, AI030205, AA586054.

20

SEQ ID NO. 8:

U08218, L38909, Y11095, AC002431, Z23069, S77418, U39060, L38580, AF053367, Z36506,
M18102, J03624, AA102264, AA730686, H47968, AA357170, AA130974, C06054,
25 AA626429, F00559, AA604528, AA383348, AA040127, N84965, D54884, D54883, R94309,
AA373184, AA128091, W68194, H58283, R76347, AA343938, AA305144, AI049611,
AA384516, AA720553, N57395, R97387, D52674, AA169408, H66293, AA456362, T74258,
AA730145, AA101952, N86388, AA355003, AA307640, AA385679, AA354542, N99075,
N83528, H87678, R84494, R35720, AA670111, AA186452, W32370, D55392, W05161,
30 AA641280, AA120503, C77063, AA146393, AA620177, AA509478, C77481, AA427148,
AA474531, W83304, AA207424, AA763436, AA958473, AA799243, AA493061, AA967792,
AA145256, AA089338, AA756259, AA789767, AA980112, AA866640, AA914516,
AA821675, AA466770, AA015387, AA816036, AA246546, AA941789, AA955779,
AA997768, AA997534, T43805, AA956150, T18836, T23333, AA525666, T18787, AA800483,
35 C64685, AA851367, C91730, AA143899, T23399.

SEQ ID NO. 9:

40 AP000056, U43491, Z74919, L81498, Z94054, AC002503, L81499, AA740188, AA630241,
AA974724, AA806907, N88859, N98242, H12649, R06485, R06511, AA546258, C76846,
AA208416, AA959219, AA276381, W10055, AA462844, AA444278, W13447, W97802,
AA542324, AA137880, AA269331, AA175695, W59029, AA003372, AA146233, AI045761,
C93154, C94084, C94208, D68027, C12780, AA687005, AA080598, C12876, C12390,
45 AA848674, AA924440, T15031, AA451569, H35524.

SEQ ID NO. 10:

U25640, AA127328, H24207, H08275, AA283063, AA826096, AA417382, AA464874, W05562, AA453370, N51211, AA495859, R33871, H00927, AA623997, AA220442, AA178568, AA605493, AA394557, AA956116, AA999037, AA818246.

5

SEQ ID NO. 11:

- AB001740, AF039956, AA581972, AA594539, AA236870, AA464410, AA237069, AA694199, AI038896, AA167314, AA577381, AA430117, N23143, R53610, W37647,
- 10 AA724229, AA313202, AA860618, W16866, AA134966, AA255556, AA305224, R50528, AA844913, W32042, W37383, AA908394, W93357, W31353, R55254, N79251, AA456077, AA477700, AA477701, AA989005, AA455580, N32722, N22935, R50622, AA135047, R51941, T34020, T30416, T32309, AA883332, W93445, AA166984, AA026749, T08224, AA255572, W03768, AA033670, W31880, AA772832, AA230974, AA511207, W82274,
- 15 AA230365, AA671085, AA511230, AA606681, AA023735, AA444535, W98518, W14718, W85455, AA980318, AA137525, AA035840, AA692158, AA007919, W48013, AA444534, AA981497, AA002566, W48089, W99869, AA960396, AA960580, AA145259, AA145683, AA388960, AA389941, AA266272, AA145124, AA267212, AA959753, AA407991, A175818, AA943997, AA899476, AA899756, AA943998, AA955446, AA012783, AA924956,
- 20 AA892219, AA955331, AI012225, AA891436.

SEQ ID NO. 12:

- 25 U72994, AC004022, AF043493, U43252, U43251, U81830, U58105, U68242, Z93242, AL009029, M29872, U12980, M81118, M30471, Z56258, AF012943, AC004080, AC002563, AF024533, AF002991, Z63771, AP000042, AF064863, U80017, AC004087, Z55235, L05920, AA508139, N90748, AA450240, AA948158, AA828938, AA165115, AI003312, AA436633, AA419100, AA743442, AA961990, AA885286, AA861312, T84801, AI040166, AA494115,
- 30 AA652324, AA181105, AA095541, R59256, AA503712, AA700364, AA603821, T60326, AA779097, AI023884, AA603785, H79111, W39526, AA506607, W94361, N66078, R01605, H22694, W86762, W99303, AA745640, AA678312, AA431870, W41927, AA874648, C92734, C23102, C53080, C91168, D65098, C32959, C50029, M80125, C34452, C83862, C24659, T21473, AA874720, C06696, W43071, AI043300, C53907.

35

SEQ ID NO. 13:

- X94232, U90437, AC003052, U59809, AC004001, M95396, Z67884, X77486, U70051,
- 40 X14805, AF022976, Z83823, X77485, J04171, AF036007, U05768, U88315, Z98048, AF036009, AC005179, U41277, U32517, AE001138, D64060, M84387, H29022, AA814221, N26314, AA935912, AA873506, AA608576, AA453605, AA232674, Z38725, AA772022, AA025212, AA318330, R48115, AA234084, H18508, N64543, AA970508, R36933, AA306944, H49559, AA325555, H85834, H89988, AA343974, AA648643, H65664, T62713,
- 45 H16554, N21122, AA351037, AA484621, AA221492, AA259314, C76383, C76336, AA607924, C76394, AA408562, AA921258, AI006352, W41405, AA153317, AA015435, AA027405, AA794066, AA498038, AA184222, AI011068, AA859614, AA899776, AA955080, AA799674, AA849652, AI009788, AA900928, AI007950, AA109392, AA753592, U92780, AA957632, AA567950, AI009495.

SEQ ID NO. 14:

AC000075, U66140, R14195, AA220229, T31199, R19104, R19148, Z46126, AA417619,
5 Z45284, H14105, R84666, AA090321, AA350108, W52840, R48497, R13097, T66255,
W44467, AA247676, AA198489, AA388175, AA261453, AA237111, AA790730, AA162394,
AA816498, AI013729, AA684961, AA979759.

10 SEQ ID NO. 15:

AF069301, D10651, U11419, U11287, M91562, U90278, U72724, X57855, X79424, M16512,
M64542, Z14152, AF016667, L01488, Z75955, AF024504, M13968, W67775, AA934587,
AA617696, AA913577, AA628682, W74527, AA969876, AA995606, AA622402, AA027090,
15 AA620556, AA085733, AA187157, AI031865, AA972318, AA897169, W79046, AA531124,
AA733183, T90909, Z25096, AA721771, AA115089, T49643, R00622, N93780, R00626,
AA365494, T71475, N74066, AA027130, T83325, AA115569, AA658299, T55344, T83700,
AA426250, AA393863, AA282967, R08138, AI000112, AA807574, AA077926, AA397527,
W87761, AA243026, R56368, H16371, AA958697, AA003997, AA008542, AA036229,
20 AA397074, AA250467, AA260498, AA968175, AA253686, AA727785, AI019478, AA474978,
AA543461, AA990281, AA245791, AA617042, AA015355, AA983015, AA982200,
AA120064, AA462778, AA242574, AA986993, AA986911, AA882490, AA223057,
AA543989, W65528, AA848318, AA874979, AA800547, AA945302, AA140994, AA991110,
AA851120.

25

SEQ ID NO. 16:

Z68106, X14199, M14872, Z63497, M31670, AC002123, Z63498, AA280070, AA215687,
30 H93207, AA070367, W95534, AA682436, AA741066, AA173269, AA641255, AA215688,
AA724798, N23259, AA442155, AA634563, AA074699, AA642322, AA861347, AA283655,
AI002587, W95419, AA357042, AA761253, AA197191, T54480, AA133029, AA378991,
AA114599, AA219925, AA174327, AA003800, C86661, AA990433, AA277014, AA445101,
AA671205, AI036728, AA241221, AA213304, AI035350, W08919, W36663, AA061406,
35 AA144736, AA240583, AI006563, AA980152, AA250075, AA088967, W17488, AA098269,
W10200, AA543712, AA755434, AI012680, AA820868, AA949519, AA391130, AA202576,
AA979150, AA012391, AA539472.

40 SEQ ID NO. 17:

J03592, M24103, AB009386, U44832, J02966, M24102, U27316, U10404, X70847, D12771,
D12770, J02683, J03591, U27315, M76669, U39779, M13783, J04982, X74510, X61667,
M57424, L78810, AC004000, Z75206, U68723, Z75207, AF009661, X53264, J03320, U66060,
45 AB011800, M77194, AE000021, L07268, AE000936, U03115, AF009663, AA582128,
AA916851, AA576667, AA915921, AA916853, N58735, AA428106, AA427849, AI024255,
H69807, H11315, N36980, H69597, AA826334, W05080, N37044, AA385873, N48222,
AA394173, AA837522, AI002511, AA292870, T96300, AA360716, AA379604, AA862844,
AA430455, AA479859, AA133899, AA669954, H92542, AA095298, AA995794, AI003667,

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SEQ ID NO. 20:

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SEQ ID NO. 21:

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SEQ ID NO. 22:

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SEQ ID NO. 23:

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35 SEQ ID NO. 28:

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5 SEQ ID NO. 29:

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- 10 AA323006, AA451780, T09445, R55858, AA324456, R87202, F11317, T30876, AA322117, AA357101, AA853747, AA325651, AA683394, W69297, H46499, AA055270, AA350932, H14250, AA024634, AA234283, L44408, AA604064, N55150, AA462547, AA146273, AA789450, AA873999, AA791509, W64849, W85596, AA444524, AA572240, AA032529, AA469889, R75180, W53226, AA020101, AA762779, AA869090, R74897, AA238408,
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SEQ ID NO. 31:

- X17644, AC002310, U95742, L37045, Z92835, L38828, L07843, X56910, AF025468, X62379,
- 40 X53599, X73911, X57331, U25851, AC004217, AA488455, AA112360, AA085969, W39758, AA450255, AA385764, AA306361, F08788, AA133458, AA331334, AA357236, N83925, AA319543, AA907882, AA295194, AA780612, AA805179, AA091629, AA233394, T52577, AA352655, AA211401, AA223759, AA187286, T51341, R66786, H17719, T08767, AA865254, AA761172, AA219613, AA169748, AA761180, AA878125, M62053, H97773,
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SEQ ID NO. 32:

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SEQ ID NO. 105:

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SEQ ID NO. 109:

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SEQ ID NO. 111:

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SEQ ID NO. 113:

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SEQ ID NO. 115:

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SEQ ID NO. 117:

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SEQ ID NO. 119:

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SEQ ID NO. 121:

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SEQ ID NO. 123:

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SEQ ID NO. 125:

U63333, AF035625, AF055320, AF032984.

SEQ ID NO. 127:

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SEQ ID NO. 129:

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SEQ ID NO. 131:

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SEQ ID NO. 135:

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SEQ ID NO. 137:

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SEQ ID NO. 141:

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SEQ ID NO. 143:

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SEQ ID NO. 145:

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Z69030, L42375, U37352, D26445, U38192, U38191, U37770, U38190, U37353, U59418, L76702.

45 SEQ ID NO. 147:

L07872, L34544, L34543, X17459, S63463, M81871, L08904, U60093, U60094, L07873, L07874.

SEQ ID NO. 149:

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SEQ ID NO. 151:

M13451, X03445, X03444, M13452, X66870, X76297, X14170, X99257, D14850, D13181, L12399.

15

SEQ ID NO. 153:

U28918, U17714, X82021, Z98048, D17265, D17092, Z82022, L04270.

20

SEQ ID NO. 155:

X54859, Z86000, AC003043, X77738, X77737, L35930, AC003084, AC000111, M89651, 25 AP000031, U67588, X03991, AC004660, AL010261, V01515, M86251, L29376, Z71417, L78442, U00921, AC004692, AC003698, AE000742, Z49128, Z73417, Z71418, AA424638, AA442084, AA805748, AA835489, AA713576, AA502343, AA765949, AA812332, AA831755, AA417718, AA776946, AA152295, AA731660, R48791, AA150237, N51650, N52616, N52586, AA533556, AA305755, AA760877, AA729913, AA731659, AA910594, 30 AA904521, AA372550, R48898, N50390, R08712, H83343, AA417867, AA090407, AA009846, AA927286, AA678135, AI033148, AI041408, AA235113, AA398662, M62215, W27276, AA885767, AA460155, AA742433, R19908, AA040696, AA555240, AA043160, AA292844, R53160, AA536080, N70013, N35921, N70096, AA277029, AA560610, AI046716, AA237153, W15784, AA547132, AA231089, AA170968, D46090, C61892, 35 C64408, D34777, D35175, D35914, D37381, AA559708, D37143, C60784, AI008855, AI021808, AI009216, D68214, AA220863, D70434.

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SEQ ID NO. 157:

U43195, U58512, U61266, D89493, U36909.

45

SEQ ID NO. 159:

AF069442, AF001295, M13820, M10081, AB010077, AA491075, AA446881, AA588390, AA479958, N20112, R86178, R97894, T64868, W68074, AA365195, AA928749, AI037069, AA882303, AA791693, AA822133, AI037224, AA404165, AI036575, AA499662, AA864136, AA561223, AA183703, AA647218, AA792208, W48100, D40621, AJ225487, AA294595,

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SEQ ID NO. 167:

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SEQ ID NO. 169:

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SEQ ID NO. 170:

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SEQ ID NO. 172:

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35 SEQ ID NO:265

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15 SEQ ID NO: 270

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SEQ ID NO: 277

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30 SEQ ID NO: 278

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- 10 AB002334, M73718, M27717, AC002067, Z49235, AC004740, AB011102, M37814, Z98744, D13641, AF000152, AC004015, U81556, U32326, Z78417, Z68316, AC004544, Z75539, S45406, AA884499, AA358171, AA476618, AA923299, N31318, AA767128, T16272, AA130639, AA122201, R81382, AI050868, AA548662, AA429467, AA376220, T85339, AA632310, W46587, N73476, H08150, Z30154, AI038648, AA969830, AA971607, 15 AA836443, AA653179, AA578086, H99657, AA833921, AA807902, W67693, D55907, AA187521, AI017410, AA814462, AA214503, AA209422, W63794, N28354, H03910, AI015056, AA888526, AA604383, AA586610, AI052722, N31612, AI027159, AA888334, AI027906, AA179400, AA922771, AA706343, AA682625, AA525897, AA485217, AA306471, AA282221, N29656, H27823, R13913, F05001, Z19816, AA782560, H23416, AA581660, 20 AA069521, H22320, R62283, AA778382, AA226827, AA035607, W37761, N27024, R63378, AA806971, AA639817, AA188936, N25005, AI025572, AA490953, AA490879, AA228362, AA182881, W40267, N21523, H16846, T66803, AA858168, H81767, N22843, AA657613, H73918, N20117, N24401, AA057815, AA504563, AA523596, N20388, AA939766, AA794705, AA863940, AA123123, AA217673, AA096644, AA855480, AA474154, C89108, 25 AA162338, AA389552, AA168055, W14081, AA895478, L11835, AA517590, AA543798, AA145689, Z36404, AI037527, AA174418, T37837, T38875, C68354, F14422, C49410, C47200, C42796, C42668, AA660084, D75577, AA113533, AA228253.

30 SEQ ID NO: 280

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SEQ ID NO: 281

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35 SEQ ID NO: 316

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10 C94126, D34450, AA191793, C09440, C65405, AA851621, C65618, AI045939, C84167,
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20 SEQ ID NO: 507

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35 SEQ ID NO: 508

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SEQ ID NO: 513

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45 SEQ ID NO: 514

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5 SEQ ID NO: 519

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 T08932, T08932 EST06824 Homo sapiens cDNA clone HIBBM46 5' end. 537 e-150
 AA488258, AA488258 ad08f07.r1 Soares NbHFB Homo sapiens cDNA ... 533 e-149
 T19350, T19350 h03012t Testis 1 Homo sapiens cDNA clone h0301... 496 e-138
 H87681, H87681 yw15e04.r1 Homo sapiens cDNA clone 252318 5'. 490 e-136

 H81522, H81522 yu61h08.r1 Homo sapiens cDNA clone 230655 5'. 466 e-129
 T49620, T49620 ya77g03.s1 Homo sapiens cDNA clone 67732 3'. 452 e-125
 R14363, R14363 yf80d10.r1 Homo sapiens cDNA clone 28995 5' si... 446 e-123
 AA211476, AA211476 zp75h11.s1 Stratagene HeLa cell s3 937216 ... 430 e-118
 N46636, N46636 yy48a09.r1 Homo sapiens cDNA clone 276760 5'. 424 e-116
 Z17358, HSDHII065 H. sapiens partial cDNA sequence; clone HL... 416 e-114
 R40737, R40737 yf80d10.s1 Homo sapiens cDNA clone 28995 3'. 400 e-109
 AA410278, AA410278 zv32f05.r1 Soares ovary tumor NbHOT Homo s... 383 e-104
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 N34907, N34907 yy48a09.s1 Homo sapiens cDNA clone 276760 3'. 371 e-100
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 R31593, R31593 yh76f03.s1 Homo sapiens cDNA clone 135677 3'. 317 e-84
 AA984591, AA984591 am89d10.s1 Stratagene schizo brain S11 Hom... 313 e-83
 AA338831, AA338831 EST43831 Fetal brain I Homo sapiens cDNA 5... 238 e-60
 T07305, T07305 EST05194 Homo sapiens cDNA clone HFBEG86. 230 e-58
 AA159942, AA159942 zo79c05.r1 Stratagene pancreas (#937208) H... 204 e-50
 R57355, R57355 F2878 Fetal heart Homo sapiens cDNA clone F287... 196 e-48
 AA729237, AA729237 nx35c08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 192 e-46
 AA877709, AA877709 nr09g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 172 e-41
 AA969195, AA969195 op51c03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 107 e-21
 AA327432, AA327432 EST30768 Colon I Homo sapiens cDNA 5' end 80 e-12
 AA854147, AA854147 aj71f01.s1 Soares parathyroid tumor NbHPA ... 74 e-11
 AA983156, AA983156 oq51g09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 66 e-08
 H09529, H09529 yl95h10.s1 Homo sapiens cDNA clone 46129 3'. 66 e-08
 AA286791, AA286791 zs54h07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 66 e-08
 W04418, W04418 za43c06.r1 Soares fetal liver spleen 1NFLS Hom... 58 e-06
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 AA706183, AA706183 ag93e01.s1 Stratagene hNT neuron (#937233)... 40 e-02
 AA393069, AA393069 zt69e09.r1 Soares testis NHT Homo sapiens ... 40 e-02
 AA371600, AA371600 EST83650 Pituitary gland, subtracted (prol... 40 e-02
 AA977820, AA977820 oq78a09.s1 NCI_CGAP_Kid6 Homo sapiens cDNA... 38 e-02
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 AA584615, AA584615 no08g12.s1 NCI_CGAP_Phe1 Homo sapiens cDNA... 38 e-02
 AA229827, AA229827 nc48c04.r1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 38 e-02
 W21398, W21398 zb50a11.r1 Soares fetal lung NbHL19W Homo sapi... 38 e-02

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AA869501, AA869501 vq08g11.r1 Barstead stromal cell line MPLR... 833 0.0
AA221749, AA221749 my28g01.r1 Barstead mouse pooled organs MP... 789 0.0
AA271363, AA271363 va71d08.r1 Soares mouse 3NME12 5 Mus muscu... 781 0.0
AA544727, AA544727 vk35d01.r1 Soares mouse mammary gland NbMM... 773 0.0
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AA153324, AA153324 ms61e11.r1 Stratagene mouse embryonic carc... 617 e-175
AA673899, AA673899 vo86g07.r1 Barstead mouse irradiated colon... 583 e-164
AA797488, AA797488 vw28a05.r1 Soares mouse mammary gland NbMM... 519 c-145
W71831, W71831 me45b06.r1 Soares mouse embryo NbME13.5 14.5 M... 472 e-131
AA213358, AA213358 mu74e04.r1 Stratagene mouse embryonic carc... 444 e-123
W75918, W75918 me82f05.r1 Soares mouse embryo NbME13.5 14.5 M... 444 e-123
AA038141, AA038141 mi81e05.r1 Soares mouse p3NMF19.5 Mus musc... 359 3e-97
AA038288, AA038288 mi83b04.r1 Soares mouse p3NMF19.5 Mus musc... 323 1e-86
AA017742, AA017742 mh40c03.r1 Soares mouse placenta 4NbMP13.5... 297 8e-79
AA771297, AA771297 vt17g04.r1 Barstead mouse myotubes MPLRB5 ... 297 8e-79
AA105228, AA105228 mp45b11.r1 Barstead MPLRB1 Mus musculus cD... 295 3e-78
AA068340, AA068340 mm53f01.r1 Stratagene mouse embryonic carc... 293 1e-77
AA612347, AA612347 vo05c08.r1 Stratagene mouse skin (#937313)... 281 5e-74
AA038300, AA038300 mi83d04.r1 Soares mouse p3NMF19.5 Mus musc... 270 2e-70
AA500952, AA500952 vg01h04.r1 Soares mouse NbMH Mus musculus ... 252 4e-65
W08368, W08368 mb41f07.r1 Soares mouse p3NMF19.5 Mus musculus... 212 4e-53
AA052280, AA052280 ma82e12.r1 Soares mouse p3NMF19.5 Mus musc... 123 3e-26
AA064466, AA064466 ml49c05.r1 Stratagene mouse testis (#93730... 107 2e-21
AA271566, AA271566 vb74b09.r1 Soares mouse 3NME12 5 Mus muscu... 60 3e-07
C86222, C86222 Mus musculus fertilized egg cDNA 3'-end seque... 42 0.078
W83632, W83632 mf31a04.r1 Soares mouse embryo NbME13.5 14.5 M... 42 0.078
AA423627, AA423627 ve80f01.r1 Soares mouse mammary gland NbMM... 42 0.078
AA036586, AA036586 mi41h08.r1 Soares mouse embryo NbME13.5 14... 42 0.078
AA207496, AA207496 mv78g02.r1 GuayWoodford Beier mouse kidney... 42 0.078
AA120433, AA120433 mp82h11.r1 Soares 2NbMT Mus musculus cDNA ... 42 0.078
W08185, W08185 mb42h02.r1 Soares mouse p3NMF19.5 Mus musculus... 38 1.2
AA065563, AA065563 ml71b06.r1 Stratagene mouse kidney (#93731... 38 1.2
AA288756, AA288756 mr46h07.r1 Life Tech mouse embryo 15 5dpc ... 38 1.2
AA119334, AA119334 mp80e10.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
AA163051, AA163051 ms24a10.r1 Stratagene mouse skin (#937313)... 38 1.2
N28074, N28074 MDB1392R Mouse brain, Stratagene Mus musculus ... 38 1.2
AA288757, AA288757 mr46h08.r1 Life Tech mouse embryo 15 5dpc ... 38 1.2
AA122857, AA122857 mq06a02.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
AA617519, AA617519 vj77d05.r1 Knowles Solter mouse blastocyst... 38 1.2

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 AI047837, AI047837 ud64c11.x1 Sugano mouse liver mlia Mus mus... 38 1.2
 AA840310, AA840310 vw91a10.r1 Stratagene mouse skin (#937313)... 36 4.8
 AA986428, AA986428 ue13b04.x1 Sugano mouse embryo mewa Mus mu... 36 4.8
 W47677, W47677 mc89g07.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
 AA057996, AA057996 mj56c10.r1 Soares mouse embryo NbME13.5 14... 36 4.8
 AA183858, AA183858 mo95h01.r1 Stratagene mouse testis (#93730... 36 4.8
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 W41067, W41067 mc39a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.8
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 AA000433, AA000433 me76e09.r1 Soares mouse embryo NbME13.5 14... 36 4.8
 AA023983, AA023983 mh94a07.r1 Soares mouse placenta 4NbMP13.5... 36 4.8
 AA013726, AA013726 mh12c09.r1 Soares mouse placenta 4NbMP13.5... 36 4.8
 AA274648, AA274648 vb08c01.r1 Soares mouse NML Mus musculus c... 36 4.8
 AA140347, AA140347 mq89g06.r1 Stratagene mouse heart (#937316... 36 4.8
 AA499377, AA499377 vi89c07.r1 Stratagene mouse heart (#937316... 36 4.8
 C88747, C88747 Mus musculus early blastocyst cDNA, clone 01B... 36 4.8
 AA726125, AA726125 vu88c06.r1 Stratagene mouse skin (#937313)... 36 4.8
 AA760311, AA760311 vv71c12.r1 Stratagene mouse skin (#937313)... 36 4.8
 AA763007, AA763007 vw60b05.r1 Soares mouse mammary gland NMLM... 36 4.8
 AA929878, AA929878 vz44d03.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
 W59064, W59064 md67e10.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
 AA103519, AA103519 mo24b12.r1 Life Tech mouse embryo 13 5dpc ... 36 4.8
 AA222310, AA222310 my14d08.r1 Barstead mouse heart MPLRB3 Mus... 36 4.8
 W83557, W83557 mf32d02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
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 W98818, W98818 mf94e06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
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 AA692113, AA692113 vt19d03.r1 Barstead mouse myotubes MPLRB5 ... 36 4.8
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 AA110893, AA110893 mm02b04.r1 Stratagene mouse kidney (#93731... 36 4.8

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 C71833, C71833 Rice cDNA, partial sequence (E0428_1A) 44 0.017
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 AA875699, AA875699 TENU0170 T.cruzi epimastigote normalized c... 42 0.069
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 C74504, C74504 Rice cDNA, partial sequence (E31753_1A) 40 0.27
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 AA246440, AA246440 LD05311.5prime LD Drosophila melanogaster ... 38 1.1
 AA801776, AA801776 GM12975.5prime GM Drosophila melanogaster ... 38 1.1
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 AA202696, AA202696 LD03182.5prime LD Drosophila melanogaster ... 38 1.1
 AA392367, AA392367 LD11287.5prime LD Drosophila melanogaster ... 38 1.1
 AA264629, AA264629 LD08245.5prime LD Drosophila melanogaster ... 38 1.1
 AA735318, AA735318 LD21104.5prime LD Drosophila melanogaster ... 38 1.1
 AA264558, AA264558 LD08333.5prime LD Drosophila melanogaster ... 38 1.1
 AA536476, AA536476 LD17106.5prime LD Drosophila Embryo Drosop... 38 1.1
 AA957774, AA957774 UI-R-E1-fv-f-04-0-UI.s1 UI-R-E1 Rattus nor... 38 1.1
 AA567991, AA567991 HL02092.5prime HL Drosophila melanogaster ... 38 1.1
 AA957876, AA957876 UI-R-E1-fv-f-04-0-UI.s2 UI-R-E1 Rattus nor... 38 1.1
 AA892488, AA892488 EST196291 Normalized rat kidney, Bento Soa... 38 1.1
 AA699001, AA699001 HL06668.5prime HL Drosophila melanogaster ... 36 4.3
 C19706, C19706 Rice cDNA, partial sequence (E10809_1A) 36 4.3
 D41773, RICS4574A Rice cDNA, partial sequence (S4574_2A). 36 4.3
 C40680, C40680 C.elegans cDNA clone yk247c4 : 5' end, single... 36 4.3
 AA698625, AA698625 HL05354.5prime HL Drosophila melanogaster ... 36 4.3
 C82819, C82819 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3
 D46016, RICS10393A Rice cDNA, partial sequence (S10393_3A). 36 4.3
 AA536314, AA536314 LD16858.5prime LD Drosophila melanogaster ... 36 4.3
 AA801012, AA801012 EST190509 Normalized rat muscle, Bento Soa... 36 4.3
 D46541, RICS11289A Rice cDNA, partial sequence (S11289_1A). 36 4.3
 D47315, RICS12612A Rice cDNA, partial sequence (S12612_1A). 36 4.3
 AA735857, AA735857 GM09977.5prime GM Drosophila melanogaster ... 36 4.3
 AA753921, AA753921 97BS0370 Rice Immature Seed Lambda ZAPII c... 36 4.3
 D47243, RICS12505A Rice cDNA, partial sequence (S12505_1A). 36 4.3
 AA978395, AA978395 LD28411.5prime LD Drosophila melanogaster ... 36 4.3

D15134, RICC0136A	Rice cDNA, partial sequence (C0136A).	36	4.3
D46483, RICS11185A	Rice cDNA, partial sequence (S11185_1A).	36	4.3
D46618, RICS11395A	Rice cDNA, partial sequence (S11395_1A).	36	4.3
D46659, RICS11457A	Rice cDNA, partial sequence (S11457_1A).	36	4.3
D46719, RICS11572A	Rice cDNA, partial sequence (S11572_1A).	36	4.3
D48579, RICS14880A	Rice cDNA, partial sequence (S14880_2A).	36	4.3
AA802334, AA802334	GM04219.5prime GM Drosophila melanogaster ...	36	4.3
D46066, RICS10470A	Rice cDNA, partial sequence (S10470_1A).	36	4.3
D47037, RICS12104A	Rice cDNA, partial sequence (S12104_1A).	36	4.3
D46874, RICS11807A	Rice cDNA, partial sequence (S11807_2A).	36	4.3
D47174, RICS12340A	Rice cDNA, partial sequence (S12340_2A).	36	4.3
T04578, T04578	625 Lambda-PRL2 Arabidopsis thaliana cDNA clon...	36	4.3
C83675, C83675	Oryctolagus cuniculus corneal endothelial cDN...	36	4.3
D47950, RICS13762A	Rice cDNA, partial sequence (S13762_1A).	36	4.3
R90044, R90044	16399 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	36	4.3
D46994, RICS12013A	Rice cDNA, partial sequence (S12013_2A).	36	4.3
AA440820, AA440820	LD15713.5prime LD Drosophila melanogaster ...	36	4.3
C72089, C72089	Rice cDNA, partial sequence (E0963_1A)	36	4.3
Z84004, SSZ84004	S.scrofa mRNA; expressed sequence tag (5'; ...	36	4.3
D47519, RICS13070A	Rice cDNA, partial sequence (S13070_1A).	36	4.3
C19735, C19735	Rice cDNA, partial sequence (E10858_1A)	36	4.3
D47231, RICS12462A	Rice cDNA, partial sequence (S12462_1A).	36	4.3
D47147, RICS12293A	Rice cDNA, partial sequence (S12293_1A).	36	4.3
AA950198, AA950198	LD30147.5prime LD Drosophila melanogaster ...	36	4.3
Z47624, ATTS4480	A. thaliana transcribed sequence; clone TAI...	36	4.3
D45955, RICS10259A	Rice cDNA, partial sequence (S10259_1A).	36	4.3
D47137, RICS12280A	Rice cDNA, partial sequence (S12280_1A).	36	4.3
D69927, CELK093H2F	C.elegans cDNA clone yk93h2 : 5' end, sin...	36	4.3
AA392275, AA392275	LD11117.5prime LD Drosophila melanogaster ...	36	4.3

SEQ ID NO:546

D87455, D87455	Human mRNA for KIAA0266 gene, complete cds	1164	0.0
Z99129, HS425C14	Human DNA sequence from clone 425C14 on chr...	42	0.20
D90900, D90900	Synechocystis sp. PCC6803 complete genome, 2/...	40	0.80
Z74281, SCYDL233W	S.cerevisiae chromosome IV reading frame O...	38	3.1
AL021528, HS394P21	Homo sapiens DNA sequence from PAC 394P21...	38	3.1
Z49155, HSL83D3	Human DNA from cosmid L83d3, Huntington's Di...	38	3.1
U33761, HSU33761	Human cyclin A/CDK2-associated p45 (Skp2) mR...	38	3.1
AF052832, AF052832	Trypanosoma cruzi CL Brener cosmid 1b21 ch...	38	3.1
Z98600, SPAC20G4	S.pombe chromosome I cosmid c20G4	38	3.1

Y09438, SPHUSPLUS *S.pombe* hus1+ gene 38 3.1
D29951, MUSKIF Mouse mRNA for kinesin family protein KIF1a, ... 38 3.1

HUMAN ESTs

AA151187, AA151187 zo03c11.r1 Stratagene colon (#937204) Homo... 694 0.0
AA824593, AA824593 oc83d10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 670 0.0
AA954862, AA954862 op20c03.s1 NCI_CGAP_Co12 Homo sapiens cDNA... 581 e-164
T16360, T16360 NIB1193 Normalized infant brain, Bento Soares ... 517 e-145
R54592, R54592 yg81h10.s1 Homo sapiens cDNA clone 40102 3'. 511 e-143
AA373594, AA373594 EST85631 HSC172 cells I Homo sapiens cDNA ... 507 e-142
AA100660, AA100660 zl90a05.r1 Stratagene colon (#937204) Homo... 383 e-104
R42009, R42009 yg05b04.s1 Homo sapiens cDNA clone 31336 3'. 379 e-103
AA249614, AA249614 k3041.seq.F Human fetal heart, Lambda ZAP ... 252 5e-65
AA360633, AA360633 EST69800 T-cell lymphoma Homo sapiens cDNA... 182 4e-44
AA053498, AA053498 zl70b11.r1 Stratagene colon (#937204) Homo... 38 1.5
AA992442, AA992442 or85h03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 1.5

AA065677, AA065677 mm43c03.r1 Stratagene mouse melanoma (#937... 297 4e-79
AA529728, AA529728 vi38g12.r1 Beddington mouse embryonic regi... 42 0.035
W91608, W91608 MTA.D10.092.A MTA adult mouse thymus library M... 42 0.035
AA177186, AA177186 mt51a11.r1 Stratagene mouse embryonic carc... 42 0.035
AA048008, AA048008 mj26h10.r1 Soares mouse embryo NbME13.5 14... 36 2.2
AA637535, AA637535 vu10c02.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
AA726355, AA726355 vu90c09.r1 Stratagene mouse skin (#937313)... 36 2.2
AA404025, AA404025 va31c11.r1 GuayWoodford Beier mouse kidney... 36 2.2
AA060014, AA060014 ml34d07.r1 Stratagene mouse testis (#93730... 36 2.2
AA870617, AA870617 vq23h10.r1 Barstead stromal cell line MPLR... 36 2.2
AA414112, AA414112 vc64f08.s1 Knowles Solter mouse 2 cell Mus... 36 2.2
AA764250, AA764250 vv49e09.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2

H34350, H34350 EST111226 Rat PC-12 cells, NGF-treated (9 days... 36 1.9
C40718, C40718 *C.elegans* cDNA clone yk247f9 : 5' end, single... 36 1.9
AA817925, AA817925 UI-R-A0-af-g-04-0-UI.s1 UI-R-A0 Rattus nor... 36 1.9
AA955650, AA955650 UI-R-E1-fc-e-10-0-UI.s1 UI-R-E1 Rattus nor... 36 1.9

SEQ ID NO:547

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.35
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.35
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.35
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4

AC004301, AC004301 Drosophila melanogaster DNA sequence (PI D... 40 1.4
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
 AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.67
 AA946650, AA946650 oq38h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA806381, AA806381 oc22g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA577174, AA577174 nm86e11.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.67
 AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.67
 AA262229, AA262229 zs25b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA969632, AA969632 op38h05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.67
 AI005324, AI005324 ou13h07.x1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.67
 AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA814296, AA814296 nz07d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA873216, AA873216 oh70f04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.67
 W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.67
 AA974988, AA974988 on59b06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
 AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
 N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.67
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.67
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.67
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.67

AA903406, AA903406 ok62c11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.67
 AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 AA927863, AA927863 om18a08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 AA587486, AA587486 nn84e09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.67
 W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.67

 AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.67
 AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.67
 AA872272, AA872272 oh72a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.67
 N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.67
 N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.67
 AA813115, AA813115 aj44d06.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA826741, AA826741 85f12.s1 NCI_CGAP_Pr24 Homo sapiens cDNA... 40 0.67
 AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.67
 AI040354, AI040354 oy33d12.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.67
 AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.67
 AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 Homo sapiens c... 40 0.67
 AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 AI005204, AI005204 ou60c12.x1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.67
 N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.67
 AA824270, AA824270 aj29f01.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA504907, AA804907 oa89a01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.67
 AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 AA618498, AA618498 np30a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.67
 AA503727, AA503727 ne49g02.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.67
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.67
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.67
 AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
 AA759377, AA759377 ah54a10.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA629243, AA629243 zu77e03.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA262162, AA262162 zs25b12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 2.6
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.6
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.6
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.6
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.6
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.6
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.6
 H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 2.6
 R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 2.6

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.24
 AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24

 AA103139, AA103139 mol17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.24
 AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.24
 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24
 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.24
 AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.24
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.24
 AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.24
 AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.24
 AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.24
 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.24
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24
 AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.24
 AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.24
 AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.24
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24
 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.24
 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24
 AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.94
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.7
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.7
 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.7
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.7
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.7
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.7
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.7
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.7

AI047609, AI047609	uh63g07.r1 Soares mouse embryonic stem cel...	36	3.7
AA692425, AA692425	vt59b05.r1 Barstead mouse irradiated colon...	36	3.7
AA966976, AA966976	ua38f11.r1 Soares mouse mammary gland NbMM...	36	3.7
AA856298, AA856298	vw99b01.r1 Soares 2NbMT Mus musculus cDNA ...	36	3.7
W20935, W20935	mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus...	36	3.7
AA230661, AA230661	mw15f08.r1 Soares mouse 3NME12 5 Mus muscu...	36	3.7
AA111190, AA111190	mp66b11.r1 Soares 2NbMT Mus musculus cDNA ...	36	3.7
AA840087, AA840087	uc99h12.r1 Soares mouse uterus NMPu Mus mu...	36	3.7
AA089210, AA089210	mo05d10.r1 Stratagene mouse lung 937302 Mu...	36	3.7
AI035925, AI035925	ub49e05.r1 Soares mouse mammary gland NbMM...	36	3.7
AA824205, AA824205	vy20g08.r1 Stratagene mouse macrophage (#9...	36	3.7
AA793845, AA793845	vr35e12.r1 Barstead mouse myotubes MPLRB5 ...	36	3.7
AA239210, AA239210	mx89e02.r1 Soares mouse NML Mus musculus c...	36	3.7
AA711873, AA711873	vu28e06.r1 Barstead mouse myotubes MPLRB5 ...	36	3.7
AA645119, AA645119	vs72d03.r1 Stratagene mouse skin (#937313)...	36	3.7
AA957268, AA957268	UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor...	42	0.053
C83463, C83463	Oryctolagus cuniculus corneal endothelial cDN...	38	0.84
AA859448, AA859448	UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor...	38	0.84
AA874930, AA874930	UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor...	38	0.84
C82607, C82607	Oryctolagus cuniculus corneal endothelial cDN...	38	0.84
AI009631, AI009631	EST204082 Normalized rat lung, Bento Soare...	38	0.84
AA801145, AA801145	EST190642 Normalized rat ovary, Bento Soar...	38	0.84
AI012760, AI012760	EST207211 Normalized rat placenta, Bento S...	38	0.84
AA956139, AA956139	UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor...	38	0.84
AA801144, AA801144	EST190641 Normalized rat ovary, Bento Soar...	38	0.84
AA660819, AA660819	00713 MtRHE Medicago truncatula cDNA 5'	38	0.84
AA859865, AA859865	UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor...	38	0.84
AI009035, AI009035	EST203486 Normalized rat embryo, Bento Soa...	38	0.84
AA859542, AA859542	UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor...	38	0.84
T00613, T00613	wEST01334 Caenorhabditis elegans cDNA clone CE...	38	0.84
H32878, H32878	EST108396 Rat PC-12 cells, untreated Rattus sp...	36	3.3
AA125602, AA125602	JM00M011.QM3 Miracidia Sjc 3/96 Schistosom...	36	3.3
D45997, RICS10346A	Rice cDNA, partial sequence (S10346_1A).	36	3.3
AA943364, AA943364	EST198863 Normalized rat brain, Bento Soar...	36	3.3
C68472, C68472	C.elegans cDNA clone yk305a12 : 5' end, singl...	36	3.3
AA785775, AA785775	h4b05a1.fl Aspergillus nidulans 24hr asexu...	36	3.3
D46069, RICS10475A	Rice cDNA, partial sequence (S10475_1A).	36	3.3
AA660859, AA660859	00754 MtRHE Medicago truncatula cDNA 5' si...	36	3.3
Z33974, ATTS3035	A. thaliana transcribed sequence; clone PAP...	36	3.3
Z32603, ATTS2731	A. thaliana transcribed sequence; clone PAP...	36	3.3
AA955567, AA955567	UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor...	36	3.3
AA842765, AA842765	M-EST080 Sugarcane mature stalk Saccharum ...	36	3.3
Z32602, ATTS2730	A. thaliana transcribed sequence; clone PAP...	36	3.3

SEQ ID NO:548

U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.34
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.34
 U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.34
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.3
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.3
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.3
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.3

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
 AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 3e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.16
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.64
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.64
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.64
 AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.64
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.64
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.64
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.64
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.64
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.64
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.64
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.5
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.5
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.5
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.5
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.5
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.23
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.23
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.23
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.23

 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.23
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.23
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.23
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.91
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6
 AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6
 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.6
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.6
 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.6
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.6
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.6
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.6
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.6
 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.6
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.6
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.6
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.6
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.6
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.6
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.6
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.6
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.6
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.6
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.6

 AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.052
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.81
 AA660819, AA660819 00713 MtrHE Medicago truncatula cDNA 5' ... 38 0.81
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.81
 D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.2
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.2
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.2
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.2
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.2
 AA660859, AA660859 00754 MtrHE Medicago truncatula cDNA 5' si... 36 3.2

D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.2
 Z32603, ATTS2731 *A. thaliana* transcribed sequence; clone PAP... 36 3.2
 AA785775, AA785775 h4b05a1.f1 *Aspergillus nidulans* 24hr asexu... 36 3.2
 C68472, C68472 *C.elegans* cDNA clone yk305a12 : 5' end, singl... 36 3.2
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.2
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.2
 Z32602, ATTS2730 *A. thaliana* transcribed sequence; clone PAP... 36 3.2

SEQ ID NO:549

U79271, HSU79271 Human clones 23920 and 23921 mRNA sequence 650 0.0
 AC000395, AC000395 Genomic sequence from Human 9q34, complete... 42 0.28
 AC004636, AC004636 *Homo sapiens* chromosome 5, P1 clone 1268h6... 42 0.28
 M94579, HUMCEL Human carboxyl ester lipase (CEL) gene, comple... 42 0.28
 AC002097, AC002097 *Homo sapiens* chromosome 9q34, clone 246H5,... 42 0.28
 AB006709, AB006709 *Vibrio alginolyticus* rpoN gene for RNA po... 42 0.28
 Z47074, CEK07C10 *Caenorhabditis elegans* cosmid K07C10, compl... 40 1.1
 AC004755, AC004755 *Homo sapiens* chromosome 19, fosmid 37502, ... 40 1.1
 Z28051, SCYKL051W *S.cerevisiae* chromosome XI reading frame O... 40 1.1
 AF022655, AF022655 *Homo sapiens* cep250 centrosome associated ... 40 1.1
 AB006708, AB006708 *Arabidopsis thaliana* genomic DNA, chromos... 40 1.1
 AF049105, AF049105 *Homo sapiens* centrosomal Nek2-associated p... 40 1.1
 Z28050, SCYKL050C *S.cerevisiae* chromosome XI reading frame O... 40 1.1
 X75781, SCXI286K *S.cerevisiae* chromosome XI (28.6 kb) DNA fo... 40 1.1
 Y16899, DMY16899 *Drosophila melanogaster* mRNA for optomotor-... 38 4.3
 M87854, RATBARK1 *Rattus norvegicus* beta-adrenergic receptor k... 38 4.3
 M74822, RATMHTLL Rat MHC class I TL-like protein gene, comple... 38 4.3
 M80776, HUMBARK1A Human beta-adrenergic receptor kinase 1 mRN... 38 4.3
 D84549, YSACA *Candida tropicalis* DNA for carnitine acetyltra... 38 4.3
 L23127, RATRMCI *Rattus norvegicus* germline MHC class I gene, ... 38 4.3
 AC004257, AC004257 *Homo sapiens* chromosome 19, cosmid R33209,... 38 4.3
 U70850, CELF28F9 *Caenorhabditis elegans* cosmid F28F9 38 4.3
 U88309, CELT23B3 *Caenorhabditis elegans* cosmid T23B3 38 4.3
 X53421, DVCHOS18 *D. virilis* s18, s15, s19, s16 chorion prote... 38 4.3
 D89245, D89245 *Schizosaccharomyces pombe* mRNA, partial cds, ... 38 4.3
 AF009623, AF009623 *Parascaris univalens* PUMA1 (puma1) mRNA, c... 38 4.3
 S48813, S48813 beta-adrenergic receptor kinase [rats, brain, ... 38 4.3
 Z67883, CEK02A4 *Caenorhabditis elegans* cosmid K02A4, complet... 38 4.3
 U90567, GGU90567 *Gallus gallus* glutamine rich protein mRNA, p... 38 4.3
 M98498, BOVEZRINA *Bos taurus* ezrin mRNA, complete cds. 38 4.3
 M34073, MUSMHT10C *Mus musculus* (clone T10-c) MHC class I cell... 38 4.3

S81843, S81843 beta-adrenergic receptor kinase 1 [Syrian hams... 38 4.3
 X61157, HSBARK H.sapiens mRNA for beta-adrenergic receptor k... 38 4.3
 U08438, HSNBARKS4 Human beta-adrenergic receptor kinase (ADRB... 38 4.3
 U39674, CELC06E2 Caenorhabditis elegans cosmid C06E2. 38 4.3

HUMAN ESTs

W29097, W29097 56d11 Human retina cDNA randomly primed sublib... 1045 0.0
 AA886109, AA886109 ny44f05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA... 656 0.0
 AA829894, AA829894 oe51e12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 650 0.0
 AA879456, AA879456 oj91g03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 650 0.0
 AA029201, AA029201 zk12f08.s1 Soares pregnant uterus NbHPU Ho... 650 0.0
 AA102109, AA102109 zk87g11.s1 Soares pregnant uterus NbHPU Ho... 650 0.0
 AA843811, AA843811 ak09c08.s1 Soares parathyroid tumor NbHPA ... 650 0.0
 W72147, W72147 zd70f08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0
 N51485, N51485 yz04e06.s1 Homo sapiens cDNA clone 282082 3'. 650 0.0
 AI033069, AI033069 ow93f02.s1 Soares_fetal_liver_spleen_1NFLS... 642 0.0
 AA161465, AA161465 zo73a06.s1 Stratagene pancreas (#937208) H... 638 0.0
 N51277, N51277 yz14d07.s1 Homo sapiens cDNA clone 283021 3'. 636 e-180
 N64528, N64528 yz91e06.s1 Homo sapiens cDNA clone 290434 3'. 636 e-180
 H99906, H99906 yx32h10.s1 Homo sapiens cDNA clone 263491 3'. 636 e-180
 AA812519, AA812519 ai79b03.s1 Soares testis NHT Homo sapiens ... 636 e-180
 R71679, R71679 yj85e08.s1 Homo sapiens cDNA clone 155558 3'. 628 e-178
 AA744290, AA744290 ny51d02.s1 NCI_CGAP_Pr18 Homo sapiens cDNA... 626 e-177
 AI038590, AI038590 ox34e03.s1 Soares_total_fetus_Nb2HF8_9w Ho... 624 e-177
 AA099913, AA099913 zk87g11.r1 Soares pregnant uterus NbHPU Ho... 624 e-177
 AA083859, AA083859 zn16d06.s1 Stratagene neuroepithelium NT2R... 622 e-176
 AA883684, AA883684 al58a05.s1 Soares NFL T GBC S1 Homo sapien... 613 e-173
 R39448, R39448 yc95d03.s1 Homo sapiens cDNA clone 23921 3'. 593 e-167
 R36854, R36854 yf52c07.s1 Homo sapiens cDNA clone 25899 3'. 591 e-167
 H98684, H98684 yx17g01.s1 Homo sapiens cDNA clone 262032 3'. 585 e-165
 R07471, R07471 ye97a06.s1 Homo sapiens cDNA clone 125650 3'. 581 e-164
 AA910762, AA910762 ol25h06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 559 e-157
 AA083954, AA083954 zn17d06.s1 Stratagene neuroepithelium NT2R... 555 e-156
 AA346369, AA346369 EST52776 Fetal heart II Homo sapiens cDNA ... 545 e-153
 R54092, R54092 yg98d07.s1 Homo sapiens cDNA clone 41818 3'. 539 e-151
 H09074, H09074 yl97a06.s1 Homo sapiens cDNA clone 46164 3'. 535 e-150
 N21975, N21975 yw30c10.s1 Homo sapiens cDNA clone 253746 3'. 533 e-149
 D59844, HUM070E11A Human fetal brain cDNA 3'-end GEN-070E11. 466 e-129
 H11525, H11525 ym15h07.s1 Homo sapiens cDNA clone 48232 3'. 442 e-122
 AA971254, AA971254 op73c08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 442 e-122
 W77907, W77907 zd70f08.r1 Soares fetal heart NbHH19W Homo sap... 428 e-118
 AA878973, AA878973 oj26d11.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 389 e-106
 AA715235, AA715235 nv10g01.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 357 2e-96

AA328928, AA328928 EST32475 Embryo, 12 week I Homo sapiens cD... 355 7e-96
 AA860455, AA860455 aj80f02.s1 Soares parathyroid tumor NbHPA ... 283 2e-74
 AA026096, AA026096 ze97a04.r1 Soares fetal heart NbHH19W Homo... 268 1e-69
 AA026516, AA026516 ze97a04.s1 Soares fetal heart NbHH19W Homo... 172 6e-41
 T26899, T26899 ESTDIR509 Homo sapiens cDNA clone CDDIR509 3'. 170 2e-40

 N71178, N71178 yw30c10.r1 Homo sapiens cDNA clone 253746 5'. 165 1e-38
 AA372290, AA372290 EST84170 Raji cells, cyclohexamide treated... 98 3e-18
 AI038890, AI038890 ox84g12.x1 Soares_senescent_fibroblasts_Nb... 40 0.53
 D81647, HUM180D08B Human fetal brain cDNA 5'-end GEN-180D08. 38 2.1
 AA452630, AA452630 zx33f08.r1 Soares total fetus Nb2HF8 9w Ho... 38 2.1
 AA682624, AA682624 zi19g01.s1 Soares fetal liver spleen 1NFLS... 38 2.1
 AA742364, AA742364 ny89c12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.1
 AA907234, AA907234 ol03h08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 2.1
 T09391, T09391 EST07284 Homo sapiens cDNA clone HIBBT71 5' en... 38 2.1
 AA161236, AA161236 zo59h07.s1 Stratagene pancreas (#937208) H... 38 2.1
 AA252941, AA252941 zr50g09.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
 AA252245, AA252245 zr64g07.s1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
 AA780678, AA780678 ac70h01.s1 Stratagene fetal retina 937202 ... 38 2.1
 W05501, W05501 za84a12.r1 Soares fetal lung NbHL19W Homo sapi... 38 2.1
 AI039908, AI039908 ox25f07.x1 Soares_total_fetus_Nb2HF8_9w Ho... 38 2.1
 AA280664, AA280664 zs99f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.1
 AA973566, AA973566 oo46f09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 2.1
 N27253, N27253 yx17g01.r1 Homo sapiens cDNA clone 262032 5'. 38 2.1
 AA995707, AA995707 os29c09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 38 2.1
 AI016407, AI016407 ot72e09.s1 Soares_total_fetus_Nb2HF8_9w Ho... 38 2.1
 N70619, N70619 za84a12.s1 Homo sapiens cDNA clone 299230 3'. 38 2.1
 AA242923, AA242923 zr64g07.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
 AA938631, AA938631 oo96f07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 38 2.1
 AA985290, AA985290 am74g03.s1 Stratagene schizo brain S11 Hom... 38 2.1

 AA690806, AA690806 vt25h10.r1 Barstead mouse myotubes MPLRB5 ... 377 e-103
 AA155014, AA155014 mr99h05.r1 Stratagene mouse embryonic carc... 180 8e-44
 AA269966, AA269966 va57d06.r1 Soares mouse 3NME12 5 Mus muscu... 172 2e-41
 AA089195, AA089195 mo05h11.r1 Stratagene mouse lung 937302 Mu... 163 2e-38
 AA466212, AA466212 vg86g02.r1 Barstead mouse pooled organs MP... 68 8e-10
 AA423476, AA423476 ve76d07.r1 Soares mouse mammary gland NbMM... 60 2e-07
 AA597213, AA597213 vo28a05.r1 Barstead mouse irradiated colon... 40 0.19
 AA396266, AA396266 vb45c01.r1 Soares mouse lymph node NbMLN M... 40 0.19
 AA967806, AA967806 uh05d06.r1 Soares mouse hypothalamus NMHy ... 38 0.75
 AA591111, AA591111 vm12c06.r1 Knowles Solter mouse blastocyst... 38 0.75
 W65797, W65797 me14g02.r1 Soares mouse embryo NbME13.5 14.5 M... 38 0.75
 AA153891, AA153891 mq56e05.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.75

AI019772, AI019772 ua90h02.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA472253, AA472253 vh10g05.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA230895, AA230895 mw14g07.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.0
 W18052, W18052 mb83g03.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.0
 AA797681, AA797681 vx66c12.r1 Stratagene mouse skin (#937313)... 36 3.0

 W66734, W66734 mc26g05.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0
 AA968020, AA968020 uh07g01.r1 Soares mouse hypothalamus NMHy ... 36 3.0
 AA051644, AA051644 mj55d12.r1 Soares mouse embryo NbME13.5 14... 36 3.0
 AA162797, AA162797 mr29g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
 AA549644, AA549644 vk80f08.s1 Knowles Solter mouse 2 cell Mus... 36 3.0
 AA273295, AA273295 vc01e01.r1 Soares mouse lymph node NbMLN M... 36 3.0
 AA048480, AA048480 mj33d08.r1 Soares mouse embryo NbME13.5 14... 36 3.0
 AA098207, AA098207 mn83d01.r1 Stratagene mouse Tcell 937311 M... 36 3.0
 AA027381, AA027381 mi05c06.r1 Soares mouse placenta 4NbMP13.5... 36 3.0
 AA544474, AA544474 vk33h06.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA416466, AA416466 vd15c09.s1 Knowles Solter mouse 2 cell Mus... 36 3.0
 AA285999, AA285999 vb88h08.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
 AA175025, AA175025 ms85f06.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
 AA544386, AA544386 vk33f06.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA175557, AA175557 ms96g04.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
 AA711924, AA711924 vu59f09.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA734052, AA734052 vv22c10.r1 Stratagene mouse heart (#937316... 36 3.0
 W53738, W53738 md12a12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0
 AA611837, AA611837 vo82a06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.0
 AA879531, AA879531 vv96f06.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA288625, AA288625 vb23g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0

 AA784124, AA784124 d2b06a1.f1 Aspergillus nidulans 24hr asexu... 38 0.67
 AI044911, AI044911 UI-R-C1-kk-e-05-0-UI.s1 UI-R-C1 Rattus nor... 36 2.6
 AA550452, AA550452 1605m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 2.6
 F20017, ATTS6056 A. thaliana transcribed sequence; clone TAP... 36 2.6
 AA786697, AA786697 k5d01a1.f1 Aspergillus nidulans 24hr asexu... 36 2.6
 AA433457, AA433457 SW3ICA2345SK Brugia malayi infective larva... 36 2.6

SEQ ID NO:550

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.20
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.20
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.20
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 0.80

AC004301, AC004301 *Drosophila melanogaster* DNA sequence (P1 D... 40 0.80
 U86662, LEU86662 *Lycopersicon esculentum* VPS41 (tVPS41) mRNA,... 40 0.80
 Y14330, HSY14330 *Homo sapiens* partial mRNA for jagged2 protein 38 3.2
 AF003521, AF003521 *Homo sapiens* Jagged 2 mRNA, complete cds 38 3.2
 AF029778, AF029778 *Homo sapiens* Jagged2 (JAG2) mRNA, complete... 38 3.2

 AF020201, AF020201 *Homo sapiens* Jagged 2 mRNA, complete cds 38 3.2
 Z71523, SCYNL247W *S.cerevisiae* chromosome XIV reading frame ... 38 3.2
 AF029779, AF029779 *Homo sapiens* hJAG2.del-E6 (JAG2) mRNA, alt... 38 3.2
 U70049, RNU70049 *Rattus norvegicus* jagged2 precursor gene, pa... 38 3.2
 X96722, SCCHXIVL *S.cerevisiae* DNA region from chromosome XIV... 38 3.2
 AF005938, AF005938 *Cavia porcellus* L-type voltage-dependent c... 38 3.2
 X78972, SBSTRBF *S.bluesensis* ISP 5564 genes strB and strF 38 3.2
 X94912, HSPR22 *H.sapiens* Pr22 gene 38 3.2

HUMAN ESTs

AA860926, AA860926 ak22d06.s1 Soares testis NHT *Homo sapiens* ... 650 0.0
 AA348243, AA348243 EST54707 Hippocampus I *Homo sapiens* cDNA 5... 513 e-144
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 *Homo sapiens* cDNA ... 363 2e-98
 AA327309, AA327309 EST30621 Colon I *Homo sapiens* cDNA 5' end 353 2e-95
 AA344913, AA344913 EST50856 Gall bladder II *Homo sapiens* cDNA... 337 1e-90
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) *Homo*... 317 1e-84
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) *Homo*... 317 1e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR *Homo sapie*... 42 0.098
 AI005204, AI005204 ou60c12.x1 NCI_CGAP_Br2 *Homo sapiens* cDNA... 40 0.39
 AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39
 AI005324, AI005324 ou13h07.x1 Soares_NFL_T_GBC_S1 *Homo sapien*... 40 0.39
 AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 *Homo sapiens* c... 40 0.39
 AA262162, AA262162 zs25b12.r1 NCI_CGAP_GCB1 *Homo sapiens* cDNA... 40 0.39
 AA824270, AA824270 aj29f01.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA826741, AA826741 85f12.s1 NCI_CGAP_Pr24 *Homo sapiens* cDNA... 40 0.39
 AA813115, AA813115 aj44d06.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39
 AA804907, AA804907 oa89a01.s1 NCI_CGAP_GCB1 *Homo sapiens* cDNA... 40 0.39
 AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA618498, AA618498 np30a11.s1 NCI_CGAP_Pr22 *Homo sapiens* cDNA... 40 0.39
 AA503727, AA503727 ne49g02.s1 NCI_CGAP_Co3 *Homo sapiens* cDNA ... 40 0.39
 AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39
 AA759377, AA759377 ah54a10.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA629243, AA629243 zu77e03.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA903406, AA903406 ok62c11.s1 NCI_CGAP_GC4 *Homo sapiens* cDNA ... 40 0.39
 AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.39

AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.39
 AA577174, AA577174 nm86e11.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.39
 AA969632, AA969632 op38h05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
 N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.39
 AA974988, AA974988 on59b06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39

 W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.39
 N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.39
 AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.39
 AA814296, AA814296 nz07d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
 AA806381, AA806381 oc22g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
 AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.39
 W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.39
 AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.39
 AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.39
 AA927863, AA927863 om18a08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
 AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.39
 W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.39
 AA262229, AA262229 zs25b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
 AA587486, AA587486 nn84e09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.39
 AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA872272, AA872272 oh72a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
 W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.39
 N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.39
 N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.39
 AI040354, AI040354 oy33d12.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.39
 AA946650, AA946650 oq38h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
 AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.39
 AA873216, AA873216 oh70f04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
 R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 1.5
 H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 1.5
 AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 1.5
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 1.5
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 1.5
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 1.5
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 1.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 6e-44
 AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.14
 AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.14

AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.14
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.14

 AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.14
 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.14
 AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.14
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.14
 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.14
 AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.14
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.14
 AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.14
 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14
 AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.14
 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.14
 AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.14
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.14
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.55
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 2.2
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 2.2
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 2.2
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 2.2
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 2.2
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 2.2
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 2.2
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.2
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 2.2
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 2.2
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 2.2
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 2.2
 AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 2.2
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 2.2

AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 2.2

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.031
 AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.48
 AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.48
 AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
 C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48
 AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
 C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48
 AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.48
 AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.48
 AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.48
 AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.48
 AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 1.9
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 1.9
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 1.9
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 1.9
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 1.9
 AA660859, AA660859 00754 MtrHE Medicago truncatula cDNA 5' si... 36 1.9
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 1.9
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 1.9
 AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 1.9

SEQ ID NO:551

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.36
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.36
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.36
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo 317 2e-84

 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.68
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.68
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.68
 AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.68
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.68
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.68
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.68
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.68
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.68
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.68
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.7
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.7
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.7
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.7
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.7
 R14449, R14449 yf81h09.r1 Homo sapiens cDNA clone 29034 5'. 38 2.7
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.7

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.24
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.24
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.24
 AA250010, AA250010 mz59b12.r1 Soares mouse lymph node NbMLN M... 38 0.97
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.97
 AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 0.97
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.8
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.8
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 36 3.8
 AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 36 3.8

AA840087, AA840087	uc99h12.r1 Soares mouse uterus NMPu Mus mu...	36	3.8
AA543280, AA543280	vj80h05.r1 Soares mouse mammary gland NbMM...	36	3.8
AA007762, AA007762	mg76b03.r1 Soares mouse embryo NbME13.5 14...	36	3.8
AA014223, AA014223	mh20a03.r1 Soares mouse placenta 4NbMP13.5...	36	3.8
AA591243, AA591243	vm18c04.r1 Knowles Solter mouse blastocyst...	36	3.8
AA921560, AA921560	vy52c06.r1 Stratagene mouse lung 937302 Mu...	36	3.8
W20935, W20935	mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus...	36	3.8
AA793845, AA793845	vr35e12.r1 Barstead mouse myotubes MPLRB5 ...	36	3.8
AA856298, AA856298	vw99b01.r1 Soares 2NbMT Mus musculus cDNA ...	36	3.8
AA833479, AA833479	uc91c03.r1 Soares mouse uterus NMPu Mus mu...	36	3.8
AA218431, AA218431	my07e05.r1 Barstead mouse lung MPLRB2 Mus ...	36	3.8
AA089210, AA089210	mo05d10.r1 Stratagene mouse lung 937302 Mu...	36	3.8
AI047609, AI047609	uh63g07.r1 Soares mouse embryonic stem cel...	36	3.8
AA797372, AA797372	vw27b08.r1 Soares mouse mammary gland NbMM...	36	3.8
AA138067, AA138067	mq37c11.r1 Barstead MPLRB1 Mus musculus cD...	36	3.8
W83172, W83172	mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus...	36	3.8
AA542324, AA542324	vk53e07.r1 Stratagene mouse Tcell 937311 M...	36	3.8
AA967316, AA967316	vj47a03.r1 Stratagene mouse skin (#937313)...	36	3.8
AI035925, AI035925	ub49e05.r1 Soares mouse mammary gland NbMM...	36	3.8
AA497479, AA497479	vh29b12.r1 Soares mouse mammary gland NbMM...	36	3.8
W87202, W87202	mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M...	36	3.8
AA016868, AA016868	mh36e12.r1 Soares mouse placenta 4NbMP13.5...	36	3.8
AA467482, AA467482	ve01a10.r1 Soares mouse NbMH Mus musculus ...	36	3.8
AA014768, AA014768	mi66h04.r1 Soares mouse embryo NbME13.5 14...	36	3.8
AA711859, AA711859	vu59c10.r1 Soares mouse mammary gland NbMM...	36	3.8
AA530735, AA530735	vj32g11.r1 Stratagene mouse diaphragm (#93...	36	3.8
AA009071, AA009071	mg87b11.r1 Soares mouse embryo NbME13.5 14...	36	3.8
AA711873, AA711873	vu28e06.r1 Barstead mouse myotubes MPLRB5 ...	36	3.8
AA645119, AA645119	vs72d03.r1 Stratagene mouse skin (#937313)...	36	3.8
AA106301, AA106301	ml81a09.r1 Stratagene mouse kidney (#93731...	36	3.8
AA111190, AA111190	mp66b11.r1 Soares 2NbMT Mus musculus cDNA ...	36	3.8
C87249, C87249	Mus musculus fertilized egg cDNA 3'-end seque...	36	3.8
AA796056, AA796056	vo65d01.r1 Soares mouse mammary gland NbMM...	36	3.8
AA230661, AA230661	mw15f08.r1 Soares mouse 3NME12 5 Mus muscu...	36	3.8
AA033481, AA033481	mi42b07.r1 Soares mouse embryo NbME13.5 14...	36	3.8
AA000268, AA000268	mg32e09.r1 Soares mouse embryo NbME13.5 14...	36	3.8
AI048515, AI048515	uh61e08.r1 Soares mouse embryonic stem cel...	36	3.8
W61547, W61547	md57a02.r1 Soares mouse embryo NbME13.5 14.5 M...	36	3.8
AA790448, AA790448	vw04f09.r1 Soares mouse mammary gland NbMM...	36	3.8
AA824205, AA824205	vy20g08.r1 Stratagene mouse macrophage (#9...	36	3.8
AA475425, AA475425	vh20g09.r1 Soares mouse mammary gland NbMM...	36	3.8
W62989, W62989	md88h12.r1 Soares mouse embryo NbME13.5 14.5 M...	36	3.8
W77724, W77724	me84h06.r1 Soares mouse embryo NbME13.5 14.5 M...	36	3.8
AA239210, AA239210	mx89e02.r1 Soares mouse NML Mus musculus c...	36	3.8

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AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.055
 AA891284, AA891284 EST195087 Normalized rat heart, Bento Soar... 40 0.22
 Z83055, RNZ83055 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22
 AI010967, AI010967 EST205418 Normalized rat muscle, Bento Soa... 40 0.22
 AA852049, AA852049 EST194818 Normalized rat spleen, Bento Soa... 40 0.22

 H33489, H33489 EST109542 Rat PC-12 cells, NGF-treated (9 days... 40 0.22
 AA799616, AA799616 EST189113 Normalized rat heart, Bento Soar... 40 0.22
 Z83044, RNZ83044 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22
 AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.86
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.86
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.86
 AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 3.4
 AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.4
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.4
 C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.4
 AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.4
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.4
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.4
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.4
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.4
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.4
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.4
 D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.4
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.4
 AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.4
 D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.4

SEQ ID NO:552

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.38
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.38
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.38
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.5
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.5
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.5

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
~~AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84~~
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.18
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.72
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.72
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.72
 AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.72
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.72
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.72
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.72
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.72
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.72
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.72
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.8
 N25839, N25839 yx22e05.r1 Homo sapiens cDNA clone 262496 5'. 38 2.8
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.8
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.8
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.8
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.8
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.8

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.26
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.26
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.26
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.26
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.26
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.26
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.26
 AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 1.0
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 1.0
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 4.0
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 36 4.0
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 4.0
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 4.0
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.0
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 4.0
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 4.0

AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 4.0
AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 4.0
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 4.0
~~AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 36 4.0~~
AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 36 4.0
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 36 4.0
AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 4.0
AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 4.0
AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 36 4.0
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 4.0
AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 36 4.0
W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 4.0
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 36 4.0
AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 4.0
AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 4.0
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 4.0
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 4.0
W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0
AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 36 4.0
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 36 4.0
AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.0
AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 36 4.0
W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.0
AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 36 4.0
AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 36 4.0
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 4.0
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0
AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 36 4.0
AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 36 4.0
W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0
W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.0
AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 4.0
AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.0
AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 36 4.0
AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 36 4.0
AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 4.0
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 4.0

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.058
T00613, T00613 wEST01334 *Caenorhabditis elegans* cDNA clone CE... 38 0.90
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.90
AA660819, AA660819 00713 MtRHE *Medicago truncatula* cDNA 5' 38 0.90
AA125602, AA125602 IM00M011 QM3 *Miracidia* Sjc 3/96 *Schistosom*... 36 3.6

Z33974, ATTS3035 *A. thaliana* transcribed sequence; clone PAP... 36 3.6
C68472, C68472 *C.elegans* cDNA clone yk305a12 : 5' end, singl... 36 3.6
AA785775, AA785775 h4b05a1.fl *Aspergillus nidulans* 24hr asexu... 36 3.6
Z32602, ATTS2730 *A. thaliana* transcribed sequence; clone PAP... 36 3.6
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.6
Z32603, ATTS2731 *A. thaliana* transcribed sequence; clone PAP... 36 3.6
AA842765, AA842765 M-EST080 Sugarcane mature stalk *Saccharum* ... 36 3.6
D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.6
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.6
AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.6
AA660859, AA660859 00754 MtRHE *Medicago truncatula* cDNA 5' si... 36 3.6
AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.6
D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.6
H32878, H32878 EST108396 Rat PC-12 cells, untreated *Rattus* sp... 36 3.6

SEQ ID NO:553

Z99297, HS262D12 *Homo sapiens* DNA sequence from PAC 262D12 o... 1963 0.0
Z81540, CEF46B3 *Caenorhabditis elegans* cosmid F46B3, complet... 40 0.89
U67488, U67488 *Methanococcus jannaschii* section 30 of 150 of ... 38 3.5
AE000786, AE000786 *Borrelia burgdorferi* plasmid lp28-2, compl... 38 3.5
L02053, OMMGSHTR1 *Ommastrephes sloani* glutathione transferase... 38 3.5
AC004521, ATAC004521 *Arabidopsis thaliana* chromosome II BAC F... 38 3.5
L41250, DROGPDHN *Drosophila nebulosa* glycerol-3-phosphate deh... 38 3.5
AE000619, HPAE000619 *Helicobacter pylori* section 97 of 134 of... 38 3.5
U39720, *Mycoplasma genitalium* ackA, licA, mucB, rpL10, rpL32... 38 3.5
AC004533, HUAC004533 *Homo sapiens* Chromosome 16 BAC clone CIT... 38 3.5
U62292, HSU62292 Human elastin (ELN) gene, partial cds 38 3.5

HUMAN ESTs

W02630, W02630 za52c02.r1 Soares fetal liver spleen 1NFLS Hom... 1009 0.0
AA557183, AA557183 nl74f12.s1 NCI_CGAP_Br2 *Homo sapiens* cDNA ... 874 0.0
AA761171, AA761171 nz09e11.s1 NCI_CGAP_GCB1 *Homo sapiens* cDNA... 866 0.0
AA976975, AA976975 oq26g11.s1 NCI_CGAP_GC4 *Homo sapiens* cDNA ... 854 0.0
AA449515, AA449515 zx06b11.r1 Soares total fetus Nb2HF8 9w Ho... 848 0.0

AA678392, AA678392 zi26h10.s1 Soares fetal liver spleen 1NFLS... 848 0.0
 AA909198, AA909198 ol12d06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 831 0.0
 W79208, W79208 zd79g05.r1 Soares fetal heart NbHH19W Homo sap... 813 0.0
 W03125, W03125 za53c02.r1 Soares fetal liver spleen 1NFLS Hom... 807 0.0
 W94750, W94750 ze13h08.r1 Soares fetal heart NbHH19W Homo sap... 785 0.0

 AA354894, AA354894 EST63217 Jurkat T-cells V Homo sapiens cDN... 771 0.0
 H70075, H70075 yr92b03.r1 Homo sapiens cDNA clone 212717 5'. 745 0.0
 W77859, W77859 zd70b08.r1 Soares fetal heart NbHH19W Homo sap... 728 0.0
 AA425424, AA425424 zw48f03.s1 Soares total fetus Nb2HF8 9w Ho... 718 0.0
 AA476893, AA476893 zu29f09.r1 Soares ovary tumor NbHOT Homo s... 688 0.0
 AA456676, AA456676 aa01h02.s1 Soares NhHMPu S1 Homo sapiens c... 688 0.0
 AA662309, AA662309 nu97c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 668 0.0
 W72135, W72135 zd70b08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0
 N74362, N74362 za52c02.s1 Homo sapiens cDNA clone 296162 3'. 622 e-176
 N66917, N66917 za47d09.s1 Homo sapiens cDNA clone 295697 3'. 585 e-165
 AA251287, AA251287 zs04c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 583 e-164
 AA971082, AA971082 op70h01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 567 e-160
 W78165, W78165 zd79g05.s1 Soares fetal heart NbHH19W Homo sap... 565 e-159
 AA253290, AA253290 zr71g03.r1 Soares NhHMPu S1 Homo sapiens c... 559 e-157
 AA729063, AA729063 nw22f08.s1 NCI_CGAP_GCB0 Homo sapiens cDNA... 557 e-157
 AA987313, AA987313 or81h06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 553 e-155
 AA300954, AA300954 EST13832 Testis tumor Homo sapiens cDNA 5'... 541 e-152
 AA425594, AA425594 zw48f03.r1 Soares total fetus Nb2HF8 9w Ho... 529 e-148
 N24014, N24014 yx87g10.s1 Homo sapiens cDNA clone 268770 3'. 523 e-146
 AA947355, AA947355 od86e12.s1 NCI_CGAP_Ov2 Homo sapiens cDNA ... 504 e-140
 AA121074, AA121074 zl88b06.s1 Stratagene colon (#937204) Homo... 460 e-127
 AA742964, AA742964 ny15d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 454 e-126
 AA306814, AA306814 EST177885 Colon carcinoma (HCC) cell line ... 452 e-125
 W87699, W87699 zh65b11.r1 Soares fetal liver spleen 1NFLS S1 ... 446 e-123
 W87700, W87700 zh65b11.s1 Soares fetal liver spleen 1NFLS S1 ... 438 e-121
 AA449084, AA449084 zx06b11.s1 Soares total fetus Nb2HF8 9w Ho... 398 e-109
 N99231, N99231 zb76f11.s1 Soares senescent fibroblasts NbHSF ... 391 e-106
 N49900, N49900 yv24d04.s1 Homo sapiens cDNA clone 243655 3'. 383 e-104
 AA782911, AA782911 ai62a10.s1 Soares testis NHT Homo sapiens ... 365 6e-99
 AA936553, AA936553 on23g11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 361 9e-98
 N74414, N74414 za53c02.s1 Homo sapiens cDNA clone 296258 3'. 353 2e-95
 AA834628, AA834628 od98a10.s1 NCI_CGAP_Ov2 Homo sapiens cDNA ... 341 8e-92
 AA693756, AA693756 zi55f11.s1 Soares fetal liver spleen 1NFLS... 341 8e-92
 AA909616, AA909616 ol09d06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 341 8e-92
 H69662, H69662 yr92b03.s1 Homo sapiens cDNA clone 212717 3'. 321 8e-86
 AA249558, AA249558 jj7521.seq.F Human fetal heart, Lambda ZAP... 317 1e-84
 AA911960, AA911960 oh88g08.s1 NCI_CGAP_Co8 Homo sapiens cDNA ... 317 1e-84
 AA969099, AA969099 op55e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 303 2e-80
 AA766191, AA766191 oa12g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 212 5e-53
 AA689312, AA689312 nx05e10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 200 2e-49

AA418586, AA418586 zv93e05.r1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44
AA418570, AA418570 zv93e05.s1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44
AA534939, AA534939 nf82f03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 167 3e-39
AA888430, AA888430 nw74e05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA... 167 3e-39
N50003, N50003 yv24d04.r1 Homo sapiens cDNA clone 243655 5' s... 149 6e-34
AA535102, AA535102 nr84f06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 135 1e-29
AA262335, AA262335 zr71g03.s1 Soares NhHMPu S1 Homo sapiens c... 129 6e-28
AA766681, AA766681 oa34c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 105 9e-21
AA761492, AA761492 nz27a05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 101 1e-19
AA688350, AA688350 nv15a05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 90 5e-16
AA347041, AA347041 EST53285 Fetal heart II Homo sapiens cDNA ... 76 8e-12
T94395, T94395 ye35e02.s1 Homo sapiens cDNA clone 119738 3'. 46 0.007
AA833565, AA833565 aj46a02.s1 Soares testis NHT Homo sapiens ... 46 0.007
AA095460, AA095460 l4630.seq.F Fetal heart, Lambda ZAP Expres... 40 0.43
AA904415, AA904415 ok07e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.43
AI018800, AI018800 ov32h04.x1 Soares_testis_NHT Homo sapiens ... 38 1.7
AA631083, AA631083 nq77e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 1.7

AA399772, AA399772 vd70g05.r1 Beddington mouse embryonic regi... 347 5e-94
AA467106, AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 309 1e-82
AI046844, AI046844 uh55c11.r1 Soares mouse embryonic stem cel... 208 3e-52
AA475075, AA475075 vh11g05.r1 Soares mouse mammary gland NbMM... 194 4e-48
AA646094, AA646094 vs31e06.r1 Stratagene mouse Tcell 937311 M... 186 1e-45
AA390020, AA390020 vb30e07.r1 Soares mouse lymph node NbMLN M... 170 6e-41
AA245553, AA245553 my52g04.r1 Barstead mouse pooled organs MP... 170 6e-41
AA930741, AA930741 vs57b02.r1 Stratagene mouse skin (#937313)... 155 4e-36
W62610, W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 117 8e-25
AA239270, AA239270 my40e01.r1 Barstead mouse pooled organs MP... 109 2e-22
AA015148, AA015148 mh16e01.r1 Soares mouse placenta 4NbMP13.5... 54 1e-05
AA764095, AA764095 vw09h02.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.61
AA238570, AA238570 my35h02.r1 Barstead mouse pooled organs MP... 38 0.61
AA600576, AA600576 vm75f08.r1 Knowles Solter mouse blastocyst... 38 0.61
AA636273, AA636273 vq76a10.s1 Knowles Solter mouse 2 cell Mus... 36 2.4
AA051407, AA051407 mj41f08.r1 Soares mouse embryo NbME13.5 14... 36 2.4
AA823136, AA823136 vw41b03.r1 Soares mouse mammary gland NbMM... 36 2.4
W83831, W83831 mf26a06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4
D77944, MUSC0D06 Mouse embryonal carcinoma F9 cell cDNA, C0D06 36 2.4
AA915408, AA915408 vz29h04.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.4
AI047229, AI047229 uh63a09.r1 Soares mouse embryonic stem cel... 36 2.4
AA271880, AA271880 va73d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4
AA475165, AA475165 vg95f01.r1 Barstead mouse pooled organs MP... 36 2.4
AA619774, AA619774 vl58a05.s1 Knowles Solter mouse 2 cell Mus... 36 2.4

AA673116, AA673116 vn49g11.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4
 AA870623, AA870623 vq24a07.r1 Barstead stromal cell line MPLR... 36 2.4
 W58907, W58907 md52f12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4
 AA690593, AA690593 vu53d05.r1 Soares mouse mammary gland NbMM... 36 2.4
 AA754801, AA754801 vu21f03.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4
 AA271607, AA271607 va72a12.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4
 AA064256, AA064256 mj66a03.r1 Soares mouse p3NMF19.5 Mus muscu... 36 2.4
 AA475144, AA475144 vg95d01.r1 Barstead mouse pooled organs MP... 36 2.4
 AA197736, AA197736 mv02g08.r1 GuayWoodford Beier mouse kidney... 36 2.4

AA817944, AA817944 UI-R-A0-ag-e-01-0-UI.s1 UI-R-A0 Rattus nor... 40 0.14
 F14714, SSC8B01 S.scrofa mRNA; expressed sequence tag (5'; c... 38 0.54
 H91505, H91505 SWMFCA089SK Brugia malayi microfilaria cDNA (S... 36 2.1
 AA998610, AA998610 UI-R-C0-if-c-04-0-UI.s1 UI-R-C0 Rattus nor... 36 2.1
 AA893562, AA893562 EST197365 Normalized rat liver, Bento Soar... 36 2.1
 AI008397, AI008397 EST202848 Normalized rat embryo, Bento Soa... 36 2.1

SEQ ID NO:554

Z92544, HS313D11 Human DNA sequence from cosmid 313D11 from ... 700 0.0
 Z46940, HSPRMTNP2 H.sapiens PRM1 gene, PRM2 gene and TNP2 gene 44 0.048
 U85039, TMU85039 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
 U85251, TMU85251 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
 AF003630, AF003630 Theileria mutans clone 15, 32 kDa immunodo... 42 0.19
 AF003629, AF003629 Theileria mutans clone 9, 32 kDa immunodom... 42 0.19
 AB007884, AB007884 Homo sapiens KIAA0424 mRNA, partial cds 42 0.19
 U85040, TMU85040 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
 Z97343, ATFCA8 Arabidopsis thaliana DNA chromosome 4, ESSA I... 40 0.75
 L19655, TOSRNA1X Tomato ringspot virus polyprotein (RNA-1) ge... 40 0.75
 M73822, TOSRNA1A Tomato ringspot virus RNA1 gene, 5' end. 40 0.75
 L02543, BOVMTNNT Bos taurus nicotinamide nucleotide transhydr... 40 0.75
 J03534, BOVNAD Bovine mitochondrial nicotinamide nucleotide t... 40 0.75
 M62862, TRBRTE Trypanosoma cruzi retrotransposon encoding gag... 40 0.75
 X72711, MMREPCFC M.musculus mRNA for replication factor C, l... 38 3.0
 M88489, MUSNBP Mus musculus nonamer binding protein mRNA, com... 38 3.0
 U36441, MMU36441 Mus musculus differentiation specific elemen... 38 3.0
 AB002354, AB002354 Human mRNA for KIAA0356 gene, complete cds 38 3.0
 J03149, CATFMSC Cat (F.domesticus) c-fms proto-oncogene mRNA ... 38 3.0
 J05475, CHKVICOLL Chicken type VI collagen alpha 2 (VI) subun... 38 3.0

AF038163, AF038163 Homo sapiens interleukin-15 (IL-15) gene, ... 38 3.0
 X75917, HSFBMBF H.sapiens mRNA for fetal beta-MHC binding fa... 38 3.0
 X06542, DMHSPG3 Drosophila heat shock gene 3 from 67B locus 38 3.0
 D17315, DRODAGK Fruit fly mRNA for diacylglycerol kinase, co... 38 3.0
 Z58600, HS45E3F H.sapiens CpG DNA, clone 45e3, forward read ... 38 3.0

~~D78638, D78638 Xenopus laevis mRNA for DNA (cytosine-5-) met...~~ 38 3.0
 Z49204, MMNADPTRH M.musculus mRNA for NADP transhydrogenase. 38 3.0
 L10425, BPEMETC Bordetella avium beta-cystathionase-lyase (me... 38 3.0
 U01222, U01222 Mus musculus activator 1 large subunit (A1-p14... 38 3.0
 U15037, MMU15037 Mus musculus replication factor C large subu... 38 3.0
 K01643, FCSSMONC Feline sarcoma virus (McDonough strain) tran... 38 3.0
 Z57538, HS183C6F H.sapiens CpG DNA, clone 183c6, forward rea... 38 3.0
 U07157, MMU07157 Mus musculus ISRE-binding protein (IBF-1) mR... 38 3.0
 Z64961, HS183F7R H.sapiens CpG DNA, clone 183f7, reverse rea... 38 3.0

HUMAN ESTs

SEQ ID NO:555

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 916 0.0
 S51239, S51239 calreticulin [Aplysia californica=marine snail... 48 0.005
 Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.019
 AF022814, AF022814 Fugu rubripes transcription factor (SLP-1)... 44 0.073
 X82638, CSCYTOX C.sordellii cytotoxin gene 42 0.29
 U63063, SCU63063 Saccharomyces cerevisiae something about sil... 42 0.29
 X63501, SCRPC53 S.cerevisiae RPC53 gene for RNA polymerase C... 42 0.29
 U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.29
 Z74201, SCYDL153C S.cerevisiae chromosome IV reading frame O... 42 0.29
 U66032, MTU66032 Methanosarcina thermophila CO dehydrogenase/... 42 0.29
 Z95620, SPBC3D6 S.pombe chromosome II cosmid c3D6 42 0.29
 X97751, SCIV23 S.cerevisiae chrIV genes STE7, CLB3, MSH5, RP... 42 0.29
 X65541, ATCAN A.thaliana mRNA for carbonic anhydrase 42 0.29
 L14750, ATHCARANHY Arabidopsis thaliana carbonic anhydrase ge... 42 0.29
 U00995, U00995 Rattus norvegicus TA1 mRNA, complete cds. 40 1.1
 S73876, S73876 FPR3=FKBP-70 [Saccharomyces cerevisiae, Genomi... 40 1.1
 U12825, SCU12825 Saccharomyces cerevisiae transcription facto... 40 1.1
 Z74237, SCYDL189W S.cerevisiae chromosome IV reading frame O... 40 1.1
 U76906, REU76906 Rhizobium etli FixK (fixK), FixN (fixN), mon... 40 1.1

AF050157, MMHC135G15	Mus musculus major histocompatibility lo...	40	1.1
X58857, SCPPH22	S.cerevisiae PPH22 gene for protein phosphat...	40	1.1
X79379, SCPROIS	S.cerevisiae gene for proline isomerase	40	1.1
Z68341, CEF01G4	Caenorhabditis elegans cosmid F01G4, complet...	40	1.1
M17192, MUSHOX1	Mouse homeodomain protein (Hox1.1) mRNA, comp...	40	1.1
U50307, CELF43H9	Caenorhabditis elegans cosmid F43H9.	40	1.1
S73144, S73144	bone sialoprotein [cattle, fetal bone cells, m...	40	1.1
L34569, YSCFPR3A	Saccharomyces cerevisiae (clone pBYNG1) prol...	40	1.1
D78303, D78303	Rattus norvegicus YT521 mRNA for RNA splicing...	40	1.1
X83276, SCDNAIV	S.cerevisiae DNA for ORFs from chromosome IV	40	1.1
U54558, HSU54558	Human translation initiation factor eIF3 p66...	40	1.1
Z50109, CEC09H10	Caenorhabditis elegans cosmid C09H10, compl...	40	1.1
X56983, EAVATP1	E.arvense gene for catalytic 70kDa V-ATPase ...	40	1.1
AB011125, AB011125	Homo sapiens mRNA for KIAA0553 protein, p...	40	1.1
Z46373, SC8248	S.cerevisiae chromosome XIII cosmid 8248	40	1.1
AF039042, CELZK697	Caenorhabditis elegans cosmid ZK697	40	1.1
Z28028, SCYKL028W	S.cerevisiae chromosome XI reading frame O...	40	1.1
AC005266, AC005266	Homo sapiens chromosome 19, cosmid F23465,...	38	4.5
U60822, HSU60822	Human dystrophin (DMD) gene, exons 7, 8 and ...	38	4.5
AJ003141, HVAJ3141	Hordeum vulgare mRNA for stress-related p...	38	4.5
M26250, CRAGAP43	Goldfish (C.auratus) growth-associated prote...	38	4.5
X95267, GGRYR3	G.gallus mRNA for ryanodine receptor type 3	38	4.5
L37092, MUSCDPK	Mus musculus cyclin-dependent kinase homologue...	38	4.5
Z72507, CEF17C11	Caenorhabditis elegans cosmid F17C11, compl...	38	4.5
U29608, DMU29608	Drosophila melanogaster large tumor suppress...	38	4.5
Z49072, CET24A11	Caenorhabditis elegans cosmid T24A11, compl...	38	4.5
M83142, RATBGASTR	Rattus norvegicus beta-galactoside-alpha 2,...	38	4.5
Z20656, HSCAMHCA	Homo sapiens of cardiac alpha-myosin heavy ...	38	4.5
M82937, YSACS2A	Candida albicans chitin synthase 2 (CHS2) gen...	38	4.5
U28888, MMU28888	Mus musculus neurogenic differentiation fact...	38	4.5
S66408, S66408	c-erbB=proto-oncogene {exon 1, promoter} [chic...	38	4.5
AC002396, AC002396	Arabidopsis thaliana chromosome I BAC F316...	38	4.5
AE000665, MMAE000665	Mus musculus TCR beta locus from bases 5...	38	4.5
L39837, DROWARTS	Drosophila melanogaster tumor suppressor (war...	38	4.5
AG000377, AG000377	Homo sapiens genomic DNA, 21q region, clo...	38	4.5
X05632, HSMHCAG1	Human alpha-MHC gene for myosin heavy chain...	38	4.5
AC002108, AC002108	Genomic sequence from Mouse 4, complete se...	38	4.5
U37219, HSU37219	Human cyclophilin-like protein CyP-60 mRNA, ...	38	4.5
M58633, MUSP58GTA	Mouse p58/GTA protein kinase mRNA, complete...	38	4.5
M25162, HUMMYHC08	Human cardiac alpha-myosin heavy chain (MYH...	38	4.5
Z46259, SCRPD3COS	S.cerevisiae FY1676 RPD3 gene.	38	4.5
U09558, LJU09558	Lactobacillus johnsonii ATCC 11506 insertion...	38	4.5
U66160, MMUSC104	Mus musculus extracellular matrix associated...	38	4.5
Z73126, SCYLL021W	S.cerevisiae chromosome XII reading frame ...	38	4.5
U83981, HSU83981	Homo sapiens apoptosis associated protein (G...	38	4.5

U59897, MRU59897	Macropus robustus hypoxanthine phosphoribosy...	38 4.5
D38256, YSCSCT1	Yeast gene for suppressor of ctr mutation	38 4.5
X69838, HSG9A	H.sapiens mRNA for G9a	38 4.5
X52952, RNCMOSO	Rat mRNA for c-mos	38 4.5
U37221, HSU37221	Human cyclophilin-like protein mRNA, partial...	38 4.5
X65880, DPRH4OP1	D.pseudoobscura rh4 opsin gene, exon 1	38 4.5
U58971, NTU58971	Nicotiana tabacum calmodulin-binding protein...	38 4.5
Z35773, SCYBL012C	S.cerevisiae chromosome II reading frame O...	38 4.5
X67668, MMHMG2	M.musculus mRNA for high mobility group 2 pro...	38 4.5
L81727, HSL81727	Homo sapiens (subclone 1_d5 from P1 H69) DNA...	38 4.5
AL023800, HS833B2	Human DNA sequence *** SEQUENCING IN PROGR...	38 4.5
X62438, HVPERO	H.vulgare mRNA for peroxidase	38 4.5
AC004096, AC004096	Mouse Cosmid ma66a100 from 14D1-D2, comple...	38 4.5
AL008980, PFSC03050	Plasmodium falciparum DNA *** SEQUENCING...	38 4.5
U64827, MMU64827	Mus musculus extracellular matrix associated...	38 4.5
AC003010, HUAC003010	Homo sapiens Chromosome 16 BAC clone CIT...	38 4.5
AE001002, AE001002	Archaeoglobus fulgidus section 105 of 172 ...	38 4.5
U86662, LEU86662	Lycopersicon esculentum VPS41 (tVPS41) mRNA,...	38 4.5
M20386, CHKEGFR	Chicken epidermal growth factor receptor (CER...	38 4.5
M77637, CHKEGF	Gallus gallus EGF/TGF-alpha receptor (c-erbB) ...	38 4.5
U08185, MMU08185	Mus musculus BALB/c zinc-finger protein Blim...	38 4.5
AC004231, AC004231	Homo sapiens chromosome 17, clone hRPC.111...	38 4.5
Z50100, HVC39SAT	H.vulgare GAA-satellite DNA	38 4.5
X53731, SCSPA2G	S. cerevisiae SPA2 gene	38 4.5
U37220, HSU37220	Human cyclophilin-like protein mRNA, partial...	38 4.5
X97560, SC32KBF	S.cerevisiae 32kb DNA fragment of chromosome...	38 4.5
AB011479, AB011479	Arabidopsis thaliana genomic DNA, chromos...	38 4.5
U89340, LVU89340	Lytechinus variegatus Endo16 homolog (LvEndo1...	38 4.5
U73850, TCU73850	Trypanosoma cruzi 29 kDa proteasome subunit ...	38 4.5
AB006698, AB006698	Arabidopsis thaliana genomic DNA, chromos...	38 4.5
D37888, CYIMYC2	Cyprinus carpio c-myc gene for c-Myc, comple...	38 4.5
AF017349, MMDSGIII	7 Mus musculus desmoglein 3 (Dsg3) gene, i...	38 4.5
X91807, OSTA136	O.sativa mRNA for alpha-tubulin (clone OSTA-...	38 4.5
Z71587, SCYNL311C	S.cerevisiae chromosome XIV reading frame ...	38 4.5
AE000742, AE000742	Aquifex aeolicus section 74 of 109 of the ...	38 4.5

HUMAN ESTs

AA324311, AA324311	EST27136 Cerebellum II Homo sapiens cDNA 5...	593 e-167
AA639190, AA639190	ns04a01.r1 NCI_CGAP_Ew1 Homo sapiens cDNA ...	513 e-143
AA172199, AA172199	zo96a06.r1 Stratagene ovarian cancer (#937...	505 e-141
AA588066, AA588066	nk10d08.s1 NCI_CGAP_Co2 Homo sapiens cDNA ...	502 e-140
AA412036, AA412036	zt68d09.s1 Soares testis NHT Homo sapiens ...	502 e-140
AA508745, AA508745	ni23a03.s1 NCI_CGAP_Co4 Homo sapiens cDNA ...	502 e-140

AA480337, AA480337 ne33a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 502 e-140
AA902270, AA902270 ok69e04.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 502 e-140
AA947303, AA947303 ok20d04.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom... 502 e-140
R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'. 490 e-136
AA811913, AA811913 ob51d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 464 e-128
AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 464 e-128
AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 400 e-109
R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 359 5e-97
AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 315 6e-84
R58372, R58372 G3243 Fetal heart Homo sapiens cDNA clone G324... 262 8e-68
AA389703, AA389703 M421 Fetal heart, Lambda ZAP Express Homo ... 202 6e-50
W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 4e-20
W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 1e-08
T65784, T65784 yc11f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.14
AA179601, AA179601 zp49f10.r1 Stratagene HeLa cell s3 937216 ... 42 0.14
AA928679, AA928679 on48e08.s1 NCI_CGAP_Co8 Homo sapiens cDNA ... 40 0.55
AA887972, AA887972 nq95g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.55
W46946, W46946 zc40c05.s1 Soares senescent fibroblasts NbHSF ... 40 0.55
AA887862, AA887862 nq99b08.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.55
AA554819, AA554819 ni34d08.s1 NCI_CGAP_Lu1 Homo sapiens cDNA ... 40 0.55
AA557362, AA557362 nl81d12.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
AA252258, AA252258 zr29e04.s1 Stratagene NT2 neuronal precurs... 40 0.55
N34310, N34310 yy52b10.s1 Homo sapiens cDNA clone 277147 3' s... 40 0.55
AA552228, AA552228 nk06b04.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 40 0.55
AI017648, AI017648 ou99b02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA... 40 0.55
T17395, T17395 NIB846 Normalized infant brain, Bento Soares H... 40 0.55
AA219659, AA219659 zr05e10.s1 Stratagene NT2 neuronal precurs... 40 0.55
AA463841, AA463841 zx67f06.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.55
N66817, N66817 za09b11.s1 Homo sapiens cDNA clone 292029 3' s... 40 0.55
AA167358, AA167358 zp06f12.s1 Stratagene ovarian cancer (#937... 40 0.55
AA063505, AA063505 zf70d02.r1 Soares pineal gland N3HPG Homo ... 40 0.55
AA731625, AA731625 nw64a04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
AA100119, AA100119 zl80g04.s1 Stratagene colon (#937204) Homo... 40 0.55
AA181572, AA181572 zp51d04.s1 Stratagene HeLa cell s3 937216 ... 40 0.55
AA327182, AA327182 EST30459 Colon I Homo sapiens cDNA 5' end ... 40 0.55
R48608, R48608 yj65f07.s1 Homo sapiens cDNA clone 153637 3' s... 40 0.55
AA678485, AA678485 ah06e04.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA082353, AA082353 zn38c11.r1 Stratagene endothelial cell 937... 40 0.55
AA633213, AA633213 nq57c06.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.55
W38410, W38410 zc77g09.s1 Pancreatic Islet Homo sapiens cDNA ... 40 0.55
AA345893, AA345893 EST51967 Gall bladder I Homo sapiens cDNA ... 40 0.55
N26876, N26876 yx97f06.s1 Homo sapiens cDNA clone 269699 3' s... 40 0.55
N95279, N95279 zb60c09.s1 Soares fetal lung NbHL19W Homo sapi... 40 0.55
AI041637, AI041637 ox92h08.x1 Soares_senescent_fibroblasts_Nb... 40 0.55
N67830, N67830 za05d12.s1 Homo sapiens cDNA clone 291671 3' s... 40 0.55

AA535094, AA535094 nf84e06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
AA514414, AA514414 nf57d11.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
T56802, T56802 ya71h07.s2 Homo sapiens cDNA clone 67165 3' co... 40 0.55
N68147, N68147 yz55f12.s1 Homo sapiens cDNA clone 286991 3' s... 40 0.55
AA535811, AA535811 nf93g10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
AA115591, AA115591 z105g09.s1 Soares pregnant uterus NbHPU Ho... 40 0.55
N75851, N75851 za96g11.s1 Homo sapiens cDNA clone 300452 3'. 40 0.55
AA534433, AA534433 nf80a08.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
H99778, H99778 yx36g01.s1 Homo sapiens cDNA clone 263856 3' s... 40 0.55
AA970859, AA970859 oo81h03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.55
F02131, HSC0PF092 H. sapiens partial cDNA sequence; clone c-... 40 0.55
AA810279, AA810279 od14g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
AA595146, AA595146 nl84b01.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
AA632386, AA632386 np67e06.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
AA135124, AA135124 zo24c04.s1 Stratagene colon (#937204) Homo... 40 0.55
AA143500, AA143500 zo31b10.s1 Stratagene colon (#937204) Homo... 40 0.55
AA854992, AA854992 aj53g12.s1 Soares testis NHT Homo sapiens ... 40 0.55
AA156872, AA156872 z120h07.s1 Soares pregnant uterus NbHPU Ho... 40 0.55
AA160994, AA160994 zq41c12.s1 Stratagene hNT neuron (#937233)... 40 0.55
AA961724, AA961724 or60a10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 40 0.55
AA551210, AA551210 nj27e09.s1 NCI_CGAP_AA1 Homo sapiens cDNA ... 40 0.55
R44103, R44103 yg27c10.s1 Homo sapiens cDNA clone 33636 3'. 40 0.55
AA938086, AA938086 oj08h08.s1 NCI_CGAP_Mel3 Homo sapiens cDNA... 40 0.55
AA576021, AA576021 nm57d11.s1 NCI_CGAP_Br3 Homo sapiens cDNA ... 40 0.55
AA722725, AA722725 zg86b09.s1 Soares fetal heart NbHH19W Homo... 40 0.55
AA678948, AA678948 ah08h11.s1 Gessler Wilms tumor Homo sapien... 40 0.55
W07435, W07435 za96g11.r1 Soares fetal lung NbHL19W Homo sapi... 40 0.55
T34639, T34639 EST72167 Homo sapiens cDNA 5' end similar to s... 40 0.55
AA632245, AA632245 np67b09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.55
R76418, R76418 yi58a10.s1 Homo sapiens cDNA clone 143418 3'. 40 0.55
AI028447, AI028447 ow08b09.x1 Soares parathyroid tumor NbHPA ... 40 0.55
AI002929, AI002929 an15e12.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA779388, AA779388 ae26a03.s1 Soares NbHFB Homo sapiens cDNA ... 40 0.55
AA776220, AA776220 ah10f02.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA815223, AA815223 oc05c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
W60807, W60807 zd27b08.s1 Soares fetal heart NbHH19W Homo sap... 40 0.55
AA666007, AA666007 ag71g01.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA643849, AA643849 np26f07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.55
AA846740, AA846740 aj99b12.s1 Soares parathyroid tumor NbHPA ... 40 0.55
AA598498, AA598498 ae38h01.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA535972, AA535972 nf95a01.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
AA488544, AA488544 ab37g06.r1 Stratagene HeLa cell s3 937216 ... 40 0.55
AA866044, AA866044 oh52g07.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.55
C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.55

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 167 1e-39
 AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.78
~~AA413261, AA413261 ve52f04.r1 Beddington mouse embryonic regi... 38 0.78~~
 AA097645, AA097645 mm36f09.r1 Stratagene mouse skin (#937313)... 38 0.78
 AA122578, AA122578 mn25b08.r1 Beddington mouse embryonic regi... 38 0.78
 AA122581, AA122581 mn25c08.r1 Beddington mouse embryonic regi... 38 0.78
 AA646168, AA646168 vn11e06.r1 Stratagene mouse Tcell 937311 M... 36 3.1
 AA200881, AA200881 mu03c09.r1 Soares mouse 3NbMS Mus musculus... 36 3.1
 AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 3.1
 AA217675, AA217675 mv01b09.r1 Soares mouse lymph node NbMLN M... 36 3.1
 AI006387, AI006387 ua71d09.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.1
 AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 3.1
 AA207387, AA207387 mv89a11.r1 GuayWoodford Beier mouse kidney... 36 3.1
 AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 3.1
 AA123112, AA123112 mn30g01.r1 Beddington mouse embryonic regi... 36 3.1
 AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 3.1
 AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 3.1
 W12171, W12171 ma59a10.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.1
 AA208446, AA208446 mv85e01.r1 GuayWoodford Beier mouse kidney... 36 3.1
 AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 3.1
 AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 3.1
 AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 3.1
 AA561847, AA561847 vl27a12.r1 Stratagene mouse Tcell 937311 M... 36 3.1
 AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 3.1
 AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.1
 AA052080, AA052080 mf69f12.r1 Soares mouse embryo NbME13.5 14... 36 3.1
 AA000646, AA000646 mg23f09.r1 Soares mouse embryo NbME13.5 14... 36 3.1
 AA510521, AA510521 vh59a05.r1 Soares mouse mammary gland NbMM... 36 3.1
 AI006122, AI006122 ua86h01.r1 Soares mouse mammary gland NbMM... 36 3.1
 AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 3.1
 W77413, W77413 me64d06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.1
 AA114809, AA114809 mn17e09.r1 Beddington mouse embryonic regi... 36 3.1
 AA793564, AA793564 vn54c05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.1
 AA174537, AA174537 mt10f09.r1 Soares mouse 3NbMS Mus musculus... 36 3.1
 W62181, W62181 md87d08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.1
 AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.1
 AA286005, AA286005 va30e05.r1 GuayWoodford Beier mouse kidney... 36 3.1
 AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 3.1
 AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 3.1

AA519228, AA519228 TgESTzz39h02.s1 TgME49 invivo Bradyzoite c... 44 0.011

AA520185, AA520185	TgESTzz39d03.s1	TgME49 invivo Bradyzoite c...	44	0.011
AA531917, AA531917	TgESTzz48f01.r1	TgME49 invivo Bradyzoite c...	44	0.011
AA519997, AA519997	TgESTzz36h03.r1	TgME49 invivo Bradyzoite c...	44	0.011
AA520811, AA520811	TgESTzz64d05.r1	TgME49 invivo Bradyzoite c...	44	0.011
AA520866, AA520866	TgESTzz68e05.r1	TgME49 invivo Bradyzoite c...	44	0.011
AA519844, AA519844	TgESTzz36c03.r1	TgME49 invivo Bradyzoite c...	44	0.011
AA274295, AA274295	TgESTzz24c11.s1	TgME49 invivo Bradyzoite c...	44	0.011
AA520901, AA520901	TgESTzz65a05.r1	TgME49 invivo Bradyzoite c...	44	0.011
AA519829, AA519829	TgESTzz36a02.r1	TgME49 invivo Bradyzoite c...	44	0.011
AA531839, AA531839	TgESTzz47h05.r1	TgME49 invivo Bradyzoite c...	44	0.011
C70525, C70525	C.elegans cDNA clone yk409g6 : 5' end, single...		44	0.011
AA520235, AA520235	TgESTzz53c06.r1	TgME49 invivo Bradyzoite c...	42	0.044
T42800, T42800	6063 Lambda-PRL2 Arabidopsis thaliana cDNA clo...		42	0.044
R29976, R29976	12581 Lambda-PRL2 Arabidopsis thaliana cDNA cl...		42	0.044
H32045, H32045	EST106774 Rat PC-12 cells, untreated Rattus sp...		40	0.18
AA819924, AA819924	MF5MA171.AE3 S. mansoni female adult Lambd...		40	0.18
H37128, H37128	15257 Lambda-PRL2 Arabidopsis thaliana cDNA cl...		40	0.18
T04367, T04367	414 Lambda-PRL2 Arabidopsis thaliana cDNA clon...		40	0.18
R90528, R90528	16883 Lambda-PRL2 Arabidopsis thaliana cDNA cl...		40	0.18
AA660422, AA660422	00298 MtrHE Medicago truncatula cDNA 5'		40	0.18
U94861, RRU94861	Rattus norvegicus clone HCY3 mRNA sequence		40	0.18
F14275, ATTS5197	A. thaliana transcribed sequence; clone YBY...		38	0.69
W43730, W43730	23107 CD4-16 Arabidopsis thaliana cDNA clone H...		38	0.69
N65025, N65025	20065 Lambda-PRL2 Arabidopsis thaliana cDNA cl...		38	0.69
AI001628, AI001628	EST0210 Tilapia brain cDNA library in pUC1...		38	0.69
H74687, H74687	383 Brassica napus cDNA clone R25R.		38	0.69
AA395597, AA395597	27394 Lambda-PRL2 Arabidopsis thaliana cDN...		38	0.69
AA753070, AA753070	97AS2091 Rice Immature Seed Lambda ZAPII c...		38	0.69
D41274, RICS3647A	Rice cDNA, partial sequence (S3647_1A).		38	0.69
Z25731, ATTS1208	A. thaliana transcribed sequence; clone VCV...		38	0.69
N82780, N82780	TgESTzy34e03.r1 TgRH Tachyzoite cDNA Toxoplas...		38	0.69
AA597822, AA597822	29889 Lambda-PRL2 Arabidopsis thaliana cDN...		38	0.69
AA948906, AA948906	LD27590.5prime LD Drosophila melanogaster ...		38	0.69
AI013695, AI013695	EST208370 Normalized rat spleen, Bento Soa...		38	0.69
AA753263, AA753263	96BS0294 Rice Immature Seed Lambda ZAPII c...		38	0.69
F14402, ATTS5324	A. thaliana transcribed sequence; clone TAP...		36	2.7
T46158, T46158	9421 Lambda-PRL2 Arabidopsis thaliana cDNA clo...		36	2.7
C91400, C91400	Dictyostelium discoideum slug cDNA, clone SSK169		36	2.7
T46009, T46009	9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo...		36	2.7
AA440655, AA440655	LD15510.5prime LD Drosophila melanogaster ...		36	2.7
AA559374, AA559374	MU002092.NH3 York-Harrop-lung-A Schistosom...		36	2.7
Z32623, ATTS2751	A. thaliana transcribed sequence; clone YAP...		36	2.7
T43683, T43683	6946 Lambda-PRL2 Arabidopsis thaliana cDNA clo...		36	2.7
AA263535, AA263535	LD06645.5prime LD Drosophila melanogaster ...		36	2.7
C37095, C37095	C.elegans cDNA clone yk482c11 : 3' end, singl...		36	2.7

C57017, C57017 *C.elegans* cDNA clone yk308h9 : 3' end, single... 36 2.7
 C93857, C93857 *Dictyostelium discoideum* slug cDNA, clone SSL794 36 2.7
 C92242, C92242 *Dictyostelium discoideum* slug cDNA, clone SSD283 36 2.7
 Z33976, ATTS3037 *A. thaliana* transcribed sequence; clone YAP... 36 2.7
 R62091, R62091 EST351 *Strongylocentrotus purpuratus* cDNA 5' end. 36 2.7

 AA567455, AA567455 HL01288.5prime HL *Drosophila melanogaster* ... 36 2.7
 C74456, C74456 Rice cDNA, partial sequence (E31357_1A) 36 2.7
 AA753227, AA753227 97AS2316 Rice Immature Seed Lambda ZAPII c... 36 2.7
 C92456, C92456 *Dictyostelium discoideum* slug cDNA, clone SSE569 36 2.7
 T20458, T20458 2466 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7
 R29905, R29905 12510 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 2.7
 M79841, M79841 wEST00378 *Caenorhabditis elegans* cDNA clone CE... 36 2.7
 Z17562, ATTS0136 *A. thaliana* transcribed sequence; clone TAT... 36 2.7
 D71983, CELK084H2R *C.elegans* cDNA clone yk84h2 : 3' end, sin... 36 2.7
 T20404, T20404 2412 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7
 AI012789, AI012789 EST207240 Normalized rat placenta, Bento S... 36 2.7
 U83048, BTU83048 *Bos taurus* clone 0429 mRNA sequence 36 2.7
 AA660182, AA660182 00022 MtRHE *Medicago truncatula* cDNA 5' si... 36 2.7
 D48514, RICS14740A Rice cDNA, partial sequence (S14740_1A). 36 2.7
 C90110, C90110 *Dictyostelium discoideum* slug cDNA, clone SSI103 36 2.7
 H36880, H36880 15009 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 2.7
 AA699152, AA699152 HL07807.5prime HL *Drosophila melanogaster* ... 36 2.7
 C11922, C11922 *C.elegans* cDNA clone yk144a11 : 5' end, singl... 36 2.7
 AA816691, AA816691 LD03795.5prime LD *Drosophila melanogaster* ... 36 2.7

SEQ ID NO:556

X99668, MM22A3 *M.musculus* mRNA for exon from unknown gene 22A3 260 5e-67
 Z83760, CICOS41 *Ciona intestinalis* DNA sequence from cosmid ... 40 0.94
 Z75710, CED1081 *Caenorhabditis elegans* cosmid D1081, complet... 40 0.94
 U73628, HSU73628 Human chromosome 11 101h11 cosmid, complete ... 40 0.94
 X99757, DMDYDTRO *D.melanogaster* mRNA for dystrophin 38 3.7
 U51189, HIVU51189 HIV-1 clone 93th253 from Thailand, complete... 38 3.7
 AC004118, AC004118 *Drosophila melanogaster* (P1 DS06238 (D26))... 38 3.7
 U50313, CELF44C4 *Caenorhabditis elegans* cosmid F44C4. 38 3.7
 AC004503, AC004503 *Homo sapiens* chromosome 5, P1 clone 1354A7... 38 3.7
 M16840, WHTCPA2 Wheat Asp-tRNA gene. 38 3.7
 Y13381, RNAMPH1 *Rattus norvegicus* mRNA for amphiphysin, amph1 38 3.7
 AC002994, AC002994 *Homo sapiens* chromosome 17, clone HRPC987K... 38 3.7
 AB008271, AB008271 *Arabidopsis thaliana* genomic DNA, chromos... 38 3.7
 D49701, ASNNIAD *Aspergillus oryzae* niaD gene for nitrate red... 38 3.7

X59422, HSPLD1 H.sapiens Pl d1 repetitive DNA 38 3.7
 Z98555, PFSC03027 Plasmodium falciparum DNA *** SEQUENCING I... 38 3.7

HUMAN ESTs

AA315671, AA315671 EST187451 Colon carcinoma (HCC) cell line ... 932 0.0
 U56653, HSU56653 Human heat shock inducible mRNA 769 0.0
 AA487685, AA487685 ab23b09.r1 Stratagene lung (#937210) Homo ... 751 0.0
 AA044797, AA044797 zk67g12.r1 Soares pregnant uterus NbHPU Ho... 749 0.0
 AA314922, AA314922 EST186735 HCC cell line (matatasis to liv... 698 0.0
 AA082278, AA082278 zn42d12.r1 Stratagene endothelial cell 937... 668 0.0
 H22613, H22613 yn64f03.r1 Homo sapiens cDNA clone 173213 5'. 624 e-177
 AA044743, AA044743 zk67g12.s1 Soares pregnant uterus NbHPU Ho... 622 e-176
 AA487470, AA487470 ab23b09.s1 Stratagene lung (#937210) Homo ... 601 e-170
 AA121057, AA121057 zm22b03.r1 Stratagene pancreas (#937208) H... 581 e-164
 AA194396, AA194396 zq05g05.s1 Stratagene muscle 937209 Homo s... 535 e-150
 AA384283, AA384283 EST97787 Thyroid Homo sapiens cDNA 5' end 535 e-150
 AA669015, AA669015 ab88f01.s1 Stratagene lung (#937210) Homo ... 535 e-150
 AA194336, AA194336 zq05g05.r1 Stratagene muscle 937209 Homo s... 505 e-141
 R96173, R96173 yt84e09.r1 Homo sapiens cDNA clone 231016 5'. 486 e-135
 AA028934, AA028934 zk08b09.s1 Soares pregnant uterus NbHPU Ho... 484 e-134
 AA564849, AA564849 nj22c04.s1 NCI_CGAP_AA1 Homo sapiens cDNA ... 442 e-122
 AA932576, AA932576 oo57g10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 440 e-121
 AA876265, AA876265 oi12g09.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 434 e-120
 AA025525, AA025525 ze86a11.s1 Soares fetal heart NbHH19W Homo... 430 e-118
 U56654, HSU56654 Human heat shock inducible mRNA 426 e-117
 AA746600, AA746600 nx18c02.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 406 e-111
 AA876346, AA876346 oj24a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 406 e-111
 W23082, W23082 78D1 Human retina cDNA Tsp509I-cleaved sublibr... 402 e-110
 AI034059, AI034059 ow14h11.x1 Soares parathyroid tumor NbHPA ... 357 2e-96
 AA662934, AA662934 nu92d09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 323 2e-86
 AA844331, AA844331 ai95f01.s1 Soares parathyroid tumor NbHPA ... 301 8e-80
 AA249866, AA249866 y0761.seq.F Human fetal heart, Lambda ZAP ... 297 1e-78
 R19215, R19215 yg24b07.r1 Homo sapiens cDNA clone 33126 5'. 280 3e-73
 T39355, T39355 ya04g08.r1 Homo sapiens cDNA clone 60542 5'. 254 2e-65
 AA731264, AA731264 nw57c08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 220 2e-55
 AA768549, AA768549 oa67c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 220 2e-55
 AA668506, AA668506 ac49a11.s1 Stratagene hNT neuron (#937233)... 216 4e-54
 T55337, T55337 yb79b05.s1 Homo sapiens cDNA clone 77361 3'. 198 8e-49
 AA860575, AA860575 aj86a09.s1 Soares parathyroid tumor NbHPA ... 198 8e-49
 AA335548, AA335548 EST39962 Epididymus Homo sapiens cDNA 5' end 109 6e-22
 R13183, R13183 yf73f02.r1 Homo sapiens cDNA clone 27960 5'. 58 2e-06
 T80034, T80034 yd04c06.r1 Homo sapiens cDNA clone 24672 5'. 38 1.8
 AA595230, AA595230 nl84g02.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 38 1.8

AA871935, AA871935 vq42h02.r1 Barstead bowel MPLRB9 Mus muscu... 664 0.0
 AA062330, AA062330 ml35e10.r1 Stratagene mouse testis (#93730... 589 e-167
 AI048164, AI048164 ud71b09.v1 Sugano mouse liver mlie Mus mus... 537 e-151
 W08037, W08037 mb37h01.r1 Soares mouse p3NMF19.5 Mus musculus... 462 e-128
 AA387311, AA387311 vc19a03.r1 Ko mouse embryo 11 5dpc Mus mus... 264 6e-69
 AA163072, AA163072 ms31a11.r1 Stratagene mouse skin (#937313)... 212 2e-53
 AA596763, AA596763 vm60a10.r1 Stratagene mouse Tcell 937311 M... 178 3e-43
 AA562549, AA562549 vl63a11.r1 Knowles Solter mouse blastocyst... 143 2e-32
 AA212378, AA212378 mu44c03.r1 Soares 2NbMT Mus musculus cDNA ... 113 1e-23
 AA450862, AA450862 vg55h12.r1 Beddington mouse embryonic regi... 111 5e-23
 AA990073, AA990073 ua59a01.r1 Soares 2NbMT Mus musculus cDNA ... 86 3e-15
 AA921175, AA921175 vy54b10.r1 Stratagene mouse lung 937302 Mu... 78 8e-13
 AA261119, AA261119 mz89e01.r1 Soares mouse NML Mus musculus c... 38 0.65
 AI005952, AI005952 ua80f06.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.6
 AA123274, AA123274 mn23a08.r1 Beddington mouse embryonic regi... 36 2.6
 AI036828, AI036828 vw96c02.r1 Stratagene mouse skin (#937313)... 36 2.6

H35787, H35787 EST109178 Rat PC-12 cells, NGF-treated (9 days... 105 3e-21
 AA686082, AA686082 EST109179 Rat PC-12 cells, NGF-treated (9 ... 86 3e-15
 C23464, C23464 Jpanese flounder liver cDNA, LE5(10) 72 4e-11
 C23465, C23465 Jpanese flounder liver cDNA, LE5(10) 56 2e-06
 AA520314, AA520314 TgESTzz38h12.r1 TgME49 invivo Bradyzoite c... 38 0.57
 AA520085, AA520085 TgESTzz37g05.r1 TgME49 invivo Bradyzoite c... 38 0.57
 AA520033, AA520033 TgESTzz36f10.r1 TgME49 invivo Bradyzoite c... 38 0.57
 AA012516, AA012516 TgESTzz23f04.r1 TgME49cDNA Toxoplasma gond... 38 0.57
 AA274286, AA274286 TgESTzz24c01.s1 TgME49 invivo Bradyzoite c... 38 0.57
 AA660585, AA660585 00471 MtRHE Medicago truncatula cDNA 5' si... 38 0.57
 L35828, BNAESTBD Brassica rapa (clone F0621) expressed sequen... 38 0.57
 AA520070, AA520070 TgESTzz37e05.r1 TgME49 invivo Bradyzoite c... 38 0.57
 C30080, C30080 C.elegans cDNA clone yk236c3 : 3' end, single... 36 2.3
 C39044, C39044 C.elegans cDNA clone yk505a4 : 3' end, single... 36 2.3
 C55023, C55023 C.elegans cDNA clone yk422a3 : 3' end, single... 36 2.3
 AA542589, AA542589 fa08d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
 N25370, N25370 EST000480 Schistosoma mansoni cDNA clone SMTBA... 36 2.3
 AA820625, AA820625 LD24443.5prime LD Drosophila melanogaster ... 36 2.3
 AA494922, AA494922 fa12g10.r1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
 AA495181, AA495181 fa04d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
 D73287, CELK116G6R C.elegans cDNA clone yk116g6 : 3' end, si... 36 2.3
 C28238, C28238 Rice cDNA, partial sequence (C60429_1A) 36 2.3

SEQ ID NO:557

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 948 0.0
 S51239, S51239 calreticulin [*Aplysia californica*=marine snail ... 56 1e-05

 Z74035, CEF47G9 *Caenorhabditis elegans* cosmid F47G9, complet... 46 0.012
 U25723, CPU25723 *Cavia porcellus* alpha-2B adrenoceptor gene, ... 44 0.047
 AL021407, HS13D10 Homo sapiens DNA sequence from PAC 13D10 o... 42 0.19
 U67572, U67572 *Methanococcus jannaschii* section 114 of 150 of... 42 0.19
 V01470, ZMZE01 *Zea mays* gene encoding a zein gene (clone lam... 42 0.19
 U06631, HSU06631 Human (H326) mRNA, complete cds. 42 0.19
 X82638, CSCYTOX *C.sordelii* cytotoxin gene 42 0.19
 AE000926, AE000926 *Methanobacterium thermoautotrophicum* from ... 42 0.19
 AC004135, AC004135 Genomic sequence for *Arabidopsis thaliana* ... 42 0.19
 AC003010, HUAC003010 Homo sapiens Chromosome 16 BAC clone CIT... 40 0.74
 AF050157, MMHC135G15 *Mus musculus* major histocompatibility lo... 40 0.74
 AC002352, AC002352 Homo sapiens 12q24 PAC P256D10 complete se... 40 0.74
 X07699, MMNUCLEO Mouse nucleolin gene 40 0.74
 X02399, MMHOM6 Mouse embryonal carcinoma DNA fragment contai... 40 0.74
 M93661, RATNOTCHX Rat notch 2 mRNA. 40 0.74
 M17440, MUSMHC4H2S Mouse MHC (H-2) S region complement compon... 40 0.74
 U15972, MMU15972 *Mus musculus* homeobox (*Hoxa7*) gene, complete... 40 0.74
 AB001601, AB001601 Homo sapiens DBP2 mRNA for ATP-dependent ... 40 0.74
 U09820, HSU09820 Human helicase II (RAD54L) mRNA, complete cds. 40 0.74
 AB011149, AB011149 Homo sapiens mRNA for KIAA0577 protein, c... 40 0.74
 U26259, MMU26259 *Mus musculus* C2-H2 zinc finger protein mRNA,... 40 0.74
 L48363, MUSZFPTX *Mus musculus* zinc finger protein gene, compl... 40 0.74
 AC003113, AC003113 *Arabidopsis thaliana* BAC F24O1 chromosome ... 40 0.74
 D76432, D76432 Mouse mRNA for transcriptional repressor delt... 40 0.74
 U72937, HSU72937 Human putative DNA dependent ATPase and heli... 40 0.74
 U72915, HSATRX16 Human putative DNA dependent ATPase and heli... 40 0.74
 U00995, U00995 *Rattus norvegicus* TA1 mRNA, complete cds. 40 0.74
 Z48618, SCCHVII35 *S.cerevisiae* genes for RAD54, ACE1(CUP2), ... 40 0.74
 U75653, HSU75653 Human zinc finger helicase (Znf-HX) mRNA, co... 40 0.74
 Z72672, SCYGL150C *S.cerevisiae* chromosome VII reading frame ... 40 0.74
 Z50109, CEC09H10 *Caenorhabditis elegans* cosmid C09H10, compl... 40 0.74
 AF013969, AF013969 *Mus musculus* antigen containing epitope to... 40 0.74
 M95627, HUMAAMP1X Homo sapiens angio-associated migratory cel... 40 0.74
 U72936, HSU72936 Human putative DNA dependent ATPase and heli... 40 0.74
 M88753, DROHTCHRPI Fruitfly heterochromatin protein-1 gene, c... 40 0.74
 U76906, REU76906 *Rhizobium etli* FixK (fixK), FixN (fixN), mon... 40 0.74
 U97085, HSXNP14 Homo sapiens X-linked nuclear protein (ATRX) ... 40 0.74
 L34363, HUMNUCPRO Human X-linked nuclear protein (XNP) gene, ... 40 0.74
 U72938, HSU72938 Human putative DNA dependent ATPase and heli... 40 0.74

X56983, EAVATP1	E.arvense gene for catalytic 70kDa V-ATPase ...	40	0.74
U88539, MMU88539	Mus musculus chromatin structural protein ho...	40	0.74
U07704, HSU07704	Human protein kinase PITSLRE isoform PBETA21...	38	2.9
U07705, HSU07705	Human protein kinase PITSLRE isoform PBETA22...	38	2.9
AF019612, AF019612	Homo sapiens S2P mRNA, complete cds	38	2.9
U04818, HSU04818	Human protein kinase PITSLRE alpha 2-4 mRNA,...	38	2.9
AB002381, AB002381	Human mRNA for KIAA0383 gene, partial cds	38	2.9
AB009520, AB009520	Pyrococcus horikoshii OT3 genomic DNA, 13...	38	2.9
Z83848, HS57A13	Human DNA sequence from PAC 57A13 between ma...	38	2.9
AC004592, AC004592	Homo sapiens PAC clone DJ0244J05 from 5q31...	38	2.9
L11710, ZEFZCMYC	Brachydanio rerio c-myc oncoprotein mRNA, co...	38	2.9
D43920, CHKMETASE	Chicken mRNA for DNA (cytosine-5-)-methylt...	38	2.9
U49056, RNU49056	Rattus norvegicus CTD-binding SR-like protei...	38	2.9
U04824, HSU04824	Human protein kinase PITSLRE alpha 2-1 mRNA,...	38	2.9
U78045, HSU78045	Human collagenase and stromelysin genes, com...	38	2.9
U04816, HSU04816	Human protein kinase PITSLRE alpha 2-2 mRNA,...	38	2.9
U04817, HSU04817	Human protein kinase PITSLRE alpha 2-3 mRNA,...	38	2.9

HUMAN ESTs

AA639190, AA639190	ns04a01.r1 NCI_CGAP_Ew1 Homo sapiens cDNA ...	519	e-145
AA172199, AA172199	zo96a06.r1 Stratagene ovarian cancer (#937...	513	e-144
R23642, R23642	yh35e03.r1 Homo sapiens cDNA clone 131740 5'.	490	e-136
AA902270, AA902270	ok69e04.s1 NCI_CGAP_GC4 Homo sapiens cDNA ...	450	e-124
AA947303, AA947303	ok20d04.s1 Soares NSF_F8_9W_OT_PA_P_S1 Hom...	402	e-110
AA588066, AA588066	nk10d08.s1 NCI_CGAP_Co2 Homo sapiens cDNA ...	347	1e-93
AA412036, AA412036	zt68d09.s1 Soares testis NHT Homo sapiens ...	347	1e-93
AA480337, AA480337	ne33a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ...	347	1e-93
AA508745, AA508745	ni23a03.s1 NCI_CGAP_Co4 Homo sapiens cDNA ...	347	1e-93
AA172083, AA172083	zo96a06.s1 Stratagene ovarian cancer (#937...	315	4e-84
AA811913, AA811913	ob51d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA...	299	2e-79
AA402403, AA402403	zt68d09.r1 Soares testis NHT Homo sapiens ...	299	2e-79
AA725458, AA725458	ai16g01.s1 Soares parathyroid tumor NbHPA ...	250	2e-64
R26558, R26558	yh35e02.s1 Homo sapiens cDNA clone 131738 3'.	250	2e-64
W25749, W25749	11b4 Human retina cDNA randomly primed sublibr...	103	3e-20
W27158, W27158	22h9 Human retina cDNA randomly primed sublibr...	66	6e-09
AA737681, AA737681	nw63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA...	42	0.090
T65784, T65784	yc11f10.s1 Homo sapiens cDNA clone 80395 3' si...	42	0.090
R52021, R52021	yg84h09.r1 Homo sapiens cDNA clone 40181 5' si...	42	0.090
AA569993, AA569993	nm47h04.s1 NCI_CGAP_Br2 Homo sapiens cDNA ...	42	0.090
R50149, R50149	yj61c05.s1 Homo sapiens cDNA clone 153224 3' s...	42	0.090
R87930, R87930	yo47a11.s1 Homo sapiens cDNA clone 181052 3' s...	42	0.090
AA812204, AA812204	ob84f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA...	42	0.090
AA770224, AA770224	ah82e12.s1 Soares testis NHT Homo sapiens ...	42	0.090

D29591, HUMNK752 Human keratinocyte cDNA, clone 752 40 0.36
AA324325, AA324325 EST27219 Cerebellum II Homo sapiens cDNA 5... 40 0.36
AA053063, AA053063 zl71c03.r1 Stratagene colon (#937204) Homo... 40 0.36
T35539, T35539 EST86964 Homo sapiens cDNA 5' end similar to N... 40 0.36
AA974278, AA974278 oq14d03.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.36
W26196, W26196 22b5 Human retina cDNA randomly primed sublibr... 40 0.36

H92585, H92585 yt89c03.s1 Homo sapiens cDNA clone 231460 3'. 40 0.36
AA232334, AA232334 zr27b04.r1 Stratagene NT2 neuronal precurs... 40 0.36
N55775, N55775 J2481F Homo sapiens cDNA clone J2481 5'. 40 0.36
R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.36
C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.36
H19156, H19156 yn50c01.r1 Homo sapiens cDNA clone 171840 5'. 40 0.36
AA299557, AA299557 EST12080 Uterus tumor I Homo sapiens cDNA ... 40 0.36
W84460, W84460 zd89d12.r1 Soares fetal heart NbHH19W Homo sap... 40 0.36
T54194, T54194 ya90a02.r2 Homo sapiens cDNA clone 68906 5'. 40 0.36
AA100203, AA100203 zm16f12.r1 Stratagene pancreas (#937208) H... 38 1.4
AA993061, AA993061 ot92h08.s1 Soares_total_fetus_Nb2HF8_9w Ho... 38 1.4
R53406, R53406 yj70d07.r1 Homo sapiens cDNA clone 154093 5' s... 38 1.4
H99671, H99671 yx35b03.s1 Homo sapiens cDNA clone 263693 3'. 38 1.4
W03410, W03410 za07c09.r1 Soares melanocyte 2NbHM Homo sapien... 38 1.4
N35475, N35475 yy24b03.s1 Homo sapiens cDNA clone 272141 3'. 38 1.4
AA630851, AA630851 nt57f04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 38 1.4
N66458, N66458 yz41b08.s1 Homo sapiens cDNA clone 285591 3'. 38 1.4
AA736438, AA736438 zh31b09.s1 Soares pineal gland N3HPG Homo ... 38 1.4
AA911761, AA911761 og19b01.s1 NCI_CGAP_PNSI Homo sapiens cDNA... 38 1.4
AA085513, AA085513 zn43a10.r1 Stratagene HeLa cell s3 937216 ... 38 1.4
AA678530, AA678530 ah02e05.s1 Gessler Wilms tumor Homo sapien... 38 1.4
AA782011, AA782011 ai75b12.s1 Soares testis NHT Homo sapiens ... 38 1.4
F12352, HSC38H091 H. sapiens partial cDNA sequence; clone c-... 38 1.4
AA861288, AA861288 ak33g01.s1 Soares testis NHT Homo sapiens ... 38 1.4
AA908705, AA908705 ol01b09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 1.4
AA298850, AA298850 EST114450 Thyroid Homo sapiens cDNA 5' end 38 1.4

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 172 1e-41
AI047347, AI047347 ud65c01.y1 Sugano mouse liver mlia Mus mus... 42 0.032
AA832736, AA832736 vw45g10.r1 Soares mouse mammary gland NbMM... 42 0.032
AA960471, AA960471 vw63a05.s1 Soares mouse mammary gland NMLM... 40 0.13
AA880584, AA880584 vw92e01.r1 Stratagene mouse skin (#937313)... 40 0.13
AA107508, AA107508 mp05e07.r1 Life Tech mouse embryo 8 5dpc 1... 40 0.13
AA116682, AA116682 mn28c06.r1 Beddington mouse embryonic regi... 40 0.13
AA522310, AA522310 vi45b02.r1 Beddington mouse embryonic regi... 40 0.13
AA162231, AA162231 mn44h02.r1 Beddington mouse embryonic regi... 40 0.13

AA414037, AA414037 vc68g03.s1 Knowles Solter mouse 2 cell Mus... 40 0.13
 AA596585, AA596585 vm58e12.r1 Stratagene mouse Tcell 937311 M... 38 0.51
 AA863563, AA863563 vx05a10.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.51
 AA795177, AA795177 vq94g04.r1 Knowles Solter mouse blastocyst... 38 0.51
 AA914764, AA914764 vy92h04.r1 Soares mouse mammary gland NbMM... 38 0.51
 AA590440, AA590440 vm20c04.r1 Knowles Solter mouse blastocyst... 38 0.51

 AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.51
 AA260352, AA260352 va93c10.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.51
 AA444734, AA444734 ve75d10.r1 Soares mouse mammary gland NbMM... 38 0.51
 C85885, C85885 Mus musculus fertilized egg cDNA 3'-end seque... 38 0.51
 AA794590, AA794590 vu78h12.r1 Stratagene mouse skin (#937313)... 38 0.51
 AA529643, AA529643 vi38a09.r1 Beddington mouse embryonic regi... 38 0.51
 AA607084, AA607084 vm84a09.r1 Knowles Solter mouse blastocyst... 38 0.51
 AA636994, AA636994 vn05g06.r1 Knowles Solter mouse blastocyst... 38 0.51
 AA675676, AA675676 vr73h08.s1 Knowles Solter mouse 2 cell Mus... 38 0.51
 AA163890, AA163890 ms52f09.r1 Life Tech mouse embryo 13 5dpc ... 38 0.51
 C80539, C80539 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 38 0.51
 AA051352, AA051352 mj53a09.r1 Soares mouse embryo NbME13.5 14... 38 0.51
 W36885, W36885 mb64f09.r1 Soares mouse p3NMF19.5 Mus musculus... 38 0.51
 AA930627, AA930627 vy67c05.r1 Stratagene mouse macrophage (#9... 38 0.51
 AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 2.0
 AA967267, AA967267 vz70e08.r1 Soares mouse mammary gland NbMM... 36 2.0
 AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 2.0
 AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 2.0
 AA170036, AA170036 ms52d01.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0
 AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 2.0
 AA555634, AA555634 vk49f08.r1 Stratagene mouse Tcell 937311 M... 36 2.0
 AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 2.0
 AA606813, AA606813 vm90h12.r1 Knowles Solter mouse blastocyst... 36 2.0
 AA591610, AA591610 vk49d08.r1 Stratagene mouse Tcell 937311 M... 36 2.0
 AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 2.0
 AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 2.0
 AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 2.0
 AA612185, AA612185 vo03d05.r1 Stratagene mouse skin (#937313)... 36 2.0
 AA103424, AA103424 mo21e05.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0
 AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.0
 AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.0
 AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 2.0
 AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 2.0
 AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 2.0
 AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 2.0
 AA655241, AA655241 vq84c07.s1 Knowles Solter mouse 2 cell Mus... 36 2.0
 AA512835, AA512835 vg13f11.r1 Soares mouse NbMH Mus musculus ... 36 2.0

C70525, C70525	C.elegans cDNA clone yk409g6 : 5' end, single...	44	0.007
F15112, SSO4D09	S.scrofa mRNA; expressed sequence tag (5'; c...	42	0.029
AA684640, AA684640	EST104989 Rat PC-12 cells, untreated Rattu...	40	0.11
H32045, H32045	EST106774 Rat PC-12 cells, untreated Rattus sp...	40	0.11
AA660422, AA660422	00298 MtrHE Medicago truncatula cDNA 5'	40	0.11
C59696, C59696	C.elegans cDNA clone yk440e1 : 3' end, single...	38	0.45
AI008699, AI008699	EST203150 Normalized rat embryo, Bento Soa...	38	0.45
AA753263, AA753263	96BS0294 Rice Immature Seed Lambda ZAPII c...	38	0.45
T38461, T38461	EST103957 Saccharomyces cerevisiae cDNA 3' end.	38	0.45
C59257, C59257	C.elegans cDNA clone yk386b12 : 3' end, singl...	38	0.45
AA948906, AA948906	LD27590.5prime LD Drosophila melanogaster ...	38	0.45
AI001628, AI001628	EST0210 Tilapia brain cDNA library in pUC1...	38	0.45
H31962, H31962	EST106545 Rat PC-12 cells, untreated Rattus sp...	38	0.45
AA979509, AA979509	LD34118.5prime LD Drosophila melanogaster ...	38	0.45
D41274, RICS3647A	Rice cDNA, partial sequence (S3647_1A).	38	0.45
C58362, C58362	C.elegans cDNA clone yk366a8 : 3' end, single...	38	0.45
C57756, C57756	C.elegans cDNA clone yk298b9 : 3' end, single...	38	0.45
AA753070, AA753070	97AS2091 Rice Immature Seed Lambda ZAPII c...	38	0.45
H74687, H74687	383 Brassica napus cDNA clone R25R.	38	0.45
C10513, C10513	C.elegans cDNA clone yk147e9 : 3' end, single...	38	0.45
C55569, C55569	C.elegans cDNA clone yk191d1 : 3' end, single...	38	0.45
C94819, C94819	Sus scrofa mRNA; expressed sequence tag (5'; ...	38	0.45
C32982, C32982	C.elegans cDNA clone yk338a12 : 3' end, singl...	38	0.45
AA816691, AA816691	LD03795.5prime LD Drosophila melanogaster ...	36	1.8
AA519844, AA519844	TgESTzz36c03.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA531839, AA531839	TgESTzz47h05.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA660182, AA660182	00022 MtrHE Medicago truncatula cDNA 5' si...	36	1.8
D71983, CELK084H2R	C.elegans cDNA clone yk84h2 : 3' end, sin...	36	1.8
R29905, R29905	12510 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	36	1.8
AA519997, AA519997	TgESTzz36h03.r1 TgME49 invivo Bradyzoite c...	36	1.8
U83048, BTU83048	Bos taurus clone 0429 mRNA sequence	36	1.8
AA440655, AA440655	LD15510.5prime LD Drosophila melanogaster ...	36	1.8
AA559374, AA559374	MU002092.NH3 York-Harrop-lung-A Schistosom...	36	1.8
C93857, C93857	Dictyostelium discoideum slug cDNA, clone SSL794	36	1.8
AA520901, AA520901	TgESTzz65a05.r1 TgME49 invivo Bradyzoite c...	36	1.8
T46158, T46158	9421 Lambda-PRL2 Arabidopsis thaliana cDNA clo...	36	1.8
AA520866, AA520866	TgESTzz68e05.r1 TgME49 invivo Bradyzoite c...	36	1.8
Z17562, ATTS0136	A. thaliana transcribed sequence; clone TAT...	36	1.8
AA520811, AA520811	TgESTzz64d05.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA567455, AA567455	HL01288.5prime HL Drosophila melanogaster ...	36	1.8
AA519228, AA519228	TgESTzz39h02.s1 TgME49 invivo Bradyzoite c...	36	1.8
AA531917, AA531917	TgESTzz48f01.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA519829, AA519829	TgESTzz36a02.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA520185, AA520185	TgESTzz39d03.s1 TgME49 invivo Bradyzoite c...	36	1.8
C37095, C37095	C.elegans cDNA clone yk482c11 : 3' end, singl...	36	1.8

T46009, T46009 9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
 T20458, T20458 2466 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
 F14402, ATTS5324 A. thaliana transcribed sequence; clone TAP... 36 1.8
 T20404, T20404 2412 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
 AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 36 1.8
 AA699152, AA699152 HL07807.5prime HL Drosophila melanogaster ... 36 1.8
 AA902065, AA902065 NCM1A12T3 Mycelial Neurospora crassa cDNA ... 36 1.8

SEQ ID NO:558

AF016585, AF016585 Streptomyces caelestis cytochrome P-450 hy... 42 0.092
 U50719, MSU50719 Manduca sexta neuroglian mRNA, complete cds 40 0.36
 Z97208, SPAC15A10 S.pombe chromosome I cosmid c15A10 40 0.36
 AC003063, AC003063 Mus musculus Chromosome 16 BAC Clone b40-o... 40 0.36
 X66455, MMFGFR2 M.musculus promoter region of fibroblast gro... 40 0.36
 D83785, D83785 Human mRNA for KIAA0200 gene, complete cds 40 0.36
 AC000398, AC000398 Genomic sequence from Mouse 11, complete s... 38 1.4
 AF062345, AF062345 Caulobacter crescentus Sts1 (sts1), S-laye... 38 1.4
 X12359, RCNIFR12 Rhodobacter capsulatus nifR1 and nifR2 gene 38 1.4
 X72382, RCNIFR3 R.capsulatus nifR3 DNA 38 1.4

HUMAN ESTs

R36714, R36714 yh93g06.s1 Homo sapiens cDNA clone 137338 3'. 775 0.0
 D61030, HUM149A04B Human fetal brain cDNA 5'-end GEN-149A04. 666 0.0
 D60944, HUM141D02B Human fetal brain cDNA 5'-end GEN-141D02. 656 0.0
 H03308, H03308 yj47d09.s1 Homo sapiens cDNA clone 151889 3'. 609 e-172
 AA435561, AA435561 zt73d09.s1 Soares testis NHT Homo sapiens ... 587 e-166
 AA977877, AA977877 oq56d03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 571 e-161
 AA846787, AA846787 aj41h03.s1 Soares testis NHT Homo sapiens ... 563 e-159
 AA972542, AA972542 oo82e01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 561 e-158
 AA954270, AA954270 on72e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 557 e-157
 AA740333, AA740333 ob23c02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 557 e-157
 AA999722, AA999722 ov04c06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 555 e-156
 AA970621, AA970621 op40h08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 551 e-155
 AA932930, AA932930 oo04g11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 541 e-152
 AA725406, AA725406 ai13b11.s1 Soares parathyroid tumor NbHPA ... 539 e-152
 W74439, W74439 zd75d10.s1 Soares fetal heart NbHH19W Homo sap... 539 e-152
 AA868538, AA868538 ak43e08.s1 Soares testis NHT Homo sapiens ... 539 e-152
 R79832, R79832 yi89b08.s1 Homo sapiens cDNA clone 146391 3's... 537 e-151

R63227, R63227 yi07e06.s1 Homo sapiens cDNA clone 138562 3'. 535 e-150
AI027967, AI027967 ov84d04.x1 Soares_testis_NHT Homo sapiens ... 535 e-150
AA776717, AA776717 ah49d07.s1 Soares testis NHT Homo sapiens ... 535 e-150
AI040961, AI040961 ov53d06.x1 Soares_testis_NHT Homo sapiens ... 533 e-150
AI024835, AI024835 ov35h09.x1 Soares_testis_NHT Homo sapiens ... 533 e-150
~~AA740667, AA740667 ob01g12.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 531 e-149~~
AA994527, AA994527 ou42h06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 531 e-149
AA932728, AA932728 oo31g06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 529 e-149
AI001978, AI001978 ot39f03.s1 Soares_testis_NHT Homo sapiens ... 529 e-149
N37092, N37092 yy41g08.s1 Homo sapiens cDNA clone 273854 3'. 529 e-149
N27547, N27547 yy01e05.s1 Homo sapiens cDNA clone 269984 3'. 527 e-148
AA883578, AA883578 al46b08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 527 e-148
AA890154, AA890154 al53f07.s1 Soares_NFL_T_GBC_S1 Homo sapien... 525 e-147
AA757222, AA757222 ah56f11.s1 Soares testis NHT Homo sapiens ... 525 e-147
AA456074, AA456074 aa17b07.s1 Soares_NhHMPu_S1 Homo sapiens c... 523 e-147
AA884285, AA884285 am32f04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 523 e-147
AA969436, AA969436 op53e12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
AA952918, AA952918 on55h11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
AA971938, AA971938 op88b01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
R25112, R25112 yh36b12.s1 Homo sapiens cDNA clone 131807 3'. 519 e-146
AA865258, AA865258 og87d08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 519 e-146
AA758323, AA758323 ah65e11.s1 Soares testis NHT Homo sapiens ... 519 e-146
AA972041, AA972041 op88e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 519 e-146
R76443, R76443 yi58e11.s1 Homo sapiens cDNA clone 143468 3'. 519 e-146
AA917965, AA917965 om37e04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 517 e-145
AA505880, AA505880 ni01a09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 517 e-145
AA906270, AA906270 oj98e12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 517 e-145
AA758549, AA758549 ah70b04.s1 Soares testis NHT Homo sapiens ... 517 e-145
AA927156, AA927156 om20f05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 515 e-144
AA976254, AA976254 oo30f08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 515 e-144
R23891, R23891 yh28a12.s1 Homo sapiens cDNA clone 131038 3'. 515 e-144
AA938552, AA938552 oo78g11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 513 e-144
AA483809, AA483809 ne41c08.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 513 e-144
AA962659, AA962659 or31f10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 511 e-143
AA724803, AA724803 ai05f02.s1 Soares parathyroid tumor NbHPA ... 511 e-143
AA410432, AA410432 zv12c09.s1 Soares_NhHMPu_S1 Homo sapiens c... 511 e-143
AA775373, AA775373 ad19c07.s1 Soares_NbHFB Homo sapiens cDNA ... 511 e-143
AA758038, AA758038 ah67h09.s1 Soares testis NHT Homo sapiens ... 509 e-143
AA904368, AA904368 ol15d02.s1 Soares_NFL_T_GBC_S1 Homo sapien... 509 e-143
AA861386, AA861386 ak37b11.s1 Soares testis NHT Homo sapiens ... 507 e-142
R31547, R31547 yh72g03.s1 Homo sapiens cDNA clone 135316 3'. 505 e-141
AA843421, AA843421 ak07f11.s1 Soares parathyroid tumor NbHPA ... 504 e-141
H02479, H02479 yj35e10.s1 Homo sapiens cDNA clone 150762 3'. 504 e-141
N29346, N29346 yw85c12.s1 Homo sapiens cDNA clone 259030 3'. 504 e-141
AA815351, AA815351 ai63g05.s1 Soares testis NHT Homo sapiens ... 504 e-141

AA923373, AA923373 ol46e03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 502 e-140
 H01218, H01218 yj31c08.s1 Homo sapiens cDNA clone 150350 3'. 500 e-140
 AA988977, AA988977 or87e11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 500 e-140
 AA628621, AA628621 af40c02.s1 Soares total fetus Nb2HF8 9w Ho... 500 e-140
 AA442745, AA442745 zv60a07.s1 Soares testis NHT Homo sapiens ... 498 e-139
~~AA777492, AA777492 zj02e07.s1 Soares fetal liver spleen 1NFLS... 498 e-139~~
 R73670, R73670 yi55f03.s1 Homo sapiens cDNA clone 143165 3'. 498 e-139
 H12460, H12460 yj12d05.s1 Homo sapiens cDNA clone 148521 3'. 498 e-139
 AA875917, AA875917 oj15a08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 496 e-138
 R76230, R76230 yi71g11.s1 Homo sapiens cDNA clone 144740 3'. 494 e-138
 AA970616, AA970616 op40h03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 494 e-138
 AA912408, AA912408 ol23a05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 492 e-137
 AA910051, AA910051 ol40e08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 492 e-137
 AA815444, AA815444 ai65b11.s1 Soares testis NHT Homo sapiens ... 492 e-137
 R76814, R76814 yi62f06.s1 Homo sapiens cDNA clone 143843 3'. 488 e-136
 AA954722, AA954722 oo84c12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 488 e-136
 R65987, R65987 yi23e10.s1 Homo sapiens cDNA clone 140106 3'. 486 e-136
 R63480, R63480 yi08e11.s1 Homo sapiens cDNA clone 138668 3'. 486 e-136
 AA885425, AA885425 am12h09.s1 Soares_NFL_T_GBC_S1 Homo sapien... 486 e-136
 AA884231, AA884231 am32a01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 484 e-135
 AA885048, AA885048 am11a12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 482 e-134
 AA996162, AA996162 os14f10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 482 e-134
 AA748637, AA748637 ny10a02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 482 e-134
 AI031908, AI031908 ow47e12.x1 Soares_parathyroid_tumor_NbHPA ... 482 e-134
 AA884703, AA884703 am18e02.s1 Soares_NFL_T_GBC_S1 Homo sapien... 480 e-134
 AA928243, AA928243 on87c10.s1 Soares_NFL_T_GBC_S1 Homo sapien... 480 e-134
 AI025986, AI025986 ow03a09.s1 Soares_parathyroid_tumor_NbHPA ... 478 e-133
 AA897637, AA897637 oj72g07.s1 Soares_NFL_T_GBC_S1 Homo sapien... 472 e-131
 AA877346, AA877346 olc07.s1 NCI_CGAP_Col10 Homo sapiens cDNA... 472 e-131
 AA833569, AA833569 aj46b02.s1 Soares testis NHT Homo sapiens ... 472 e-131
 AA832163, AA832163 oc91b02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 470 e-131
 R89052, R89052 ym99e08.s1 Homo sapiens cDNA clone 167078 3'. 470 e-131
 N26589, N26589 yx91f03.s1 Homo sapiens cDNA clone 269117 3'. 460 e-128
 R73883, R73883 yi56c03.s1 Homo sapiens cDNA clone 143236 3'. 454 e-126
 AA579968, AA579968 ng51c03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 444 e-123
 AA843427, AA843427 ak07g06.s1 Soares_parathyroid_tumor_NbHPA ... 438 e-121
 AA705903, AA705903 ah42g12.s1 Soares testis NHT Homo sapiens ... 436 e-121
 AA835882, AA835882 oc81d05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 434 e-120
 AA812583, AA812583 aj43b02.s1 Soares testis NHT Homo sapiens ... 432 e-119
 AA512970, AA512970 nj16b08.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 432 e-119
 R26664, R26664 yh35g10.s1 Homo sapiens cDNA clone 131778 3'. 428 e-118
 AA429715, AA429715 zv60a07.r1 Soares testis NHT Homo sapiens ... 414 e-114
 H17430, H17430 ym40f09.s1 Homo sapiens cDNA clone 50607 3'. 404 e-111
 AA436117, AA436117 zu03d10.r1 Soares testis NHT Homo sapiens ... 402 e-110
 AA099077, AA099077 zl77a09.s1 Stratagene colon (#937204) Homo... 400 e-110

R72440, R72440 yj90h02.s1 Homo sapiens cDNA clone 156051 3'. 379 e-103
AA577436, AA577436 nm96h06.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 351 4e-95
AA516390, AA516390 nf55e03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 347 6e-94
AA534533, AA534533 nf80h06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 341 3e-92
AA541583, AA541583 ni89f05.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 311 3e-83
N72191, N72191 yz99f07.s1 Homo sapiens cDNA clone 291205 3' 303 8e-81

AA905015, AA905015 ok09b08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 303 8e-81
AA393148, AA393148 zt73d09.r1 Soares testis NHT Homo sapiens ... 287 4e-76
AA939048, AA939048 op56h04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 256 2e-66
AA412317, AA412317 zt97c05.r1 Soares testis NHT Homo sapiens ... 246 2e-63
R65986, R65986 yi23e10.r1 Homo sapiens cDNA clone 140106 5'. 238 4e-61
AA400827, AA400827 zt76c07.s1 Soares testis NHT Homo sapiens ... 232 2e-59
W00472, W00472 yz99f07.r1 Homo sapiens cDNA clone 291205 5'. 180 8e-44
AA860558, AA860558 aj81e09.s1 Soares parathyroid tumor NbHPA ... 180 8e-44
AA455577, AA455577 aa17b07.r1 Soares NhHMPu S1 Homo sapiens c... 176 1e-42
AA583931, AA583931 nn64e04.s1 NCI_CGAP_Lar1 Homo sapiens cDNA... 172 2e-41
AA907332, AA907332 ol22g11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 168 3e-40
R71169, R71169 yi53a12.r1 Homo sapiens cDNA clone 142942 5'. 159 3e-37
W79084, W79084 zd75d10.r1 Soares fetal heart NbHH19W Homo sap... 155 4e-36
AA295914, AA295914 EST101137 Thymus III Homo sapiens cDNA 5' end 135 4e-30
AA860415, AA860415 aj60d10.s1 Soares testis NHT Homo sapiens ... 100 2e-19
H01351, H01351 yi99a07.r1 Homo sapiens cDNA clone 147348 5'. 98 9e-19
AA709286, AA709286 ai21g07.s1 Soares testis NHT Homo sapiens ... 96 3e-18
AA931370, AA931370 oo03d01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 96 3e-18
AA501911, AA501911 ng54a08.s1 NCI_CGAP_Li2 Homo sapiens cDNA ... 94 1e-17
AA548419, AA548419 nj14g09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 92 5e-17
AA588892, AA588892 no23b06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 92 5e-17
AI025228, AI025228 ov40h08.x1 Soares testis_NHT Homo sapiens ... 76 3e-12
R73757, R73757 yi55f03.r1 Homo sapiens cDNA clone 143165 5'. 74 1e-11
R23710, R23710 yh35g10.r1 Homo sapiens cDNA clone 131778 5'. 56 3e-06
N40362, N40362 yy01e05.r1 Homo sapiens cDNA clone 269984 5'. 50 2e-04
H59895, H59895 yr04c12.r1 Homo sapiens cDNA clone 204310 5'. 48 7e-04
H12509, H12509 yj12d05.r1 Homo sapiens cDNA clone 148521 5'. 44 0.011
N20344, N20344 yx38d02.s1 Homo sapiens cDNA clone 264003 3'. 38 0.70
AA614692, AA614692 np52b10.s1 NCI_CGAP_Br1.1 Homo sapiens cDN... 38 0.70
H30707, H30707 yo78f07.r1 Homo sapiens cDNA clone 184069 5'. 36 2.7
H52973, H52973 yq82e04.r1 Homo sapiens cDNA clone 202302 5'. 36 2.7
AA218550, AA218550 zq96b02.r1 Stratagene NT2 neuronal precurs... 36 2.7
AA312481, AA312481 EST183215 Jurkat T-cells VI Homo sapiens c... 36 2.7
AA632009, AA632009 np74c07.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 36 2.7
H13363, H13363 yl71b10.r1 Homo sapiens cDNA clone 43343 5'. 36 2.7
AI022018, AI022018 ow64d01.x1 Soares_senescent_fibroblasts_Nb... 36 2.7
AA781996, AA781996 ai75a06.s1 Soares testis NHT Homo sapiens ... 36 2.7
N21623, N21623 yx60a09.s1 Homo sapiens cDNA clone 266104 3'. 36 2.7
AA326194, AA326194 EST29340 Cerebellum II Homo sapiens cDNA 5... 36 2.7

C76071, C76071 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 250 4e-65
 AA051612, AA051612 mj52c07.r1 Soares mouse embryo NbME13.5 14... 238 1e-61
~~AA561635, AA561635 vl01h07.r1 Knowles Solter mouse blastocyst... 234 2e-60~~
 AA288419, AA288419 vb14h01.r1 Soares mouse NML Mus musculus c... 220 3e-56
 AA212883, AA212883 mw78e10.r1 Soares mouse NML Mus musculus c... 220 3e-56
 AA268018, AA268018 vb08e07.r1 Soares mouse NML Mus musculus c... 212 8e-54
 AA692427, AA692427 vt59b07.r1 Barstead mouse irradiated colon... 200 3e-50
 W18566, W18566 mb98h02.r1 Soares mouse p3NMF19.5 Mus musculus... 192 7e-48
 AA543948, AA543948 vj69b08.r1 Knowles Solter mouse blastocyst... 147 4e-34
 W41070, W41070 mc39b06.r1 Soares mouse p3NMF19.5 Mus musculus... 123 5e-27
 Z31174, MMTEST52 M.musculus expressed sequence tag MTEST52 117 3e-25
 AA530723, AA530723 vj32f07.r1 Stratagene mouse diaphragm (#93... 74 5e-12
 AA966940, AA966940 ua38c01.r1 Soares mouse mammary gland NbMM... 72 2e-11
 AA111079, AA111079 mp50e01.r1 Barstead MPLRB1 Mus musculus cD... 44 0.004
 AA049187, AA049187 mj51a02.r1 Soares mouse embryo NbME13.5 14... 36 0.99
 AA058246, AA058246 mg74e12.r1 Soares mouse embryo NbME13.5 14... 36 0.99
 AA153730, AA153730 mq60a02.r1 Soares 2NbMT Mus musculus cDNA ... 36 0.99
 AA473959, AA473959 vd02b12.s1 Knowles Solter mouse 2 cell Mus... 36 0.99
 W47887, W47887 mc83h09.r1 Soares mouse embryo NbME13.5 14.5 M... 36 0.99
 AA033312, AA033312 mi43g01.r1 Soares mouse embryo NbME13.5 14... 36 0.99
 AA980820, AA980820 ua46a04.r1 Soares mouse mammary gland NbMM... 36 0.99
 Z31139, MMTEST427 M.musculus expressed sequence tag MTEST427 36 0.99
 C76637, C76637 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 34 3.9
 AI049314, AI049314 uc87b10.y1 Sugano mouse kidney mkia Mus mu... 34 3.9
 AA670807, AA670807 vs70b02.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA727571, AA727571 vv01h11.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA571966, AA571966 vg12f07.r1 Soares mouse NbMH Mus musculus ... 34 3.9
 W37059, W37059 mb73f10.r1 Soares mouse p3NMF19.5 Mus musculus... 34 3.9
 AA760280, AA760280 vv74h11.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA799036, AA799036 vn40c12.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA432831, AA432831 vf28g07.r1 Knowles Solter mouse 8 cell Mus... 34 3.9
 AA562435, AA562435 vk98c01.r1 Knowles Solter mouse blastocyst... 34 3.9
 AA726680, AA726680 vu93g12.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA217464, AA217464 mu87d11.r1 Soares mouse lymph node NbMLN M... 34 3.9
 AA790564, AA790564 vx71e06.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA033172, AA033172 mi37f06.r1 Soares mouse embryo NbME13.5 14... 34 3.9
 AA616204, AA616204 vo96h02.r1 Soares mouse mammary gland NbMM... 34 3.9
 AA982055, AA982055 ua37h05.r1 Soares mouse mammary gland NbMM... 34 3.9
 W47850, W47850 mc82h10.r1 Soares mouse embryo NbME13.5 14.5 M... 34 3.9
 AA537538, AA537538 vk48c12.r1 Soares mouse mammary gland NbMM... 34 3.9
 AA636986, AA636986 vn05f04.r1 Knowles Solter mouse blastocyst... 34 3.9

AI043768, AI043768 UI-R-C0-jm-d-11-0-UI.s1 UI-R-C0 Rattus nor... 174 1e-42
 AA531635, AA531635 TgESTzz29b08.r1 TgME49 invivo Bradyzoite c... 38 0.22
 AA944260, AA944260 EST199759 Normalized rat embryo, Bento Soa... 38 0.22
 AI008930, AI008930 EST203381 Normalized rat embryo, Bento Soa... 36 0.87
 D15788, RICC1258A Rice cDNA, partial sequence (C1258A). 36 0.87
~~AA963741, AA963741 UI-R-C0-gt-b-09-0-UI.s1 UI-R-C0 Rattus nor... 36 0.87~~
 AA951235, AA951235 LD31601.3prime LD Drosophila melanogaster ... 34 3.5
 C20118, C20118 Rice cDNA, partial sequence (E11542_2A) 34 3.5
 AA820317, AA820317 LD23876.5prime LD Drosophila melanogaster ... 34 3.5
 AA950448, AA950448 LD30237.3prime LD Drosophila melanogaster ... 34 3.5

SEQ ID NO:559

U83883, RNU83883 Rattus norvegicus p105 coactivator mRNA, com... 42 0.11
 V00722, MMBGL1 Mouse gene for beta-1-globin. 40 0.45
 X14061, MMBGCXD M.musculus beta-globin complex DNA for y, bh... 40 0.45
 U20824, EHVU20824 Equine herpesvirus 2, complete genome 38 1.8
 U04106, PFU04106 Pleurotus fossulatus D1822, mating group VI,... 38 1.8
 U04101, POU04101 Pleurotus ostreatus D1742, Japan, mating gro... 38 1.8
 AC005174, AC005174 Homo sapiens clone UWGC:g1564a012 from 7p1... 38 1.8
 M18680, HUMRGAPS Homo sapiens 5S rRNA pseudogene. 38 1.8
 AL022121, MTV025 Mycobacterium tuberculosis H37Rv complete g... 38 1.8
 AF038379, AF038379 Leishmania amazonensis ribosomal protein S... 38 1.8
 Z11528, THIGPMR T.harzianum mRNA for imidazoleglycerolphosphate 38 1.8
 U32622, CTU32622 Comamonas testosteroni TsaR (tsaR), toluenes... 38 1.8
 U04102, POU04102 Pleurotus ostreatus D1743, Japan, mating gro... 38 1.8
 U04105, PFU04105 Pleurotus fossulatus D1821, mating group VI,... 38 1.8
 U04109, PEU04109 Pleurotus eryngii D1832, mating group VI rib... 38 1.8
 U65606, BSU65606 Basidiomycete from a bamboo (Phyllostachys p... 38 1.8

HUMAN ESTs

R49969, R49969 yj56c07.s1 Homo sapiens cDNA clone 152748 3' s... 523 e-147
 AA834501, AA834501 of21c02.s1 NCI_CGAP_Kid6 Homo sapiens cDNA... 381 e-104
 W96422, W96422 ze43a05.s1 Soares retina N2b4HR Homo sapiens c... 315 2e-84
 R47821, R47821 yj56c07.r1 Homo sapiens cDNA clone 152748 5'. 214 7e-54
 AA761660, AA761660 nz24b09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 212 3e-53
 AA887861, AA887861 nq99b07.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 74 2e-11
 AA644044, AA644044 nm20b12.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 72 6e-11

AA115963, AA115963 zm78d11.s1 Stratagene neuroepithelium (#93... 40 0.22
AA779271, AA779271 zj43f02.s1 Soares fetal liver spleen 1NFLS... 40 0.22
T65600, T65600 yc76a04.r1 Homo sapiens cDNA clone 21496 5'. 38 0.86
AA515882, AA515882 nf67f10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 38 0.86
AA664812, AA664812 nu69b05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA... 36 3.4
~~T83365, T83365 ye03f05.s1 Homo sapiens cDNA clone 116673 3'. 36 3.4~~

AA009773, AA009773 zi04d04.s1 Soares fetal liver spleen 1NFLS... 36 3.4
AA916894, AA916894 og34g10.s1 NCI_CGAP_Br7 Homo sapiens cDNA ... 36 3.4
N27865, N27865 yy02g03.s1 Homo sapiens cDNA clone 270100 3'. 36 3.4
AA953544, AA953544 om79g06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 36 3.4
AA505576, AA505576 nh93f03.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 36 3.4
H30276, H30276 yp42f05.s1 Homo sapiens cDNA clone 190113 3'. 36 3.4
AA699914, AA699914 zi61f08.s1 Soares fetal liver spleen 1NFLS... 36 3.4
AA595583, AA595583 nk92c04.s1 NCI_CGAP_Co11 Homo sapiens cDNA... 36 3.4
AA351139, AA351139 EST58769 Infant brain Homo sapiens cDNA 5'... 36 3.4
AA810167, AA810167 ob88a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 36 3.4
H50257, H50257 yo28a07.r1 Homo sapiens cDNA clone 179220 5'. 36 3.4
W19939, W19939 zb37e09.r1 Soares parathyroid tumor NbHPA Homo... 36 3.4
R19840, R19840 yg30e11.r1 Homo sapiens cDNA clone 33837 5'. 36 3.4
AA514234, AA514234 nf56e10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 36 3.4

AA183407, AA183407 ms
AA821640, AA821640 vw
AA289310, AA289310

AA900756, AA900756 UI-R-E0-di-d-04-0-UI.s1 UI-R-E0 Rattus nor... 46 0.001
T18416, T18416 6c02e07t7 etiolated seedling Zea mays cDNA clo... 40 0.069
AA817427, AA817427 LD22827.5prime LD Drosophila melanogaster ... 36 1.1
AA274351, AA274351 TgESTzz25c09.s1 TgME49 invivo Bradyzoite c... 36 1.1
AA391823, AA391823 LD10747.5prime LD Drosophila melanogaster ... 36 1.1
AA274275, AA274275 TgESTzz24b02.s1 TgME49 invivo Bradyzoite c... 34 4.3
R86490, R86490 RABEST068T Oryctolagus cuniculus cDNA clone pR... 34 4.3
AA965817, AA965817 o5g08a1.r1 Aspergillus nidulans 24hr asexu... 34 4.3

SEQ ID NO:560

X81198, L35746, L49403, U21317, Z35640, AL010273, U09850, AF071771, Z96434,

Z50028, X72735, U13072, Z34294, AB002109, X68401, M92840, D88399, Z36238, AF000262, Z46828,

HUMAN ESTs

AA215808, AA215808 zr98b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 1082 0.0
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 AA709149, AA709149 zf98g05.s1 Soares fetal heart NbHH19W Homo... 985 0.0
 AA428341, AA428341 zw18f09.s1 Soares ovary tumor NbHOT Homo s... 967 0.0
 AA043426, AA043426 zk54h09.r1 Soares pregnant uterus NbHPU Ho... 870 0.0
 AA878521, AA878521 oj19c01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 844 0.0
 AA599696, AA599696 ag10h01.s1 Gessler Wilms tumor Homo sapien... 842 0.0
 W52304, W52304 zc47c08.r1 Soares senescent fibroblasts NbHSF ... 841 0.0
 AA043427, AA043427 zk54h09.s1 Soares pregnant uterus NbHPU Ho... 769 0.0
 N64314, N64314 yz46a12.s1 Homo sapiens cDNA clone 286078 3'. 763 0.0
 N52360, N52360 yz29g07.s1 Soares multiple sclerosis 2NbHMSP H... 753 0.0
 AA290863, AA290863 zt19a08.s1 Soares ovary tumor NbHOT Homo s... 747 0.0
 AA768023, AA768023 oa60e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 728 0.0
 AA872018, AA872018 oi05f08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 718 0.0
 AA164765, AA164765 zp01g09.s1 Stratagene ovarian cancer (#937... 716 0.0
 AA814881, AA814881 oa75e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 708 0.0
 R86915, R86915 yq30f07.r1 Homo sapiens cDNA clone 197317 5'. 692 0.0
 W56703, W56703 zd14e01.r1 Soares fetal heart NbHH19W Homo sap... 642 0.0
 R84872, R84872 yq27e01.r1 Soares fetal liver spleen 1NFLS Hom... 636 0.0
 D79691, HUM307D10B Human aorta cDNA 5'-end GEN-307D10. 630 e-179
 AA025638, AA025638 ze90d11.s1 Soares fetal heart NbHH19W Homo... 626 e-178
 AA298883, AA298883 EST114512 Pancreas tumor I Homo sapiens cD... 624 e-177
 R86903, R86903 yq30d07.r1 Homo sapiens cDNA clone 197293 5'. 622 e-176
 AA033584, AA033584 zk21b12.s1 Soares pregnant uterus NbHPU Ho... 618 e-175
 AA633335, AA633335 nq58h09.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 611 e-173
 AA298894, AA298894 EST114513 Pancreas tumor I Homo sapiens cD... 599 e-169
 R85806, R85806 yq27e01.s1 Soares fetal liver spleen 1NFLS Hom... 595 e-168
 AA872617, AA872617 oi05g07.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 591 e-167
 H71458, H71458 yu71a06.s1 Homo sapiens cDNA clone 239218 3'. 587 e-166
 AA291045, AA291045 zt19a08.r1 Soares ovary tumor NbHOT Homo s... 563 e-159
 H71587, H71587 yu71a06.r1 Homo sapiens cDNA clone 239218 5'. 543 e-153
 AA035172, AA035172 zk28g05.s1 Soares pregnant uterus NbHPU Ho... 523 e-147
 AA164764, AA164764 zp01g09.r1 Stratagene ovarian cancer (#937... 517 e-145
 AA297001, AA297001 EST112550 Adipose tissue, white II Homo sa... 502 e-140
 AA296816, AA296816 EST112381 Aorta endothelial cells Homo sap... 500 e-139
 AA769090, AA769090 oa74e12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 494 e-138
 H54447, H54447 yq91f04.s1 Homo sapiens cDNA clone 203167 3'. 438 e-121
 H54537, H54537 yq91f04.r1 Homo sapiens cDNA clone 203167 5'. 436 e-120
 AI049757, AI049757 an26g03.x1 Gessler Wilms tumor Homo sapien... 430 e-119

AA033583, AA033583 zk21b12.r1 Soares pregnant uterus NbHPU Ho... 422 e-116
D61748, HUM205G02B Human aorta cDNA 5'-end GEN-205G02. 412 e-113
AA148635, AA148635 zl26d10.r1 Soares pregnant uterus NbHPU Ho... 377 e-102
AA148636, AA148636 zl26d10.s1 Soares pregnant uterus NbHPU Ho... 373 e-101
AA025637, AA025637 ze90d11.r1 Soares fetal heart NbHH19W Homo... 371 e-101
AA932620, AA932620 oo61h04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA 365 4e-99
AA385594, AA385594 EST99296 Thyroid Homo sapiens cDNA 5' end 339 2e-91
AA361957, AA361957 EST71295 T-cell lymphoma Homo sapiens cDNA... 289 2e-76
AA383998, AA383998 EST97483 Thyroid Homo sapiens cDNA 5' end ... 274 1e-71
H22175, H22175 yl38a03.r1 Homo sapiens cDNA clone 160492 5'. 256 3e-66
R50060, R50060 yj59c10.r1 Homo sapiens cDNA clone 153042 5'. 256 3e-66
AA229414, AA229414 nc47f12.r1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 246 3e-63
D20466, HUMGS01440 Human HL60 3'directed MboI cDNA, HUMGS014... 208 6e-52
AA249061, AA249061 ll4438.seq.F Human fetal heart, Lambda ZAP... 168 5e-40
R86758, R86758 yq30f07.s1 Homo sapiens cDNA clone 197317 3'. 147 2e-33
R58025, R58025 F8018 Fetal heart Homo sapiens cDNA clone F801... 101 1e-19
AA371076, AA371076 EST82846 Prostate gland I Homo sapiens cDN... 42 0.081
AA977111, AA977111 oq24c03.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.32
AA608923, AA608923 af03b04.s1 Soares testis NHT Homo sapiens ... 38 1.3

gb|AA386999|AA386999 vc81b02.r1 Ko mouse embryo 11 5dpc Mus mus... 668 0.0
gb|AA589082|AA589082 vk24a08.r1 Knowles Solter mouse blastocyst... 658 0.0
gb|AA510881|AA510881 vh59c11.r1 Soares mouse mammary gland NbMM... 617 e-175
gb|AA763574|AA763574 vp07e08.r1 Soares mouse mammary gland NbMM... 615 e-174
gb|AA387423|AA387423 vc84b03.r1 Ko mouse embryo 11 5dpc Mus mus... 549 e-155
gb|AA915333|AA915333 vz28f05.r1 Soares 2NbMT Mus musculus cDNA ... 543 e-153
gb|AA816208|AA816208 vp43c10.r1 Barstead mouse irradiated colon... 444 e-123
gb|AA190043|AA190043 mt91h08.r1 Soares mouse lymph node NbMLN M... 424 e-117
gb|AA207393|AA207393 mv89c09.r1 GuayWoodford Beier mouse kidney... 394 e-108
emb|Z31258|MMTEST693 M.musculus expressed sequence tag MTEST693 309 8e-83
gb|AA930143|AA930143 vz52d11.s1 Soares 2NbMT Mus musculus cDNA ... 293 5e-78
gb|AA170612|AA170612 ms92c09.r1 Soares mouse 3NbMS Mus musculus... 287 3e-76
gb|AA762238|AA762238 vw58h02.r1 Soares mouse mammary gland NMLM... 266 1e-69
gb|AA689028|AA689028 vs02c12.r1 Barstead mouse irradiated colon... 264 4e-69
gb|AA959938|AA959938 vw58h02.s1 Soares mouse mammary gland NMLM... 240 6e-62
dbj|D18511|MUSGS01569 Mouse 3'-directed cDNA, MUSGS01569, clon... 172 1e-41
gb|AA474393|AA474393 vd57g07.r1 Knowles Solter mouse blastocyst... 100 1e-19
gb|W97165|W97165 mf90g05.r1 Soares mouse embryo NbME13.5 14.5 M... 74 8e-12
gb|AA512077|AA512077 vj43f05.r1 Stratagene mouse skin (#937313)... 62 3e-08
gb|AA794521|AA794521 vu68e07.r1 Stratagene mouse skin (#937313)... 54 8e-06
gb|AA155454|AA155454 mn38h12.r1 Beddington mouse embryonic regi... 48 5e-04
gb|W91000|W91000 mf83f06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.12

gb|AA219917|AA219917 mv62f05.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.45
 gb|AA529349|AA529349 vi35f08.r1 Beddington mouse embryonic regi... 36 1.8
 gb|AA754855|AA754855 vu51e08.r1 Soares mouse mammary gland NbMM... 36 1.8

gb|AA850379|AA850379 EST193146 Normalized rat ovary, Bento Soar... 569 e-161
 gb|W63375|W63375 TgESTzy68g02.r1 TgME49 Tachyzoite cDNA Toxopla... 394 e-108
 gb|AA946379|AA946379 EST201878 Normalized rat lung, Bento Soare... 353 5e-96
 gb|AA964427|AA964427 UI-R-E1-gp-a-08-0-UI.s1 UI-R-E1 Rattus nor... 335 1e-90
 gb|AA849599|AA849599 EST192366 Normalized rat muscle, Bento Soa... 307 3e-82
 gb|AA849595|AA849595 EST192362 Normalized rat muscle, Bento Soa... 307 3e-82
 gb|AA850378|AA850378 EST193145 Normalized rat ovary, Bento Soar... 278 3e-73
 gb|AA957389|AA957389 UI-R-E1-fu-b-04-0-UI.s1 UI-R-E1 Rattus nor... 157 6e-37
 gb|AI012981|AI012981 EST207432 Normalized rat spleen, Bento Soa... 147 6e-34
 dbj|C48357|C48357 C.elegans cDNA clone yk469b2 : 5' end, single... 40 0.10
 gb|AA440444|AA440444 LD15290.5prime LD Drosophila melanogaster ... 36 1.6
 dbj|C22690|C22690 Rice cDNA, partial sequence (S5274_4A) 36 1.6
 gb|AA697626|AA697626 HL02895.5prime HL Drosophila melanogaster ... 36 1.6
 gb|AA550136|AA550136 1244m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 1.6
 gb|T43579|T43579 6842 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.6
 gb|AI030501|AI030501 UI-R-C0-jc-g-02-0-UI.s1 UI-R-C0 Rattus nor... 36 1.6
 gb|AA056876|AA056876 SWMFC A987SK Brugia malayi microfilaria cDN... 36 1.6
 gb|AA440689|AA440689 LD15550.5prime LD Drosophila melanogaster ... 36 1.6

SEQ ID NO:561

emb|Z47552|HSFMO3 H.sapiens mRNA for flavin-containing monooxyg... 44 0.10
 gb|U39966|HSFMO3G7 Homo sapiens flavin containing monooxygenase... 44 0.10
 emb|AL021026|HS127D3 Homo sapiens DNA sequence from PAC 127D3 o... 44 0.10
 gb|U35007|CPU35007 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10
 gb|U35008|CPU35008 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10
 dbj|D85068|RICT3A Rice transposable element T3 gene and ret... 42 0.40
 dbj|D63711|RICT3 Rice transposon T3 DNA, complete sequence 42 0.40
 gb|U01657|U01657 Carcharhinus plumbeus Ig lambda-chain gene, co... 42 0.40
 emb|Z92540|HS179I15A Human DNA sequence from PAC 179I15, BRCA2 ... 40 1.6
 dbj|AB001569|AB001569 Carrot DNA for transposon Tdc1 40 1.6
 gb|AE000613|HPAE000613 Helicobacter pylori section 91 of 134 of... 40 1.6
 emb|X07985|DMCUT Drosophila cut locus mRNA for homeodomain-cont... 40 1.6
 gb|AC005217|AC005217 Homo sapiens chromosome 5, P1 clone 1047D6... 40 1.6

HUMAN ESTs

gb|AA401219|AA401219 zv63a03.r1 Soares total fetus Nb2HF8 9w Ho... 993 0.0
 gb|H69371|H69371 yu19h09.r1 Homo sapiens cDNA clone 234305 5' s... 44 0.049
 gb|N62576|N62576 za13d10.s1 Homo sapiens cDNA clone 292435 3' s... 42 0.19
 gb|W77763|W77763 zd69c06.r1 Soares fetal heart NbHH19W Homo sap... 40 0.77
 gb|R14832|R14832 yf93g05.r1 Homo sapiens cDNA clone 30203 5'. 40 0.77
 gb|T90524|T90524 vd40a04.s1 Homo sapiens cDNA clone 110670 3' s... 38 3.0

 gb|R91887|R91887 yq04c09.r1 Homo sapiens cDNA clone 195952 5'. 38 3.0
 gb|AA586935|AA586935 nn68h03.s1 NCI_CGAP_Lar1 Homo sapiens cDNA... 38 3.0
 gb|T46987|T46987 yb12a07.s1 Homo sapiens cDNA clone 70932 3' co... 38 3.0
 gb|AA853975|AA853975 aj51f09.s1 Soares testis NHT Homo sapiens ... 38 3.0
 gb|T97059|T97059 ye50e01.r1 Homo sapiens cDNA clone 121176 5'. 38 3.0
 gb|AA883119|AA883119 am15h02.s1 Soares NFL T GBC S1 Homo sapien... 38 3.0
 gb|AA860074|AA860074 ak45b06.s1 Soares testis NHT Homo sapiens ... 38 3.0
 gb|AA889618|AA889618 ak28f06.s1 Soares_testis_NHT Homo sapiens ... 38 3.0

 gb|AA230450|AA230450 mv73c06.r1 Soares mouse 3NME12 5 Mus muscu... 38 1.1
 gb|AA058041|AA058041 mj58e08.r1 Soares mouse embryo NbME13.5 14... 38 1.1
 gb|AA152953|AA152953 mq54a03.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1
 gb|W34414|W34414 ma98b07.r1 Soares mouse p3NMF19.5 Mus musculus... 38 1.1
 gb|AA465969|AA465969 ve90c06.s1 Knowles Solter mouse 2 cell Mus... 38 1.1
 gb|AA261173|AA261173 mz62b11.r1 Soares mouse lymph node NbMLN M... 38 1.1
 gb|AA238109|AA238109 mw97b05.r1 Soares mouse NML Mus musculus c... 38 1.1
 dbj|C86549|C86549 Mus musculus fertilized egg cDNA 3'-end seque... 38 1.1
 gb|AI048677|AI048677 ub29g09.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1
 dbj|D77921|MUSC1A08 Mouse embryonal carcinoma F9 cell cDNA, C1A08 38 1.1
 gb|AA396183|AA396183 vb45e04.r1 Soares mouse lymph node NbMLN M... 38 1.1
 gb|AA465898|AA465898 vc62f12.s1 Knowles Solter mouse 2 cell Mus... 36 4.3
 gb|AA041869|AA041869 mj05b12.r1 Soares mouse embryo NbME13.5 14... 36 4.3
 gb|AA637824|AA637824 vr21f11.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3
 gb|W82563|W82563 mf05g06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.3
 gb|AA389972|AA389972 vb30e03.r1 Soares mouse lymph node NbMLN M... 36 4.3
 gb|AA396253|AA396253 vb45f08.r1 Soares mouse lymph node NbMLN M... 36 4.3
 gb|AA920907|AA920907 vy84f04.r1 Stratagene mouse macrophage (#9... 36 4.3
 gb|AA517166|AA517166 vh98h05.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3
 gb|AA433599|AA433599 vf47a05.r1 Soares mouse NbMH Mus musculus ... 36 4.3
 gb|AA867252|AA867252 vx25c01.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.3
 dbj|C85619|C85619 Mus musculus fertilized egg cDNA 3'-end seque... 36 4.3
 gb|AA260277|AA260277 va93g05.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.3
 gb|AA172548|AA172548 mt04g11.r1 Soares mouse 3NbMS Mus musculus... 36 4.3
 gb|AA266879|AA266879 mz96a02.r1 Soares mouse lymph node NbMLN M... 36 4.3
 gb|AA473019|AA473019 vd43e06.r1 Barstead MPLRB1 Mus musculus cD... 36 4.3

gb|R47549|R47549 SW3ICA119SK *Brugia malayi* infective larva cDNA... 40 0.24
 gb|H32651|H32651 EST107947 Rat PC-12 cells, untreated *Rattus* sp... 38 0.96
 gb|AA955987|AA955987 UI-R-E1-fb-f-06-0-UI.s1 UI-R-E1 *Rattus* nor... 38 0.96
 gb|AA819638|AA819638 UI-R-A0-an-f-03-0-UI.s1 UI-R-A0 *Rattus* nor... 38 0.96
 gb|AI010914|AI010914 EST205365 Normalized rat muscle, Bento Soa... 38 0.96
 gb|AA893199|AA893199 EST197002 Normalized rat kidney, Bento Soa... 38 0.96

 gb|AA945176|AA945176 EST200675 Normalized rat liver, Bento Soar... 38 0.96
 gb|R95272|R95272 SWOvL3CA167SK *Onchocerca volvulus* infective la... 36 3.8
 gb|AA917208|AA917208 ka05f02.s1 *Onchocerca volvulus* infective l... 36 3.8
 dbj|C62023|C62023 *C.elegans* cDNA clone yk249d5 : 5' end, single... 36 3.8
 gb|AI013322|AI013322 EST207997 Normalized rat spleen, Bento Soa... 36 3.8
 gb|AI043280|AI043280 TENU0920 *T. cruzi* epimastigote normalized ... 36 3.8
 gb|AI009422|AI009422 EST203873 Normalized rat heart, Bento Soar... 36 3.8
 gb|AI012655|AI012655 EST207106 Normalized rat placenta, Bento S... 36 3.8
 dbj|C62878|C62878 *C.elegans* cDNA clone yk296d4 : 5' end, single... 36 3.8
 gb|AA915818|AA915818 SWOvL3CA1269SK *Onchocerca volvulus* infecti... 36 3.8
 gb|W00009|W00009 TgESTzy75b07.r1 TgRH *Tachyzoite* cDNA *Toxoplasma*... 36 3.8
 gb|AA943503|AA943503 EST199002 Normalized rat brain, Bento Soar... 36 3.8
 gb|AA956933|AA956933 UI-R-E1-fl-b-08-0-UI.s1 UI-R-E1 *Rattus* nor... 36 3.8
 gb|H54977|H54977 HHU16a *Sorghum bicolor* cv. TX430 *Sorghum bicol*... 36 3.8

SEQ ID NO:562

gb|AC000112|HSAC000112 Human PAC clone DJ149P21, complete seque... 44 0.082
 gb|U50197|CELF25E2 *Caenorhabditis elegans* cosmid F25E2. 44 0.082
 dbj|AB007727|AB007727 *Arabidopsis thaliana* genomic DNA, chromos... 44 0.082
 gb|U02562|BSU02562 *Bacillus subtilis* N-acetylglucosaminidase (l... 42 0.32
 dbj|D45048|BACORFX *Bacillus subtilis* gene for beta-N-acetylgluc... 42 0.32
 emb|Z70683|CEF13B12 *Caenorhabditis elegans* cosmid F13B12, compl... 40 1.3
 emb|AL023828|CEY17G7B *Caenorhabditis elegans* cosmid Y17G7B, com... 40 1.3
 gb|U39740|CELZC64 *Caenorhabditis elegans* cosmid ZC64. 40 1.3
 gb|AF006490|AF006490 *Gossypium hirsutum* adenine nucleotide tran... 40 1.3
 emb|AL010170|PFSC03098 *Plasmodium falciparum* DNA *** SEQUENCING... 40 1.3
 gb|U53701|GHU53701 *Gossypium hirsutum* alcohol dehydrogenase 2d ... 40 1.3

HUMAN ESTs

gb|AA670455|AA670455 ae62h05.s1 Stratagene lung carcinoma 93721... 852 0.0
 gb|AA251062|AA251062 zs07c10.r1 NCI_CGAP_GCB1 *Homo sapiens* cDNA... 795 0.0

gb|AA669916|AA669916 ag42h08.s1 Jia bone marrow stroma Homo sap... 638 0.0
 gb|AA300058|AA300058 EST12665 Uterus tumor I Homo sapiens cDNA ... 587 e-165
 gb|AA664277|AA664277 ac08c05.s1 Stratagene HeLa cell s3 937216 ... 549 e-154
 gb|AA373224|AA373224 EST85230 HSC172 cells I Homo sapiens cDNA ... 529 e-148
 gb|AA225705|AA225705 nc10b05.r1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 515 e-144
 gb|W27883|W27883 39h10 Human retina cDNA randomly primed sublib... 484 e-134

 gb|R24643|R24643 yh36g05.r1 Homo sapiens cDNA clone 131864 5'. 438 e-121
 gb|N93137|N93137 zb28h06.s1 Homo sapiens cDNA clone 304955 3'. 432 e-119
 gb|AA250933|AA250933 zs07d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 426 e-117
 gb|AA216370|AA216370 nc10b05.s1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 398 e-109
 gb|H26939|H26939 yl64g01.r1 Homo sapiens cDNA clone 163056 5'. 394 e-108
 gb|H30169|H30169 yo58g09.r1 Homo sapiens cDNA clone 182176 5'. 394 e-108
 gb|W38854|W38854 zb28h06.r1 Soares parathyroid tumor NbHPA Homo... 359 5e-97
 gb|AA602297|AA602297 np25a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 281 1e-73
 gb|AA167151|AA167151 zp06e09.r1 Stratagene ovarian cancer (#937... 256 6e-66
 gb|AA172387|AA172387 zo99d03.s1 Stratagene ovarian cancer (#937... 234 2e-59
 gb|AA173748|AA173748 zo99d03.r1 Stratagene ovarian cancer (#937... 224 2e-56
 gb|T83979|T83979 yd66a11.s1 Homo sapiens cDNA clone 113180 3'. 220 3e-55
 dbj|D61540|HUM415A08B Human fetal brain cDNA 5'-end GEN-415A08. 194 2e-47
 gb|N45148|N45148 yv25a05.r1 Homo sapiens cDNA clone 243728 5'. 165 2e-38
 gb|AA642960|AA642960 60f07.s1 NCI_CGAP_Lym3 Homo sapiens cDNA... 147 4e-33
 gb|R90980|R90980 yp93a03.r1 Homo sapiens cDNA clone 194956 5' s... 40 0.62
 gb|AA521500|AA521500 aa73h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.62
 gb|H82921|H82921 yq46h10.s1 Homo sapiens cDNA clone 198883 3' s... 40 0.62
 gb|AA294871|AA294871 EST100023 Pancreas tumor I Homo sapiens cD... 38 2.4
 dbj|D63191|HUM503F11B Human placenta cDNA 5'-end GEN-503F11. 38 2.4
 gb|AA211096|AA211096 zq89g01.s1 Stratagene hNT neuron (#937233)... 38 2.4

 gb|AA840137|AA840137 ud01e08.r1 Soares mouse uterus NMPu Mus mu... 383 e-104
 gb|AA145994|AA145994 mr13h04.r1 Soares mouse 3NbMS Mus musculus... 345 3e-93
 gb|AA146365|AA146365 mr05d05.r1 Soares mouse 3NbMS Mus musculus... 236 2e-60
 gb|AA203902|AA203902 mu60f02.r1 Soares mouse lymph node NbMLN M... 236 2e-60
 gb|AA204516|AA204516 mu66c10.r1 Soares mouse lymph node NbMLN M... 182 2e-44
 gb|AA137343|AA137343 mq80g08.r1 Stratagene mouse melanoma (#937... 52 6e-05
 gb|AA174717|AA174717 ms67a01.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
 gb|W34073|W34073 ma85d10.r1 Soares mouse p3NMF19.5 Mus musculus... 48 0.001
 gb|AA289493|AA289493 vb36b01.r1 Soares mouse lymph node NbMLN M... 48 0.001
 gb|AA177700|AA177700 mt33e12.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
 gb|AA146021|AA146021 mr13e03.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
 gb|AA155352|AA155352 mn43d09.r1 Beddington mouse embryonic regi... 46 0.004
 gb|AA880874|AA880874 vx33b02.r1 Stratagene mouse lung 937302 Mu... 42 0.056

gb|AA590520|AA590520 vi54b08.r1 Beddington mouse embryonic regi... 38 0.88
 gb|AA596629|AA596629 vm56e06.r1 Stratagene mouse Tcell 937311 M... 38 0.88
 dbj|D76657|MUS75H09 Mouse embryonal carcinoma F9 cell cDNA, 75H09 38 0.88
 gb|AA050336|AA050336 mj12f05.r1 Soares mouse embryo NbME13.5 14... 38 0.88
 gb|AA120196|AA120196 mn35a12.r1 Beddington mouse embryonic regi... 38 0.88
 gb|W85267|W85267 mf42c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5

 gb|AA239372|AA239372 my38f03.r1 Barstead mouse pooled organs MP... 36 3.5
 gb|AA497891|AA497891 vi73c07.r1 Stratagene mouse testis (#93730... 36 3.5
 gb|AA673053|AA673053 vn45e05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.5
 emb|Z36324|MM224 M.musculus mRNA (clone 224) for expressed sequ... 36 3.5
 gb|AI021128|AI021128 ub01f06.r1 Soares mouse mammary gland NbMM... 36 3.5
 gb|AA403424|AA403424 mz56f07.r1 Barstead mouse pooled organs MP... 36 3.5
 gb|W66683|W66683 me23g11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5
 gb|AA689022|AA689022 vs02c03.r1 Barstead mouse irradiated colon... 36 3.5
 gb|AA574590|AA574590 vn63h11.r1 Barstead mouse proximal colon M... 36 3.5

dbj|C90696|C90696 Dictyostelium discoideum slug cDNA, clone SSJ634 38 0.78
 gb|AA269052|AA269052 MA1MA052.AA3 S. mansoni adult Lambda Zap S... 38 0.78
 gb|AA998786|AA998786 UI-R-C0-im-e-11-0-UI.s1 UI-R-C0 Rattus nor... 38 0.78
 gb|H33464|H33464 EST109494 Rat PC-12 cells, NGF-treated (9 days... 38 0.78
 gb|AA390721|AA390721 LD09459.5prime LD Drosophila melanogaster ... 36 3.1
 dbj|C83908|C83908 Dictyostelium discoideum slug cDNA, clone SSA567 36 3.1
 gb|AA202425|AA202425 LD02606.5prime LD Drosophila melanogaster ... 36 3.1
 gb|AI030951|AI030951 UI-R-C0-jf-d-04-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1
 gb|N60251|N60251 TgESTzy11d04.r1 TgRH Tachyzoite cDNA Toxoplasm... 36 3.1
 gb|AA246875|AA246875 LD05855.5prime LD Drosophila melanogaster ... 36 3.1
 gb|AA803682|AA803682 GM13955.5prime GM Drosophila melanogaster ... 36 3.1
 gb|AA997528|AA997528 UI-R-C0-hw-h-11-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1
 gb|AA695197|AA695197 GM02389.5prime GM Drosophila melanogaster ... 36 3.1
 gb|AA567339|AA567339 HL01077.5prime HL Drosophila melanogaster ... 36 3.1
 gb|AA950648|AA950648 LD30547.5prime LD Drosophila melanogaster ... 36 3.1

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substantially identical to D86956

SEQ ID NO:564

gb|AC004505|AC004505 Homo sapiens chromosome 20, P1 clone 86C1 ... 176 1e-41
 gb|S78798|S78798 1-phosphatidylinositol-4-phosphate 5-kinase is... 115 4e-23
 gb|U48696|HSU48696 Human mariner-like element-containing mRNA, ... 115 4e-23
 gb|U66300|LEU66300 Lycopersicon esculentum heat shock protein (... 115 4e-23
 gb|AF045432|AF045432 Danio rerio stem cell leukemia protein (ta... 111 6e-22
 emb|Z97178|BVRNAEF2 Beta vulgaris cDNA for elongation factor 2 107 9e-21
 gb|U39066|MMU39066 Murine MAP kinase kinase 6c mRNA, complete cds. 101 6e-19
 gb|U37573|XXU37573 Shuttle expression vector pBKCMV. 96 4e-17
 gb|AF033097|AF033097 Avena sativa nonphototropic hypocotyl 1 (N... 90 2e-15
 gb|AF027174|AF027174 Arabidopsis thaliana cellulose synthase ca... 86 3e-14
 gb|U65376|CFU65376 Canis familiaris rod photoreceptor transduci... 84 1e-13
 gb|AF033565|AF033565 Mus musculus cdc2/CDC28-like protein kinas... 82 5e-13
 emb|Z49980|HS2AMCP H.sapiens mRNA for ets-like protein (clone 7... 82 5e-13
 emb|AJ001103|LLARCAB Lactococcus lactis arcA and arcB genes 80 2e-12
 gb|U52868|CFU52868 Canis familiaris retinal cyclic-GMP phosphod... 80 2e-12
 gb|G29058|G29058 chicken STS ADL368 76 3e-11
 gb|G29060|G29060 chicken STS ADL352 76 3e-11
 gb|U34048|HDU34048 Haemophilus ducreyi hemoglobin-binding prote... 76 3e-11
 gb|U44386|SLU44386 Solanum lycopersicum heat shock protein (TFH... 68 8e-09
 gb|S83098|S83098 ribosomal protein S3 [Ambystoma mexicanum=Mexi... 66 3e-08
 gb|U48697|HSU48697 Human mariner-like element-containing mRNA, ... 60 2e-06
 gb|AF033096|AF033096 Avena sativa nonphototropic hypocotyl 1 (N... 60 2e-06
 en.b|X99051|LLATTMSAT L.lagopus ATT microsatellite, locus LLST1 58 8e-06
 gb|U41811|HAU41811 Homarus americanus beta-I tubulin mRNA, comp... 46 0.029
 emb|X99055|LLCAMSAT1 L.lagopus CA microsatellite, locus LLSD5 44 0.12
 emb|X65215|BTMISATN B.taurus microsatellite DNA (624bp) 44 0.12
 gb|AE001023|AE001023 Archaeoglobus fulgidus section 84 of 172 o... 42 0.46
 emb|X80164|HSPDCM4 H.salinarium phage dcm4 Virus DNA 42 0.46
 emb|X87859|MTCMAJ12S C.major mitochondrial gene for 12S ribosom... 42 0.46
 emb|X87861|MTCPAL12S C.pallidus mitochondrial gene for 12S ribo... 42 0.46
 gb|L13767|STMSEC101A Streptomyces lividans sec101 gene, 5' end p... 42 0.46
 emb|Y08962|OSTRAMBPR O.sativa mRNA for transmembrane protein >g... 40 1.8
 gb|S65686|S65686 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 gb|J02871|HUMCP45IV Human lung cytochrome P450 (IV subfamily) B... 40 1.8
 dbj|D10450|HUMRTVE Human genomic DNA, retrovirus-like element 40 1.8
 gb|S65683|S65683 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 gb|L14950|PIGALDRED Sus scrofa aldose reductase mRNA, complete ... 40 1.8
 gb|S65693|S65693 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 gb|S65694|S65694 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 emb|AJ223292|SPAJ3292 Streptococcus pyogenes SOD gene, complete... 40 1.8
 gb|U25846|HAU25846 Homarus americanus clone LOB5 farnesoic acid... 40 1.8
 emb|X16699|HSP450P2 Human mRNA for cytochrome P-450HP 40 1.8
 gb|U37100|HSU37100 Homo sapiens aldose reductase-like peptide m... 40 1.8

HUMAN ESTs

gb|AA305996|AA305996 EST177003 Jurkat T-cells VI Homo sapiens c... 942 0.0
 gb|AA975279|AA975279 oq36e08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 900 0.0
 gb|AA426359|AA426359 zw11b02.r1 Soares NhHMPu S1 Homo sapiens c... 868 0.0
 gb|AA424296|AA424296 zv90b08.r1 Soares NhHMPu S1 Homo sapiens c... 749 0.0
 gb|AA632259|AA632259 np67d04.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 730 0.0
 gb|H80377|H80377 yu59e01.r1 Homo sapiens cDNA clone 230424 5'. 658 0.0
 gb|AA515175|AA515175 ng68f10.s1 NCI_CGAP_Lip2 Homo sapiens cDNA... 615 e-174
 gb|AA351770|AA351770 EST59616 Infant brain Homo sapiens cDNA 5'... 611 e-172
 gb|AA426522|AA426522 zw11b02.s1 Soares NhHMPu S1 Homo sapiens c... 587 e-165
 gb|AA676220|AA676220 zi22a12.s1 Soares fetal liver spleen 1NFLS... 585 e-165
 gb|R35132|R35132 yg60e09.r1 Homo sapiens cDNA clone 36874 5'. 579 e-163
 gb|H80280|H80280 yu59e01.s1 Homo sapiens cDNA clone 230424 3'. 579 e-163
 gb|H81145|H81145 yu60e01.r1 Homo sapiens cDNA clone 230520 5'. 561 e-157
 gb|AA311105|AA311105 EST18187 Heart I Homo sapiens cDNA 5' end 533 e-149
 gb|AA380530|AA380530 EST93691 Supt cells Homo sapiens cDNA 5' end 527 e-147
 gb|H81050|H81050 yu60e01.s1 Homo sapiens cDNA clone 230520 3'. 500 e-139
 gb|AA460005|AA460005 zx49g07.s1 Soares testis NHT Homo sapiens ... 482 e-134
 gb|AA076450|AA076450 zm91d12.r1 Stratagene ovarian cancer (#937... 466 e-129
 gb|N43873|N43873 yy43e09.r1 Homo sapiens cDNA clone 274024 5'. 452 e-125
 gb|AA076451|AA076451 zm91d12.s1 Stratagene ovarian cancer (#937... 418 e-115
 gb|AA907095|AA907095 ol03b12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 414 e-113
 gb|W01027|W01027 za56g07.r1 Soares fetal liver spleen 1NFLS Hom... 262 1e-67
 gb|AA127183|AA127183 zn29d11.r1 Stratagene neuroepithelium NT2R... 222 1e-55
 gb|H65491|H65491 yr56a08.s1 Homo sapiens cDNA clone 209270 3'. 222 1e-55
 gb|N48543|N48543 yy49d08.r1 Homo sapiens cDNA clone 276879 5'. 210 4e-52
 gb|R32579|R32579 yh54h06.r1 Homo sapiens cDNA clone 133595 5'. 194 2e-47
 gb|AA247827|AA247827 j0778.seq.F Human fetal heart, Lambda ZAP ... 117 5e-24
 N84048, (many others similar, but smaller)

gb|AA589598|AA589598 vl49d08.s1 Stratagene mouse skin (#937313)... 398 e-109
 gb|AA647465|AA647465 vq82f02.s1 Knowles Solter mouse 2 cell Mus... 385 e-105
 gb|AA510284|AA510284 vh58f02.r1 Soares mouse mammary gland NbMM... 345 4e-93
 gb|AA028696|AA028696 mi12e12.r1 Soares mouse p3NMF19.5 Mus musc... 307 9e-82
 gb|N28081|N28081 MDB1409R Mouse brain, Stratagene Mus musculus ... 244 1e-62
 gb|AA177452|AA177452 mt24c12.r1 Soares mouse 3NbMS Mus musculus... 226 3e-57
 gb|N28080|N28080 MDB1409 Mouse brain, Stratagene Mus musculus c... 226 3e-57
 dbj|C88310|C88310 Mus musculus fertilized egg cDNA 3'-end seque... 226 3e-57
 gb|AA763786|AA763786 vo99g12.r1 Soares mouse mammary gland NbMM... 94 2e-17
 gb|AA667535|AA667535 vv18b12.r1 Stratagene mouse heart (#937316... 40 0.31
 gb|AA208274|AA208274 mv96a01.r1 GuayWoodford Beier mouse kidney... 38 1.2

gb AA444814 AA444814	vg50e04.r1 Soares mouse mammary gland NbMM...	38	1.2
gb AA763341 AA763341	vw53b12.r1 Soares mouse mammary gland NMLM...	38	1.2
gb AA110827 AA110827	mp57a12.r1 Soares 2NbMT Mus musculus cDNA ...	38	1.2
gb AA691932 AA691932	vt06b04.r1 Barstead mouse myotubes MPLRB5 ...	38	1.2
gb W77233 W77233	me61f11.r1 Soares mouse embryo NbME13.5 14.5 M...	38	1.2
gb AA072872 AA072872	mm80g08.r1 Stratagene mouse embryonic carc...	38	1.2
gb AA980630 AA980630	ua43f05.r1 Soares mouse mammary gland NbMM...	36	4.9
gb AA065522 AA065522	ml54d09.r1 Stratagene mouse testis (#93730...	36	4.9
gb AA982398 AA982398	uh07b08.r1 Soares mouse hypothalamus NMHy ...	36	4.9
gb W62610 W62610	md58c06.r1 Soares mouse embryo NbME13.5 14.5 M...	36	4.9
gb AA286651 AA286651	vb79b02.r1 Soares mouse 3NME12 5 Mus muscu...	36	4.9
gb AA399772 AA399772	vd70g05.r1 Beddington mouse embryonic regi...	36	4.9
gb AA510475 AA510475	vg32h08.r1 Soares mouse mammary gland NbMM...	36	4.9
gb AA109064 AA109064	ml63g02.r1 Stratagene mouse testis (#93730...	36	4.9
gb AA033485 AA033485	mi42c08.r1 Soares mouse embryo NbME13.5 14...	36	4.9
gb W57221 W57221	md59g10.r1 Soares mouse embryo NbME13.5 14.5 M...	36	4.9
gb AA467106 AA467106	vd98b04.r1 Soares mouse NbMH Mus musculus ...	36	4.9
gb W97470 W97470	mf95a11.r1 Soares mouse embryo NbME13.5 14.5 M...	36	4.9
gb AA606917 AA606917	vm91c05.r1 Knowles Solter mouse blastocyst...	36	4.9
dbj C78330 C78330	Mus musculus 3.5-dpc blastocyst cDNA 3'-end s...	36	4.9
gb AA013753 AA013753	mh26h12.r1 Soares mouse placenta 4NbMP13.5...	36	4.9
gb AA145240 AA145240	mr12a03.r1 Soares mouse 3NbMS Mus musculus...	36	4.9
gb AA245533 AA245533	mx03c11.r1 Soares mouse NML Mus musculus c...	36	4.9
gb AA770893 AA770893	vt13a08.r1 Barstead mouse myotubes MPLRB5 ...	36	4.9
dbj C79987 C79987	Mus musculus 3.5-dpc blastocyst cDNA 3'-end s...	36	4.9
gb AA014027 AA014027	mh24a12.r1 Soares mouse placenta 4NbMP13.5...	36	4.9
dbj C89051 C89051	Mus musculus early blastocyst cDNA, clone 01B...	36	4.9
gb AA058308 AA058308	mj59e09.r1 Soares mouse embryo NbME13.5 14...	36	4.9
gb AA673826 AA673826	vu08h10.r1 Barstead mouse myotubes MPLRB5 ...	36	4.9
gb AA637080 AA637080	vn07h04.r1 Knowles Solter mouse blastocyst...	36	4.9
gb W44292 W44292	mc80c07.r1 Soares mouse embryo NbME13.5 14.5 M...	36	4.9
gb AA955972 AA955972	UI-R-E1-ff-d-10-0-UI.s1 UI-R-E1 Rattus nor...	159	4e-37
gb AA957275 AA957275	UI-R-E1-fq-f-08-0-UI.s1 UI-R-E1 Rattus nor...	157	2e-36
emb Z84031 SSZ84031	S.scrofa mRNA; expressed sequence tag (5'; ...	111	9e-23
gb AF041408 AF041408	Fragaria x ananassa clone FA110b	96	5e-18
gb AA933116 AA933116	SWBmL3SA048T3 Brugia malayi L3 subtracted ...	58	1e-06
gb AA933363 AA933363	SWBmL3SA615T3 Brugia malayi L3 subtracted ...	52	7e-05
gb AA660164 AA660164	00001 MtRHE Medicago truncatula cDNA 5' si...	50	3e-04
gb N37420 N37420	18647 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	44	0.018
gb H35981 H35981	14503 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	44	0.018
gb AA882627 AA882627	TENS0198 T. cruzi epimastigote normalized ...	44	0.018
gb AI026481 AI026481	TENU0693 T. cruzi epimastigote normalized ...	42	0.070
gb AA946369 AA946369	EST201868 Normalized rat lung, Bento Soare...	42	0.070

gb|AI010371|AI010371 EST204822 Normalized rat lung, Bento Soare... 42 0.070
 gb|AI010257|AI010257 EST204708 Normalized rat lung, Bento Soare... 42 0.070
 dbj|D39318|RICR3325A Rice cDNA, partial sequence (R3325_1A). 40 0.28
 gb|U40140|OSU40140 Oryza sativa clone pFDRRC22 mRNA sequence. 40 0.28
 gb|AI009132|AI009132 EST203583 Normalized rat embryo, Bento Soa... 40 0.28
 dbj|D47291|RICS12574A Rice cDNA, partial sequence (S12574_1A) 40 0.28

 dbj|D47316|RICS12613A Rice cDNA, partial sequence (S12613_1A). 40 0.28
 gb|T42265|T42265 5528 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 40 0.28
 dbj|D47631|RICS13239A Rice cDNA, partial sequence (S13239_1A). 40 0.28
 gb|AI013513|AI013513 EST208188 Normalized rat spleen, Bento Soa... 40 0.28
 gb|AA751980|AA751980 96AS0896 Rice Immature Seed Lambda ZAPII c... 40 0.28
 gb|AA660165|AA660165 00002 MtRHE Medicago truncatula cDNA 5' si... 40 0.28
 emb|Z34868|ATTS3597 A. thaliana transcribed sequence; clone FAF... 40 0.28
 dbj|D39131|RICR2302A Rice cDNA, partial sequence (R2302_1A). 40 0.28
 gb|AA963968|AA963968 UI-R-C0-gs-b-05-0-UI.s1 UI-R-C0 Rattus nor... 40 0.28
 gb|AA866346|AA866346 UI-R-A0-bm-a-05-0-UI.s1 UI-R-A0 Rattus nor... 40 0.28
 gb|AI044437|AI044437 UI-R-C1-js-e-06-0-UI.s1 UI-R-C1 Rattus nor... 40 0.28
 dbj|D41811|RICS4634A Rice cDNA, partial sequence (S4634_1A). 40 0.28
 dbj|C19261|C19261 Rice cDNA, partial sequence (E10176_1A) 40 0.28
 dbj|D48409|RICS14588A Rice cDNA, partial sequence (S14588_1A). 40 0.28
 dbj|C26556|C26556 Rice cDNA, partial sequence (C12586_1A) 40 0.28
 dbj|D47831|RICS13548A Rice cDNA, partial sequence (S13548_1A). 40 0.28
 dbj|C72152|C72152 Rice cDNA, partial sequence (E1094_3A) 40 0.28
 dbj|D46553|RICS11305A Rice cDNA, partial sequence (S11305_2A). 40 0.28
 gb|AI028926|AI0289 (and many others of similar score)

SEQ ID NO:565

emb|X68308|OOLPLIP O.ovis mRNA for lipoprotein lipase 40 1.2
 gb|AE000660|HUA000660 Homo sapiens T-cell receptor alpha delta... 40 1.2
 emb|AL022333|HS474112 Human DNA sequence *** SEQUENCING IN PROG... 38 4.6
 emb|Z12618|CFTRG C.fasciculata gene encoding trypanothione redu... 38 4.6
 gb|M81651|HUMSEMIIB Human semenogelin II (SEMGII) gene, complet... 38 4.6
 gb|M96980|HUMMYT1A Homo sapiens myelin transcription factor 1 (... 38 4.6
 gb|U89688|ACU89688 Acanthamoeba castellanii myosin-I binding pr... 38 4.6
 gb|AC002497|AC002497 Human Cosmid g1940a142 from 7q31.3, comple... 38 4.6
 gb|M81652|HUMSMNGLN Homo sapiens semenogelin II mRNA, complete ... 38 4.6
 gb|M25665|HUMNCF1A Human neutrophil cytosol factor 1 (NCF-47k) ... 38 4.6
 gb|M73325|TRFTRPREDC Crithidia fasciculata trypanothione reduct... 38 4.6
 gb|M73324|TRFTRPREDB Crithidia fasciculata trypanothione reduct... 38 4.6
 emb|X92589|MMSEMIIGN M.mulatta semenogelin II gene 38 4.6
 emb|Z47556|HSSG1SG2 H.sapiens genes for semenogelin I and semen... 38 4.6
 gb|AC004753|AC004753 Homo sapiens chromosome 16, cosmid clone R... 38 4.6
 gb|M55067|HUMNADPHO Human 47-kD autosomal chronic granulomatous... 38 4.6

gb|M73323|TRFTRPREDA Crithidia fasciculata trypanothione reduct... 38 4.6

HUMAN ESTs

gb|R11942|R11942_yf54c05.r1 Homo sapiens cDNA clone 25950 5' 656 0.0

gb|AA366384|AA366384 EST77326 Pancreas tumor III Homo sapiens c... 470 e-130

gb|T12566|T12566 CHR90086 Homo sapiens genomic clone P94_24 5' ... 133 5e-29

gb|R37032|R37032_yf54c05.s1 Homo sapiens cDNA clone 25950 3' 44 0.036

gb|AA661650|AA661650 nv02h12.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA261982|AA261982 zs20d03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

gb|AA588219|AA588219 no24c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA250891|AA250891 zs06c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

gb|AA244177|AA244177 nc05a02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 38 2.2

gb|AA715147|AA715147 nv10d05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA659887|AA659887 nv03a10.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA627890|AA627890 nq70a08.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA603596|AA603596 np27b11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA613738|AA613738 np25h09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA715248|AA715248 nv10h06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AI038487|AI038487 ow25d12.x1 Soares_parathyroid_tumor_NbHPA ... 38 2.2

gb|AA252786|AA252786 zs26f10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

gb|AA287819|AA287819 zs50h04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

gb|AA564176|AA564176 nj04c08.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2

gb|AA643870|AA643870 np26h07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA280371|AA280371 zt05f07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

gb|R00687|R00687_ye78h08.r1 Homo sapiens cDNA clone 123903 5' s... 38 2.2

gb|AA587820|AA587820 nj06h05.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2

gb|AA588443|AA588443 no22c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA568385|AA568385 nl88f06.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 38 2.2

gb|AA281831|AA281831 zt06c08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

gb|AA700438|AA700438 zj74b08.s1 Soares fetal liver spleen 1NFLS... 38 2.2

gb|AA689530|AA689530 ns66e07.r1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA688300|AA688300 nv14a09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA687962|AA687962 nv13h04.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA526586|AA526586 ni96f11.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2

gb|AA642589|AA642589 nq73f04.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA541594|AA541594 ni89g07.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2

gb|AA278713|AA278713 zs76h02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

gb|T58661|T58661_ya94a07.r1 Homo sapiens cDNA clone 69300 5' si... 38 2.2

gb|AA689473|AA689473 ns66e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2

gb|AA459023|AA459023 aa26a09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

dbj|C76752|C76752 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 60 2e-07
gb|AA123048|AA123048 mn32g01.r1 Beddington mouse embryonic regi... 36 3.2
gb|AA616529|AA616529 vo10e01.r1 Barstead mouse myotubes MPLRB5 ... 36 3.2
gb|AA254370|AA254370 va13h09.r1 Soares mouse lymph node NbMLN M... 36 3.2
gb|AA537288|AA537288 vk46c04.r1 Soares mouse mammary gland NbMM... 36 3.2
~~gb|AA462365|AA462365 vg74c05.r1 Soares mouse NbMH Mus musculus ... 36 3.2~~
gb|AA589462|AA589462 vl47g07.s1 Stratagene mouse skin (#937313)... 36 3.2
gb|AA968017|AA968017 uh06h10.r1 Soares mouse hypothalamus NMHy ... 36 3.2

dbj|C93868|C93868 Dictyostelium discoideum slug cDNA, clone SSL809 36 2.8
gb|AA531984|AA531984 TgESTzz46b06.r1 TgME49 invivo Bradyzoite c... 36 2.8
gb|N60418|N60418 TgESTzy07a10.r1 TgRH Tachyzoite cDNA Toxoplasma... 36 2.8
gb|H32045|H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 36 2.8
gb|AA956789|AA956789 UI-R-E1-fr-h-01-0-UI.s1 UI-R-E1 Rattus nor... 36 2.8
gb|H33275|H33275 EST109117 Rat PC-12 cells, NGF-treated (9 days... 36 2.8
gb|AA531938|AA531938 TgESTzz45b08.r1 TgME49 invivo Bradyzoite c... 36 2.8
dbj|D41507|RICS4044A Rice cDNA, partial sequence (S4044_1A). 36 2.8
gb|AA799411|AA799411 EST188908 Normalized rat heart, Bento Soar... 36 2.8
gb|AA519671|AA519671 TgESTzz27c10.r1 TgME49 invivo Bradyzoite c... 36 2.8
dbj|D40678|RICS2786A Rice cDNA, partial sequence (S2786_1A). 36 2.8
gb|AA012430|AA012430 TgESTzz22b12.r1 TgME49cDNA Toxoplasma gond... 36 2.8
dbj|D40551|RICS2612A Rice cDNA, partial sequence (S2612_1A). 36 2.8
gb|AI008452|AI008452 EST202903 Normalized rat embryo, Bento Soa... 36 2.8
dbj|D41253|RICS3620A Rice cDNA, partial sequence (S3620_1A). 36 2.8
gb|AA923843|AA923843 UI-R-A1-dr-f-04-0-UI.s1 UI-R-A1 Rattus nor... 36 2.8
gb|AA799410|AA799410 EST188907 Normalized rat heart, Bento Soar... 36 2.8

We claim:

1. A method of diagnosing a disorder characterized by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule, comprising:

contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an

5 expression product thereof complexed with an HLA molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and

determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.

10 2. The method of claim 1, wherein the agent is selected from the group consisting of

(a)

a nucleotide acid molecule comprising NA group 1 nucleic acid molecules
15 or a fragment thereof,

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules or
a fragment thereof,

20

(c)

a nucleic acid molecule comprising NA group 17 nucleic acid molecules
or a fragment thereof,

25

(d)

an antibody that binds to an expression product of NA group 1 nucleic
acids,

(e)

30 an antibody that binds to an expression product of NA group 3 nucleic
acids,

(f)

an antibody that binds to an expression product of NA group 17 nucleic acids,

5

(g)

and agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 1 nucleic acid,

10

(h)

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 3 nucleic acid, and

(I)

15

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 17 nucleic acid.

3.

20

The method of claim 1, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 4, at least 6, at least 7, or at least 8, at least 9 or at least 10 such agents.

25

4.

The method of claims 1-3, wherein the agent is specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

5.

30

A method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

monitoring a sample, from a patient who has or is suspected of having the condition, for a parameter selected from the group consisting of

(I)

5

the protein,

(ii)

a peptide derived from the protein,

10

(iii)

an antibody which selectively binds the protein or peptide, and

(iv)

15

cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule,
as a determination of regression, progression or onset of said condition.

6.

The method of claim 5, wherein the sample is a body fluid, a body effusion or a tissue.

20

7.

The method of claim 5, wherein the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of

(a)

25

an antibody which selectively binds the protein of (I), or the peptide of (ii),

(b)

a protein or peptide which binds the antibody of (iii), and

30

(c)

a cell which presents the complex of the peptide and MHC molecule of
(iv).

5

8. The method of claim 7, wherein the antibody, the protein, the peptide or
the cell is labeled with a radioactive label or an enzyme.

9. The method of claim 5, comprising assaying the sample for the peptide.

10

10. The method of claim 5, wherein the nucleic acid molecule is a NA Group
3 molecule.

11. The method of claim 5, wherein the nucleic acid molecule is a NA Group

15 11 molecule.

12. The method of claim 5, wherein the nucleic acid molecule is a NA Group
12 molecule.

20 13. The method of claim 5, wherein the nucleic acid molecule is a NA Group
13 molecule.

14. The method of claim 5, wherein the nucleic acid molecule is a NA Group
14 molecule.

25

15. The method of claim 5, wherein the nucleic acid molecule is a NA Group
15 molecule.

16. The method of claim 5, wherein the nucleic acid molecule is a NA Group

30 16 molecule.

17. The method of claim 5, wherein the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

5 18. A pharmaceutical preparation for a human subject comprising
an agent which when administered to the subject enriches selectively the
presence of complexes of an HLA molecule and a human cancer associated antigen, and
a pharmaceutically acceptable carrier, wherein the human cancer
associated antigen is a fragment of a human cancer associated antigen precursor encoded by a
10 nucleic acid molecule comprises a NA Group 1 molecule.

19. The pharmaceutical preparation of claim 18, wherein the agent comprises
a plurality of agents, each of which enriches selectively in the subject complexes of an HLA
molecule and a different human cancer associated antigen.

15

20. The pharmaceutical preparation of claim 19, wherein the plurality is at
least two, at least three, at least four or at least 5 different such agents.

21. The pharmaceutical preparation of claim 18, wherein the nucleic acid
20 molecule is a NA Group 3 nucleic acid molecule.

22. The pharmaceutical preparation of claim 18, wherein the agent is selected
from the group consisting of
(1) an isolated polypeptide comprising the human cancer associated
25 antigen, or a functional variant thereof,
(2) an isolated nucleic acid operably linked to a promoter for expressing
the isolated polypeptide, or functional variant thereof,
(3) a host cell expressing the isolated polypeptide, or functional variant
thereof, and

(4) isolated complexes of the polypeptide, or functional variant thereof, and an HLA molecule.

23. The pharmaceutical preparation of claims 18-22, further comprising an
5 adjuvant.

24. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative.

10 25. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide.

15 26. The pharmaceutical preparation of claim 18, wherein the agent is at least two, at least three, at least four or at least five different polypeptides, each coding for a different human cancer associated antigen or functional variant thereof.

20 27. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 2 polypeptide.

28. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

25 29. The pharmaceutical preparation of claim 25, wherein the cell expresses one or both of the polypeptide and HLA molecule recombinantly.

30 30. The pharmaceutical preparation of claim 25, wherein the cell is nonproliferative.

31. A composition comprising
an isolated agent that binds selectively a PP Group 1 polypeptide.

32. The composition of matter of claim 31, wherein the agent binds selectively
5 a PP Group 3 polypeptide.

33. The composition of matter of claim 31, wherein the agent binds selectively
a PP Group 11 polypeptide.

10 34. The composition of matter of claim 31, wherein the agent binds selectively
a PP Group 12 polypeptide.

35. The composition of matter of claim 31, wherein the agent binds selectively
a PP Group 13 polypeptide.

15 36. The composition of matter of claim 31, wherein the agent binds selectively
a PP Group 14 polypeptide.

37. The composition of matter of claim 31, wherein the agent binds selectively
20 a PP Group 15 polypeptide.

38. The composition of matter of claim 31, wherein the agent binds selectively
a PP Group 16 polypeptide.

25 39. The composition of claims 31-38, wherein the agent is a plurality of
different agents that bind selectively at least two, at least three, at least four, or at least five
different such polypeptides.

40. The composition of claims 31-38, wherein the agent is an antibody.

41. The composition of claim 39, wherein the agent is an antibody.

42. A composition of matter comprising
a conjugate of the agent of claims 31-41 and a therapeutic or diagnostic

5 agent.

43. The composition of matter of claim 42, wherein the conjugate is of the
agent and a therapeutic or diagnostic that is a toxin.

10 44. A pharmaceutical composition comprising an isolated nucleic acid
molecule selected from the group consisting of:

(1)

NA Group 1 molecules, and

15 (2)

NA Group 2 molecules, and a pharmaceutically acceptable carrier.

45. The pharmaceutical composition of claim 44, wherein the isolated nucleic
acid molecule comprises a NA Group 3 or NA Group 4 molecule.

20

46. The pharmaceutical composition of claim 44, wherein the isolated nucleic
acid molecule comprises at least two isolated nucleic acid molecules coding for two different
polypeptides, each polypeptide comprising a different human cancer associated antigen.

25 47. The pharmaceutical composition of claims 44-46 further comprising an
expression vector with a promoter operably linked to the isolated nucleic acid molecule.

48. The pharmaceutical composition of claims 44-46 further comprising a host
cell recombinantly expressing the isolated nucleic acid molecule.

30

49. A pharmaceutical composition comprising
an isolated polypeptide comprising a PP Group 1 or a PP Group 2
polypeptide, and
~~a pharmaceutically acceptable carrier~~
-

5

50. The pharmaceutical composition of claim 49, wherein the isolated
polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

- 10 51. The pharmaceutical composition of claim 49, wherein the isolated
polypeptide comprises at least two different polypeptides, each comprising a different human
cancer associated antigen.

52. The pharmaceutical composition of claim 49, wherein the isolated
15 polypeptides are PP Group 11 polypeptides or HLA binding fragments thereof.

53. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP
Group 12 polypeptides or HLA binding fragments thereof.

20

54. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP Group 13 polypeptides or HLA binding fragments thereof.

55. The pharmaceutical composition of claim 49, wherein the isolated
25 polypeptides are PP Group 14 polypeptides or HLA binding fragments thereof.

56. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP Group 15 polypeptides or HLA binding fragments thereof.

30

57. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 16 polypeptides or HLA binding fragments thereof.

58. ~~The pharmaceutical composition of claims 49-57, further comprising an~~

5 adjuvant.

59. An isolated nucleic acid molecule comprising a NA Group 3 molecule.

60. An isolated nucleic acid molecule comprising a NA Group 4 molecule.

10

61. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 11 molecule or a fragment thereof.

62. The isolated nucleic acid molecule of claims 59-60, wherein the molecule
15 is a Group 12 molecule or a fragment thereof.

63. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 13 molecule or a fragment thereof.

20 64. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 14 molecule or a fragment thereof.

65. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 15 molecule or a fragment thereof.

25

66. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 16 molecule or a fragment thereof.

67. An isolated nucleic acid molecule selected from the group consisting of

(a)

a fragment of a nucleic acid selected from the group of nucleic acid

~~consisting of SEQ ID NOs presenting nucleic acid sequences among SEQ ID NOs. 1-816, of~~

5 sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor,

(b)

complements of (a),

10

provided that the fragment includes a sequence of contiguous nucleotides

which is not identical to any sequence selected from the sequence group consisting of

(1) sequences having the GenBank accession numbers of Table 1

(correct?),

15

(2) complements of (1), and

(3) fragments of (1) and (2).

68. The isolated nucleic acid molecule of claim 67, wherein the sequence of contiguous nucleotides is selected from the group consisting of:

20

(1)

at least two contiguous nucleotides nonidentical to the sequence group,

(2)

at least three contiguous nucleotides nonidentical to the sequence group,

(3)

25

at least four contiguous nucleotides nonidentical to the sequence group,

(4)

at least five contiguous nucleotides nonidentical to the sequence group,

(5)

30

at least six contiguous nucleotides nonidentical to the sequence group,

(6)

at least seven contiguous nucleotides nonidentical to the sequence group.

69. The isolated nucleic acid molecule of claim 67, wherein the fragment has a

5 size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, and 200 nucleotides.

10 70. The isolated nucleic acid molecule of claim 67, wherein the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

71. An expression vector comprising an isolated nucleic acid molecule of
15 claims 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69 or 70 operably linked to a promoter.

72. An expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule.

20 73. An expression vector comprising a NA Group 1 or Group 2 molecule and a nucleic acid encoding an HLA molecule.

74. A host cell transformed or transfected with an expression vector of claims 71, 72, or 73.

25 75. A host cell transformed or transfected with an expression vector of claim 71 or claim 72 and further comprising a nucleic acid encoding HLA.

76. An isolated polypeptide encoded by the isolated nucleic acid molecule of
30 claims 59, 60, 61, 62, 63, 64, 65, or 66.

77. A fragment of the polypeptide of claim 76 which is immunogenic.

78. The fragment of claim 77, wherein the fragment, or a portion of the fragment, binds HLA or a human antibody.

5

79. An isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule.

10 80. The fragment of claim 79, wherein the fragment is part of a complex with HLA.

81. The fragment of claim 79, wherein the fragment is between 8 and 12 amino acids in length.

15

82. An isolated polypeptide comprising a fragment of the polypeptide of claim 76 of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

20 83. A kit for detecting the presence of the expression of a human cancer associated antigen precursor comprising
a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of

25 (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and

(b) complements of ("a"), wherein the contiguous segments are nonoverlapping.

30

84. The kit of claim 83, wherein the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule.

5 85. A method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor, comprising administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated
10 antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of

(a)

a nucleic acid molecule comprising NA group 1 nucleic acid molecules,

15

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules,

(c)

20

a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

86. The method of claim 85, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes
25 of an HLA molecule and a different human cancer associated antigen.

87. The method of claim 86, wherein the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

88. The method of claims 85-87, wherein the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17

5 polypeptides.

89. The method of claims 85-88, wherein the disorder is cancer.

90. A method for treating a subject having a condition characterized by
10 expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(I)

removing an immunoreactive cell containing sample from the subject,

15 (ii)

contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor,

20 (iii)

introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from
25 the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

91. The method of claim 90, wherein the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen.

92. The method of claim 90, wherein the host cell endogenously expresses an
5 HLA molecule which binds the human cancer associated antigen.

93. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

10 (I)
identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule

(ii)
15 transfecting a host cell with a nucleic acid selected from the group consisting of

(a) the nucleic acid molecule identified,
20

(b)
a fragment of the nucleic acid identified which includes a segment coding
for a human cancer associated antigen,
25

(c)
deletions, substitutions or additions to (a) or (b), and
30

(d)

degenerates of (a), (b), or (c);

(iii)

5 culturing said transfected host cells to express the transfected nucleic acid molecule, and;

(iv)

10 introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition.

94. The method of claim 93, further comprising:

15

(a)

identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule,

20 wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

95. The method of claim 93, wherein the immune response comprises a B-cell
25 response or a T cell response.

96. The method of claim 95, wherein the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human
30 cancer associated antigen.

97. The method of claim 93, wherein the nucleic acid molecule is a NA Group 3 molecule.

98. The method of claims 93 or 94, further comprising treating the host cells

5 to render them non-proliferative.

99. A method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

10 administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

100. The method of claim 99, wherein the antibody is a monoclonal antibody.

15

101. The method of claim 100, wherein the monoclonal antibody is a chimeric antibody or a humanized antibody.

102. A method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

20

administering to a subject a pharmaceutical composition of any one of claims 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 47, and 58 in an amount effective to prevent, delay the onset of, or inhibit the condition in
25 the subject.

103. The method of claim 102, wherein the condition is cancer.

104. The method of claims 102-103, further comprising first identifying that
30 the subject expresses in a tissue abnormal amounts of the protein.

105. A method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

(I) identifying cells from the subject which express abnormal amounts of

5 the protein;

(ii) isolating a sample of the cells;

(iii) cultivating the cells, and

(iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

10

106. The method of claim 105, wherein the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein.

15

107. The method of claim 105, further comprising rendering the cells non-proliferative, prior to introducing them to the subject.

108. A method for treating a pathological cell condition characterized by
20 aberrant expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

25 109. The method of claim 108, wherein the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

110. The method of claim 108, wherein the agent is an antisense nucleic acid
30 molecule which selectively binds to the nucleic acid molecule which encodes the protein.

111. The method of claim 108, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

112. A composition of matter useful in stimulating an immune response to a

5 plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules, comprising

a plurality of peptides derived from the amino acid sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

10

113. The composition of matter of claim 112, wherein at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto.

114. The composition of matter of claim 113, further comprising an adjuvant.

15

115. The composition of matter of claim 114, wherein said adjuvant is a saponin, GM-CSF, or an interleukin.

116. An isolated antibody which selectively binds to a complex of:

20

(i)

a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and

25

(ii)

and an MHC molecule to which binds the peptide to form the complex, wherein the isolated antibody does not bind to (i) or (ii) alone.

117. The antibody of claim 116, wherein the antibody is a monoclonal
30 antibody, a chimeric antibody or a humanized antibody.

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NY-1U-12 KESPPPKVNVNPLIGLLCEYGGSDYEEEEETPPPPQRTAQPKREEQTKKENEEDKLTDMNKLACLLCRRQFPNKEVL 970
LUCA15 PELVRNGDEENPLKRGVAAAYSGSDNEE.....ELVERLESEEEKLADWKMACLLCRRQFPNKKDAL 662
DXS8237E DLPKLASDDRPSPPRGLVAAAYSGESDSEE.....EQERGGEREEKLTDWQKLACLLCRRQFPNKEAL 233

NY-1U-12 IKHQQLSDLPKQNLEIHRKTKQSEQLAYLERRERE.GKFKGRGNDRRREKLQSFDSPEKRIKYSRETDSD..DRKLVNKKEDID 1050
LUCA15 VRHQQLSDLHKQNMIDYRRSRLSEQLALELELRERE.MKYRDRAAERREKYGIPEPPEPKRKKQFDAGTV..NYEQTKDGID 742
DXS8237E IRHQQLSGLHKQNLEIHRRAHLSENELEALEKNDMEQMKYRDRAAERREKYGIPEPPEPKRKKYGGISTASVDFEQPTRDGLG 316

NY-1U-12 TSSKGGCVQQATGWRKGTGLGYGHPGLASSEAEGRMRGSPVSGSRGTSKRQSNETYRDAVRRVMFARYKELD 1123
LUCA15 HSNIGNKMLQAMGWREGSGLGRKCQGITAPIEAQVRLKGAGLGAKGSAYGLSGADSYKDQAVRKAMFARFIEME 815
DXS8237E SDNIGSRMLQAMGWKEGSGLGRKKQGITVPIEAQTRVRGSLGARGSSYGVTSYKETLHKTMVTRFNEAQ 389

Fig. 1

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AAGGAGAGCGGGCCGTGGAGGCTTCGCCCTAGGTACTGCTATAACAGAAATTTGGTATAAAAGGATTACTTGTGGGGCCCTCTTCGATAAAAGA 100
 GATGTGGGGGGATTCTCGACCTGCTAACAGAACTGCACCTTTTCGTGGGGCCCAAGAAAGGTTTGTCTCCCGGGTGGAAACAGGGATTATCCTCTCCT 200
 1 M M G D S R P A N R T G P Y R G S Q F E R F A P S N H R D Y P P P
 CCCCCTAAGAGTCATGCTCAAGAGAGACACTCTGGCAACTTCTCGGACAGATTACATTCCTCCCTTTGATTTCCAGGGGCATTGGGGCCCTCTTTTGCAA 300
 34 P I K S R A Q E R D S G R F P G R D S L P F D F Q G H S G P P F A
 ATGTAGAGGAGCATTTCTTCAGCTATGGAGCTAGAGACGGACCGCATGCTGACTATCGAGGAGGGGAGGACCTGGACATGATTTCAGGGGGGAGATT 400
 67 H V E E H S F S Y G A R Q G P H G D Y R G G K G P G R D F R G G D F
 TTCGTCCTCTGATTTCAGAGCAGAGATTTCATCACAGTTCGACTTCAGGGGTAGGGAGATACATTCTGGGATTTCGGGATAGAGAGGACCACCTATG 500
 101 S S S D F G S R D S S Q L D F R G R D T H S G D F R E R E G P P G
 GACTATAGGGGTGGAGGGGTACTTCTATGATTATAGAGGTAGGGAGGCACCTCATATCAACTACAGACAGGGATGCTCAGCTCTGACTTACAGAG 600
 134 D Y R G G D G T S M D Y R G R E A P H H N Y R D R D A H A V D F R
 GTAGGGATGCTCCTCCATCTGACTTCAGGGGCCGGGGACTTATGATTTAGATTATTTAGAGGCCGGGATGATCCCATGACAGATTTCAGGGGAAGGATT 700
 167 G R D A P P S D F R G R G T Y D L D F R G R D G S R A D F R G R C L
 ATCAGATTTCGATTTTAGGGCCAGAGAACAGTCCCGTTCTGATTTTAGGAATAGAGATGATCTGATTCGACTTTAGAGACAAAGACGGAACACACAGTA 800
 201 S D L D F R A R E Q S R S D F R N R D V S D L D F R D K D G T Q V
 GACTTTAGAGGCCGAGGTTTCAGGTACTACTGATCTAGACTTTAGGGACAGGGATACGCCACATTTCAGATTTCAGAGGTAGACACCGGATCTAGGACTGATC 900
 234 D F R G R G S G T T D L D F R D R C T P H S D F R S R H R S R T D
 AGGATTTAGGGCCAGAGAGATGGGATCTTGTATGGAATTTAAAGATAGGGAGATGCCCCCTGTGGATCCAAATATTTTGGATTACATTCAGCCCTCTAC 1000
 267 Q D F R G R E M G S C M E F K D R E M P P V D P N I L D Y I Q P S T
 ACAAGATAGAGAACAATCTGGTATGAATGTGAACAGGAGAGAAGAATCCACACACGACCATACGATAGAAAGGCCCTGTTTGGCATTCAGAAGGGAGAA 1100
 301 Q D R R E S G H N V N R R E K S T H D H T I F R R P A F G I Q K Q K

Fig. 2

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334 TTTGAGCATTCAGAAACAAGAGAGGAGAAACACAAAGGTGTAGCCTTTGAACATGAGTCTCCAGCAGACTTTCAGAACAGACCCAAAGTCCAGTTCAGAGACC 1200
 F E H S E T R K G E T G G V A F E H E S P A D F Q N S Q S P V Q D
 367 AAGATAAGTCACAGCTTCTGGACGCTGAAGAGCAGAGTTCAGATGCTGGTCTGTTTAAAGAAAGGCGGTCTGGACTTCTTGGCGGCAAGACACACCGA 1300
 Q D K S Q L S G R K K Q S S D A G L F K E E G G L D F A G R Q D T D
 401 TTACAGAAAGCATGGAGTACCGTGTGGATCATAGGCTGCCAGGAAGCCAGATGTTTGGCTATGGCCAGAGCAAGTCTTTTCCAGAGGGGCAAAACATGCC 1400
 Y R S N F Y R D V D H R L P G S Q N F G Y G Q S K S F P E G K T A
 434 CGAGTGTCCCAACGGGACCTTCAGGATCAAGATTATAGGACCGGCCCAAGTGAAGAGAAACCCAGCAGGCTTATTCGATTAAAGTGGGTACCTGAGAGATG 1500
 R D A Q R D L Q D Q D T R T G P S E K K P S R L I R L S G V P K D
 467 CCACAAAAGAGAGATCTTAATGCTTTTCGGACTCCTGATGGCATGCTGTAAAGAACTTGCAGTTGAAGGAGTATAACACAGGTTTACGACTATGCGCTA 1600
 A T K E E I R N A F R T P D G M P V K R L Q L K E Y N T G Y D Y G Y
 501 TCTCTGCGTGGAGTTTCACTCTTTGGAAAGATGCCATCGGATGCTATCGAGGCCAACCCAGCCCAACTCTAATGATCCAGGACAAAGAAAGTTACCTTGGTGTAT 1700
 V C V E F S L L E D A I G C M E A N Q G T L H I Q D K E V T L E Y
 534 GTATCAAGCCTGGATTTTGGTACTGCAAAACGATGTAAAGGCAACATGGTGGCCAGCATCTTCTGTTCATTCTGCAAGAACCCCAAGAGAGTGTACAG 1800
 V S S L D F W Y C K R C K A N I G G H R S S C S F C K N P R E V T
 567 AGGCCAAGCAAGAAATTAATAACCTACCTCAGCCTCAGAAAACATCCATACCAGCACCATTGGAAAACAGCCCAACCCAGCCCTTAAGACAGCTGATAA 1900
 E A K Q E L I T Y P Q P Q K T S I P A P L E K Q P N Q P L R P A D K
 601 GGAACCTGAACCCAGGAAGAGGGAAGGCCCAAGAGTCACGCTTAGGACATCAAAAGAGAGAGCAAGAGGTATCTGCCTCCTTCTCGAAGGGAGGG 2000
 E P E P R K R E E G Q E S R L G H Q K R E A E R Y L P P S R R E G
 634 CCAACTTCCGAAGAGACCGGAGTGCATGGTCTGGAGAGACAGCCAGGATGGAGAGAGCAAAACTATCATGCTAAAGCGTATCTATCTGTTCCA 2100
 P T F R R D R F R E S W N G E T R Q D G E S K T I M L K R I Y R S
 667 CACCACCTGAGGTGATGTGAAGTCTGTGAGCCCTATGTCGCCCTTACTGCCACGTCCTGATCAAGAAACAGAACAGGCCCTTATGGGGGATAC 2200
 T P P E V I V E V L E P Y V R L T T A N V R I I K N R T G P M G H T

Fig. 2 (CONTINUED)

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701 CTATGGCTTTATTGACCTCGACTCCCATGTGGAAAGCTCTTCGTGTGGTGAAGATCTTTACAGAACCTTGATCCGCCATTATACCATTTGATGGGAAGATGGTA 2300
 Y G F I D L D S H V E A L R V V K I L Q N L D P P F S I D G K N V
 734 GCTGTAAACCTGGCCACTGGAAAACGAAGAAATGATTCCTCCGACCATTTCTGACCACANGCATTTACTATCAGGGTAAATAATTTCCGAGATAGCAGGG 2400
 A V N L A T G K R R N D S G D H S D H M H Y Y Q G K K Y F R D R R
 767 GAGTGGCAGAAATTCAGACTGGTCTTCAGATACAAATCGACAAGGACAAGTCATCTCTGAGTGCATACATATATGATTTCTGCTAGTGGCTACTATTATTA 2500
 G G G R N S D W S S D T N R Q G Q S S S D C Y I Y D S A S G Y Y Y
 801 VGACCCCTFGGCAGGAACTTATATGACCCCAATACCCAGCAAGAAGTCTATGTGCCCCAGGATCCTCTGGATTACCTGAGGAAGAAGATCAAGGAATAAAA 2600
 D P L A G T Y Y D P N T Q Q E V Y V P Q D P G L P E E I E H L
 834 AAACCCACAGTCAAGGAAGTCAAGTAGCAAGAAGGAATGTCTAAAGAGATGGCAAGGAGAAAAGAACACAGAGGAGTGACGAGGTTTCAGGAAATC 2700
 K P T S Q G K S S S K K E M S K R D G K E K K D R G V T R F Q E N
 867 CCAGTGAAGGGAAGGCCCTGCAGAGAGCTCTTTAAGAGCCCTCCTGCTCCTACTGTGAAGAAGGAAGAGAGTCCCCCTCCACCTAAAGTGGTAAACC 2800
 A S E G K A P A E D V F L K P L F P T V K K E E S P P P P K V V H I
 901 ACTGATCGGCCTCTTGGGTGAATAIGGACGAGACAGTCACTATGAGGAGGAAGAGAGGGAACAGACCCCTCCCCACAGCCCCCGCACAGCACAGCCCC 2900
 L I G L L G E Y G G D S D Y E E E E E Q T P P P Q P R T A Q P
 934 CAGAAGCGAGAGGAGCAACCAAGAGGAATGAAGAAGACAACACTCACTGACTGGAAATAAACTGGCTGTCTGTCTGCTTTGCAGAAAGGCAGTTTCCCAATA 3000
 Q K R E E Q T K K E M E E D K L T D W N K L A C L L C R R Q F P N
 967 AAGAAGTTCTGATCAAAACACAGCAGCTGTCAGACCTGCACAAGCAAAACCTGGAAATCCACCGGAAGATAAAACAGTCTGAGCAGGAGCTAGCCTATCT 3100
 K E V L I K R Q Q L S D L H K Q N L E I H R K I K Q S E Q E L A Y L
 1001 GGAAGGAGAGAACGAGAGGGAAGTTTAAACGAGAGGAATCATCCAGGGAAAAGTCCAGTCTTTTGACTCTCCAGAAAAGGAACCGGATTAAGTAC 3200
 E R R E R E G K F E G R D D D R R E K L Q S F D S P E R K R I H Y

Fig. 2 (CONTINUED)

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1034 TCCAGGGAACGACAGTGATCGTAAACTTGTGTGATAAAGAAGATATCGACACTAGCAGCAAAAGGAGGCTGTGTCCAACAGGCTACTGGCTGGAGGAAAG 3300
S R E T D S D R K L V D K E D I D T S S K G G C V Q Q A T G W R K
1067 GGACAGGCCCTGGGATATGGCCATCCCTGGATTGGCTTCATCAGAGGAGGCTGAAGGCCGGATGAGGGGCCCCAGTGTGGAGCCTCAGGAAGAACCAGCAA 3400
G T G L G Y G H P G L A S S E E A E G R M R G P S V G A S G R T S E
1101 AAGACAGTCCCAACGAGACTTATCGAGATGCTGTTCGAAGACTCATCTTTGCTCGATATAAAGAACTCGATTAAAGAAAGGAGACAAGCTTCCATGGGGATACA 3500
R Q S N E T Y R D A V K R V M F A R Y K E L D ***
ACCTCCCTCTTTGTTGTCCTCTCCCTTTCTTTGTTGTTACTGTCTGCTAGAACTTTTAAATAAACTGTTTCAATGTGATTAAATAAA 3599

Fig. 2 (CONTINUED)

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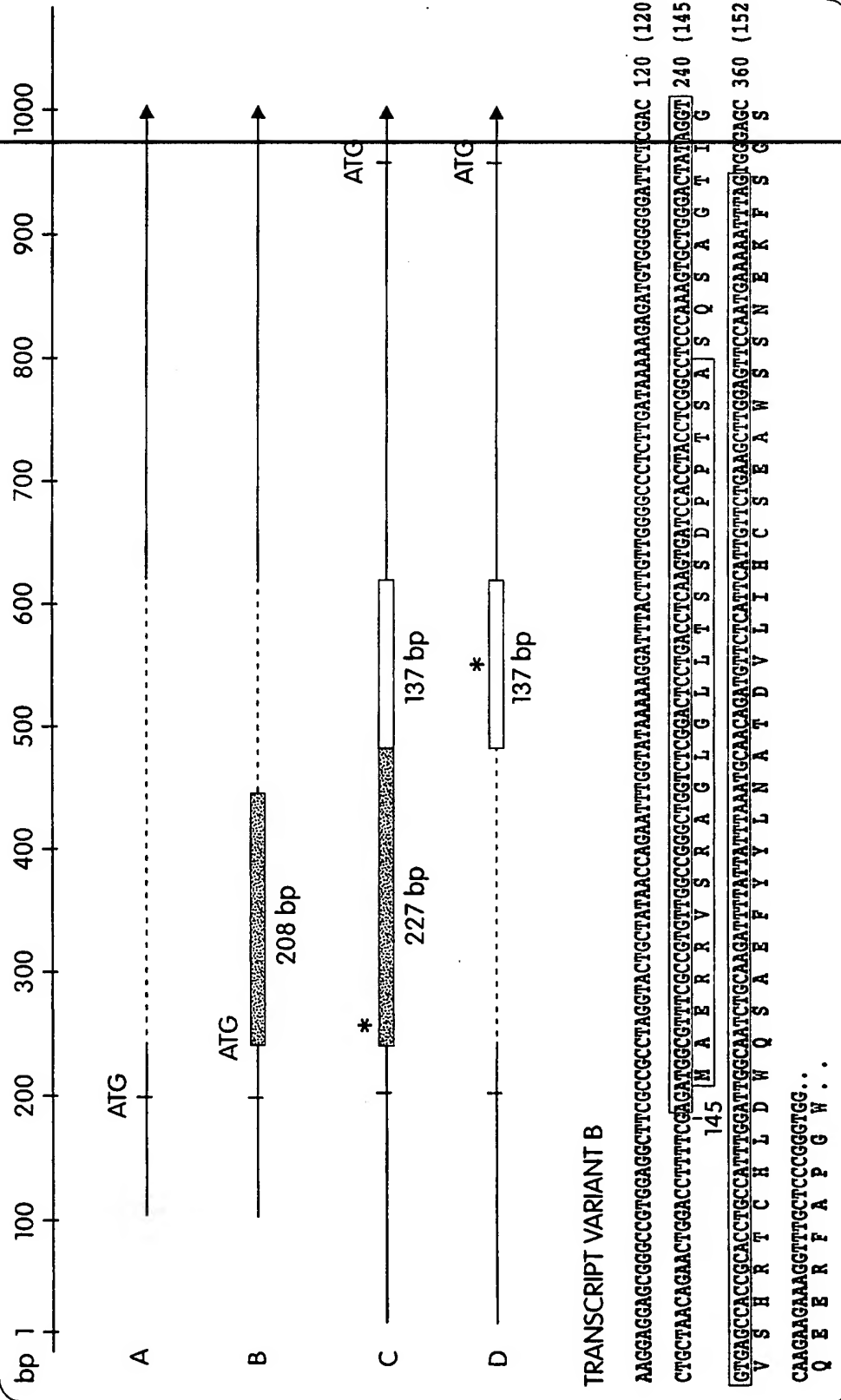


Fig. 3A

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227bp exon:
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CGTGTCTGAAATGGGAGCATAAAAGTTTACTCCGCCACTTCGTCTTAAATAGCAAAACTTTGCTGTTTCTGCAG

137bp exon:
ATCTAGGACCTTGTACAGAACTCTGCCAAAAAAATGTTTACAGAAATGTGCTGTGATTAGAGAAATA
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Fig. 3B

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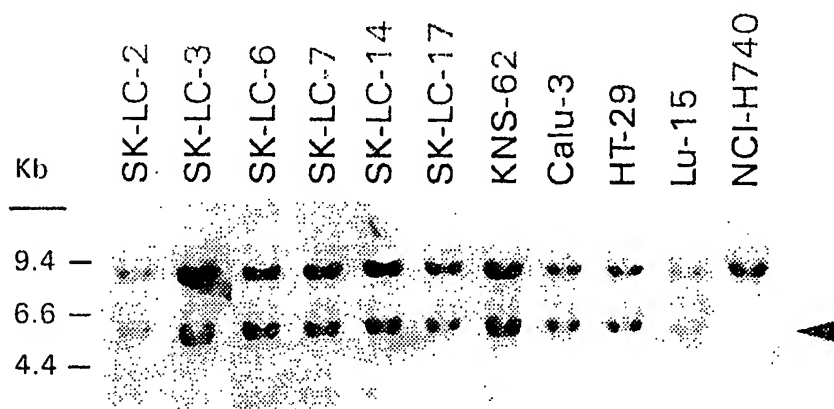


Fig. 4

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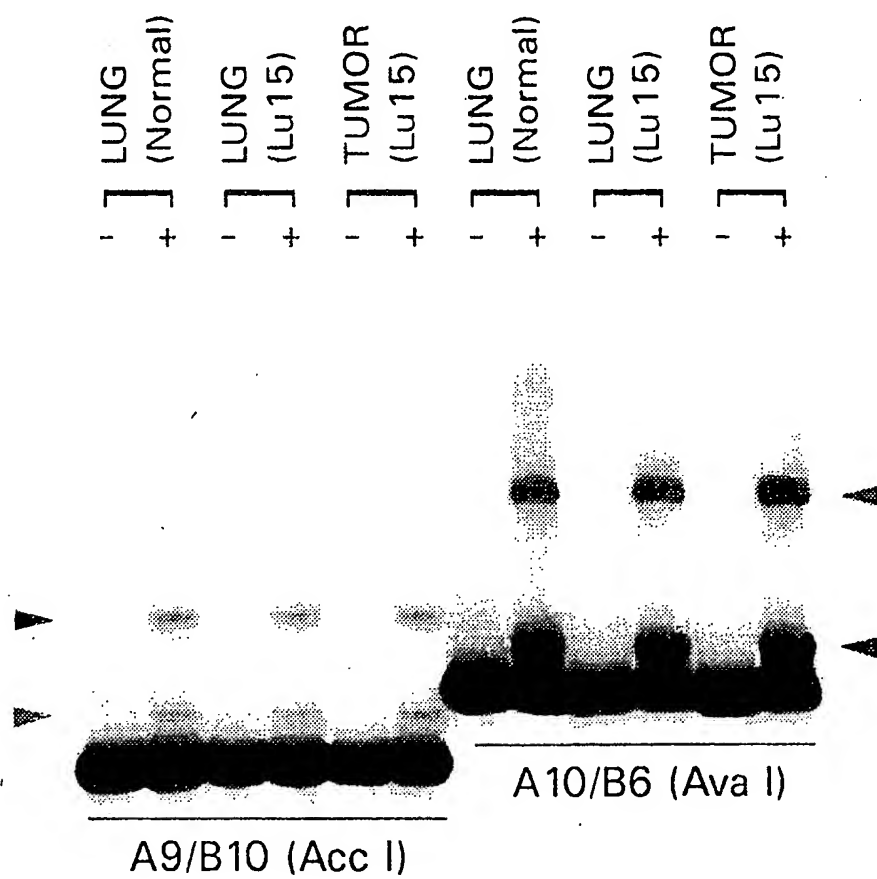


Fig. 5

SEQUENCE LISTING

<110> Ludwig Institute for Cancer Research
Old, Lloyd J.
Scanlan, Matthew J.
Stockert, Elisabeth
Gure, Ali
Chen, Yao-Tseng

Gout, Ivan
O'Hare, Michael
Obata, Yuichi
Pfreundschuh, Michael
Tureci, Ozlem
Sahin, Ugur

<120> CANCER-ASSOCIATED NUCLEIC ACIDS AND
POLYPEPTIDES

<130> L0461/7039/JRV/ERG

<140> Unknown

<141> 1998-07-15

<150> U.S. 08/896,164

<151> 1997-07-17

<150> U.S. 60/061,599

<151> 1997-10-10

<150> U.S. 60/061,765

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<151> 1997-10-10

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ctctcaaaga	tgttggtatt	attgntaact	tgantcccat	tttgcttcag	taagcctgaa	300
tacctcagct	tccaaatctc	taatccgcac	ttggaggcct	tgcacttcca	naagangngc	360
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<211> 441

<212> DNA

<213> Homo Sapiens

<400> 3

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<210> 4

<211> 247

<212> DNA

<213> Homo Sapiens

<400> 4

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aactgagggg	atctctcncg	tcacttcacc	gagttccgat	gtgattcana	agggcatttc	180
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<210> 5

<211> 486

<212> DNA

<213> Homo Sapiens

<400> 5

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<210> 6

<211> 766

<212> DNA

<213> Homo Sapiens

<400> 6

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<210> 7

<211> 567

<212> DNA

<213> Homo Sapiens

<400> 7

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<210> 8

<211> 730

<212> DNA

<213> Homo Sapiens

<400> 8

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<210> 9

<211> 585

<212> DNA

<213> Homo Sapiens

<400> 9

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<210> 10

<211> 661

<212> DNA

<213> Homo Sapiens

<400> 10

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<210> 11

<211> 1162

<212> DNA

<213> Homo Sapiens

<400> 11

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<210> 12

<211> 850

<212> DNA

<213> Homo Sapiens

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<210> 13

<211> 372
 <212> DNA
 <213> Homo Sapiens

<400> 13

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<400> 14

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<210> 15
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<400> 15

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<211> 1113

<212> DNA

<213> Homo Sapiens

<400> 16

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<210> 17

<211> 731

<212> DNA

<213> Homo Sapiens

<400> 17

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<211> 552

<212> DNA

<213> Homo Sapiens

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gtcctaantt ttaaaagaag ggnaaccaag nganatattt ggtgtaagt ttgcagtatg 3720
aanttctggt tgcaatccct ccccgctcca cantgcccc catttgagta caccgcacaa 3780
gtcaaacgnt aggnagtttg nataaaacca atttttctaa nttgttgntc atttgttgta 3840
antcaataaa gcnaaganta aacattttta tt 3872

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<210> 31
 <211> 655
 <212> DNA
 <213> Homo Sapiens

```

<400> 31
gaaatcatgg gagcacaaag aagaaataag tgaagcagag ccaggggggtg gttccttggg 60
agatggaagg ccgccagagg aaagtgccca tgaatgatg gaggaggaag aggaaatccc 120
aaaacctaa tctgtggttg caccgccagg tgctcctaag aaagagcatg taaatgtagt 180
attcattggg cacgtanatg ctggcaagtc aaccattgga ggacaaataa tgtatttgac 240
tggaatggtt gacaaaagga cgcttgaaaa gtatgaaaga gaagctaaag agaaaaacag 300
agaaaacttg tacttgtctt gggccttaga cacaatcag gaagaacgag acaagggtta 360
aacagtagaa gtgggtcgtg cctattttga aaccgaaaag aacatttcac aattctagat 420
atgaatccca gaacactgag ctcaaaaccc aaagcccaga atttgaagct caaagtccn 480
aattccanga aggtgctggag atgcttctga accccgagga aaagatcctt tgaatatctc 540
cgtaggagtt caccctctg actccttcac tcaggggttt ggggagcacc cacaggggac 600
ctgcccatag ggccacctt tgagatgccc acaggggccc tgctgtctac accgc 655

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<210> 32
 <211> 466
 <212> DNA
 <213> Homo Sapiens

<400> 32
 gaaaggtggc cagaggaagg gacagctgac ctggcacaat ctgggcttga agggggcaca 60
 acaagagcgt ctgtgagctg gtgctgtctg gagggatctt ggctcctctc cggctatctg 120
 accttctga agacctgctc gcacactgca tcccttgagc tcagttccag ctcgtgccga 180
 attcggcacg agctcgtgcc gaattcggca cgagggaagc actactccca gcgctgggcc 240
 caggaggacc tgctggagga gcagaaggat gggggccggg cagcggctgt ggctgacaag 300
 aagaaaggcc tcatggggcc actgaaccga ctggacacta aagatgtgga tgccctgctg 360
 aagaagtctg agggccagca tgaacagccg gaagatggat gcccctttgg tgccctgacg 420
 cagcgctcc tgcaggccct ggtggaggaa aatattatct tttccc 466

<210> 33
 <211> 293
 <212> DNA
 <213> Homo Sapiens

<400> 33
 gtccggcgccc tacatgagaa gcatgatgca gtcgctgagc cagaatccag atttggtgc 60
 acagatgatg ctgaatagcc cgctgtttac tgcaaatcct cagctgcagg agcagatgag 120
 gccacagctc ccagccttcc tgcagcagat gcagaatcca gacacactat cagccatgtc 180
 aaacccaaga ccaatgcagg ctttaatgca gatccagcag gggctacaga cattagccac 240
 tgaagcacct ggctgatcc cgagcttcac tccaggtgtg ggggtggggn tct 293

<210> 34
 <211> 456
 <212> DNA
 <213> Homo Sapiens

<400> 34
 caaagcctta gtcagagcc tgctagaatg tgtccagggt tacagctata ctgcacagca 60
 cttcccatgc tagtctctgt aaaacgcaaa aagccatttt caggagcagt aggcaagtca 120
 cattcaattg aaatgcagga tgggtgactg ccattccaag ttccatcttc ctggcagatc 180
 agcacagggt tccccagaag ttcatatcct ggattacagg tgtatgaaac catggtacca 240
 tacagaaagt ttgatgaatg tgtagcagga gactcctttg tattttccca ggttttagcc 300
 actgtcctca aatgataagg aggggtgagga gtcacatatg gaacttccat catgtcgtct 360
 tcttgctcaa aatatccctg gtcactcttg agtttagtac agtctccaaa atctatatga 420
 ggaggggaggc cacagtctat tggcatacca aatttt 456

<210> 35
 <211> 679
 <212> DNA
 <213> Homo Sapiens

<400> 35
 ggcggcgttc gtgtccgagg tcactagttt cccggtagtt cagctgcaca tgaatagaac 60
 agcaatgaga gccagtcaga aggactttga aaattcaata aatcaagtga aactcttgaa 120
 aaaggatcca ggaaacgaag tgaagctaaa actctacgcg ctatataagc aggccactga 180
 aggaccttgt aacatgcccc aaccagggtg atttgacttg atcaacaagg ccaaatggga 240
 cgcattggaat gcccttgcca gcctgccccaa ggaagctgcc aggcagaact atgtggattt 300
 ggtgtccagt ttgagtcctt cattggaatc ctctagttag gtggagcctg gaacagacag 360
 gaaatcaact gggtttgaaa ctctgggtgt gacctccgaa gatggcatca caaagatcat 420
 gttcaaccgg cccaaaaaga aaaatgccat aaactactgag atgtatcatg aaattatgag 480
 tgcacttaaa gctgccagca aggatgactc aatcatcact gttttaacag gaaatggtga 540
 ctattacagt agtgggaatg atctgactaa cttcactgat attccccctg gtggagtana 600
 ggagaaagct aaaaataatg ccgttttact gaagggaatt tgtgggctgt tttatagaat 660
 ttccctaagcc tctgattgc 679

<210> 36
 <211> 689
 <212> DNA
 <213> Homo Sapiens

<400> 36
 ctaaaccagt ggacatatca ggccatgggc cacgaactac taggcataaa caacaatcgg 60
 attgatcttt ccagagtgcc gggaatcagt aaagacttaa gagaagtggc cctatctgct 120
 gaaaatgatg aattctatgc taataatatg tacctgaact ttgctgagat tggtagcaat 180
 ataaagaatc tcatggaaga ttttcagaag aagaaaccaa aagaacagca aaaactagaa 240
 tcaatagcag acatgaaggc gtttgttgag aattatccac agttcaagaa aatgtctggg 300
 actgtttcaa agcatgtgac agtggttgga gaactgtctc gattggtcag tgaacggaat 360
 ctgctggagg tttcagaggc tgagcaagaa ctggcctgtc aaaatgacca ttctagtgtc 420
 ctccagaata taaaaaggct tctgcagaac cccaaagtga cagagtttga tgcgtcccgc 480
 ctggtgatgc tttatgcttt acattatgag cgacacagca gcaatagcct gccaggacta 540
 atgatggnc ctaggaataa aggtgtttct gagaagtatc gaaagctcgt gtctgcagtt 600
 gttgaatatg gtggtaaaaa gagtgcaggc aagtgcacct ctcagcccca aagatgctgt 660
 tggctatcac caacaattc ctcaaaggc 689

<210> 37
 <211> 443
 <212> DNA
 <213> Homo Sapiens

<400> 37
 ccacgcccgg ccccgagca ggcttttacg catgccccgc gcgccccctt gtgtccggaa 60
 tttattcctt ccggtgggtt cgcggtctag ctgaccaaga acggaactgg ggactttcgc 120
 agtgagagtt acagctctta aagatggcac cgaccaggc cgggcgcggt ggctcaggcc 180
 tgcaatccca gcactttggg aggcggaggc aggtgaatca cgaggtcagg aaatcgagac 240
 catcctggct aacatggtga aacccgtct cactaaaaa tacaaaaaat tagccaggca 300
 tgggtggctg cacctgtagt ccagctact tgggaggctg agccaggaaa gtggcatgaa 360
 cccgcgaggc agagcttgca ataagccgag atcgtgcca tgactccag cctgggcaac 420
 agaaggagac actgtctcaa aaa 443

<210> 38
 <211> 442
 <212> DNA
 <213> Homo Sapiens

<400> 38
 ctgcctcgg agcagccatg atggaaggcc tggacgacgg cccggacttc ctctcagaag 60
 aggaccgagg acttaaagca ataaatgtag atcttcaaag tgatgtgct ctgcagggtg 120
 acattttctga tgctcttagt gagcgggata aagtaaaatt cactgttcac acaaagattc 180
 caccagcacc accaagacct gattttgatg cttcaaggga aaaactacag aagcttggtg 240
 aaggagaagg gtcaatgacg aaggaagaat tcaçaaagat gaaacaggaa ctggaagctg 300
 aatatttggc aatattcaag aagacagttg cgatgcatga agtgttcctg tgcgtgtg 360
 cagcacatcc tattttgaga agagatttaa atttccatgt cttcttgga tataatcaag 420
 atttgagtgt gcgagga aaa aa 442

<210> 39
 <211> 692
 <212> DNA
 <213> Homo Sapiens

<400> 39

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cagggacagg ccctatctta ttttttttc catcttcac atccacttct gcttacagtt      60
tgctgcttac aataacttaa tgatggattg agttatctgg gtggtctcta gccatctggg      120
cagtgtgggt ctgtctaacc aaagggcatt ggcctcaaac cctgcatttg gtttaggggc      180
taacagagct cctcagataa tcttcacaca catgtaactg ctggagatct tattctatta      240
tgaataagaa acgagaagtt tttccaaagt gttagtcagg atctgaaggc tgtcattcag      300
ataaccagc ttttcctttt ggcttttagc ccattcagac tttgccagag tcaagccaag      360
gattgctttt ttgctacagt tttctgcaa atggcctagt tcctgagtag ctggaaacca      420
gagagaaaga ggatccagga tgtacttgga tgaggaggcc tggcttatct aggaagtcgt      480
gtctgggggtg cttattgctg ctccatacag ctgtacgtca gccccttggc cttctctgta      540
ggttcttggc ancaatgagc agctttcact caagtgcac aagtaattac tgagtcctaa      600
tttgatagcc accaactgta cctgggtang caaagtcaga tttttgagaa nctttttcct      660
gatttgaagt ttttaattacc ttaatttcct tt                                  692

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<210> 40
 <211> 619
 <212> DNA
 <213> Homo Sapiens

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<400> 40
gaggcaccag attctgctga ggggaccacc cttacagtgc tgctgaagg tgaggagttg      60
cccctgtgtg tgagtgaag caatggcctg gagctccac cctcagcagc atctgatgag      120
ccacttcagg agccactgga ggctgacagg acctcggaag agctgacaga ggccaagacc      180
ccaacctcca gccagagaa gccacaggaa ctgcgttacag ctgagggttg agctccatcc      240
acctcatctt cagccacttc ctgcctgag ggtccttcac ctgcccagacc tctcggcgt      300
cgcaccagtg ctgatgtgga aattaggggt caagggactg gtcggccagg acaaccacca      360
ggcccccagg tgcttcgaaa gctgccagga cggctggtaa ctgtggtaga ggaaaaggaa      420
ctgggtgccc ggcgccgga gcagccggga gctgccaanc accctagtgc ctgggggtctc      480
tgagactagt gccagcccg gaagcccgtc tgtccgcagc atgtcanggc canaatctc      540
ccctcccatt ggtgggccc gtgaaagctg ctccttcac cncactgcnc accccanccc      600
agnagccctt cattgcneg                                           619

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<210> 41
 <211> 153
 <212> PRT
 <213> Homo Sapiens

```

<400> 41
Pro Glu Ser Lys Pro Ile Met Thr Ser Ser Glu Ala Phe Glu Pro Pro
 1           5           10           15
Lys Tyr Leu Met Leu Gly Gln Gln Ala Val Gly Gly Val Pro Ile Gln
 20           25           30
Pro Ser Val Arg Thr Gln Met Trp Leu Thr Glu Gln Leu Arg Thr Asn
 35           40           45
Pro Leu Glu Gly Arg Asn Thr Glu Asp Ser Tyr Ser Leu Ala Pro Trp
 50           55           60
Gln Gln Gln Gln Ile Glu Phe Arg Gln Gly Ser Glu Thr Pro Met Gln
 65           70           75           80
Val Leu Thr Gly Ser Ser Arg Gln Ser Tyr Ser Pro Gly Tyr Gln Asp
 85           90           95
Phe Ser Lys Trp Glu Ser Met Leu Lys Lys Glu Gly Leu Leu Arg Gln
100           105           110
Lys Glu Ile Val Asp Arg Gln Lys Gln Ile Thr His Leu Ile Arg Asp
115           120           125
Asn Glu Leu Pro Ala His Ala Met Leu Gly His Tyr Val Asn Cys Glu
130           135           140

```

Asp Ser Tyr Val Ala Ser Leu His His
145 150

<210> 42
<211> 95
<212> PRT
<213> Homo Sapiens

<400> 42
Ile Leu Leu Glu Phe Tyr Leu Trp Gln Ile Gly Arg Tyr Ile Phe Val
1 5 10 15
His Val Asn Asn His Ile Tyr Ile Lys Leu Tyr Asn Cys Thr Phe Leu
20 25 30
Thr Ala Leu Ser Gln Val Ala Leu Ser Phe Pro Ser Ile Asn Gly Leu
35 40 45
Ile Phe Val Ser Phe Ala Phe Phe Arg Val Val Asn Ser Tyr Cys Pro
50 55 60
Leu Gln Phe Val Gln Phe Leu Arg Cys Leu Leu Leu Lys Arg Met
65 70 75 80
Leu Gly Glu Phe Ile Phe His Lys Glu Met Glu His Tyr Leu Lys
85 90 95

<210> 43
<211> 114
<212> PRT
<213> Homo Sapiens

<400> 43
Ser Lys Leu Leu Ser Gly Thr Ala Asp Gly Ala Asp Leu Arg Thr
1 5 10 15
Val Asp Pro Glu Thr Gln Ala Arg Leu Glu Ala Leu Leu Glu Ala Ala
20 25 30
Gly Ile Gly Lys Leu Ser Thr Ala Asp Gly Lys Ala Phe Ala Asp Pro
35 40 45
Glu Val Leu Arg Arg Leu Thr Ser Ser Val Ser Cys Ala Leu Asp Glu
50 55 60
Ala Ala Ala Leu Thr Arg Met Arg Ala Glu Ser Thr Ala Asn Ala Gly
65 70 75 80
Gln Ser Asp Asn Arg Ser Leu Ala Glu Ala Cys Ser Gly Asp Val Ala
85 90 95
Val Arg Lys Leu Leu Ile Glu Gly Arg Ser Val Phe Glu Leu Pro Glu
100 105 110
Glu Gly

<210> 44
<211> 132
<212> PRT
<213> Homo Sapiens

<400> 44
Gly Glu Lys Glu Gln Asp Lys Pro Pro Asn Leu Val Leu Lys Asp Lys
1 5 10 15
Val Lys Pro Lys Gln Asp Thr Lys Tyr Asp Leu Ile Leu Asp Glu Gln
20 25 30

Ala Glu Asp Ser Lys Ser Ser His Ser His Thr Ser Lys His Lys Lys
 35 40 45
 Lys Thr His His Cys Ser Glu Lys Glu Asp Glu Asp Tyr Met Pro
 50 55 60
 Ile Lys Asn Thr Asn Gln Asp Ile Tyr Arg Glu Met Gly Phe Gly His
 65 70 75 80
 Tyr Glu Glu Glu Glu Ser Cys Trp Glu Lys Gln Lys Ser Glu Lys Arg
 85 90 95
 Asp Arg Thr Gln Asn Arg Ser Arg Ser Arg Ser Arg Glu Arg Asp Gly
 100 105 110
 His Tyr Ser Asn Ser His Lys Ser Lys Tyr Gln Thr Asp Leu Tyr Glu
 115 120 125
 Arg Glu Arg Ser
 130

<210> 45
 <211> 214
 <212> PRT
 <213> Homo Sapiens

<400> 45
 Lys Thr Gln Glu Lys Pro Pro Lys Glu Leu Val Asn Glu Trp Ser Leu
 1 5 10 15
 Lys Ile Arg Lys Glu Met Arg Val Val Asp Arg Gln Ile Arg Asp Ile
 20 25 30
 Gln Arg Glu Glu Lys Val Lys Arg Ser Val Lys Asp Ala Ala Lys
 35 40 45
 Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala Lys Glu Met Ile Arg
 50 55 60
 Ser Arg Lys Ala Val Ser Lys Leu Ala Ser Lys Ala His Met Asn Ser
 65 70 75 80
 Val Leu Met Gly Met Lys Asn Gln Leu Ala Val Leu Arg Val Ala Gly
 85 90 95
 Ser Leu Gln Lys Ser Thr Glu Val Met Lys Ala Met Gln Ser Leu Val
 100 105 110
 Lys Ile Pro Glu Ile Gln Ala Thr Met Arg Glu Leu Ser Lys Glu Met
 115 120 125
 Met Lys Ala Gly Ile Ile Glu Glu Met Leu Glu Asp Thr Phe Glu Ser
 130 135 140
 Met Asp Asp Gln Glu Glu Met Glu Glu Glu Ala Glu Met Glu Ile Asp
 145 150 155 160
 Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala Leu Gly Lys Ala Pro Ser
 165 170 175
 Lys Val Thr Asp Ala Leu Pro Glu Pro Glu Pro Pro Gly Ala Met Ala
 180 185 190
 Ala Ser Glu Asp Glu Glu Glu Glu Glu Leu Glu Ala Met Gln Ser
 195 200 205
 Arg Leu Ala Thr Arg Ser
 210

<210> 46
 <211> 248
 <212> PRT
 <213> Homo Sapiens

<400> 46

Gly Ser Arg Glu Glu Thr Leu Ala Phe Val Pro Leu Leu Arg Leu Leu
 1 5 10 15
 Glu Ala Thr Leu Ser Pro Gly Arg Ala Phe Cys Ser Pro Ile Ser Ser
 20 25 30
 Lys Ile Gln Pro Ala Gln Val Ala Gly His Glu Leu Cys Ser Gly Ser
 35 40 45
 Trp Asn Leu Thr Leu Val Ala Ser Gly Pro Val Ser Met Ala Ala Glu
 50 55 60
 His Leu Leu Pro Gly Pro Pro Pro Ser Leu Ala Asp Phe Leu Glu Ala
 65 70 75 80
 Gly Gly Lys Gly Thr Glu Arg Gly Ser Gly Ser Ser Lys Pro Thr Gly
 85 90 95
 Ser Ser Gly Gly Pro Arg Met Ala Ser Phe Pro Lys Thr Lys Phe Asn
 100 105 110
 Glu Tyr Lys Asp Val Leu Pro Cys Met Thr Ser Ser Arg Gly Gly Lys
 115 120 125
 Ile Lys Ala Thr Asp Phe Met Val Ala Met Arg Cys Leu Gly Ala Ser
 130 135 140
 Pro Thr Pro Gly Glu Val Gln Arg His Leu Gln Thr His Gly Ile Asp
 145 150 155 160
 Gly Asn Gly Glu Leu Asp Phe Ser Thr Phe Leu Thr Ile Met His Met
 165 170 175
 Gln Ile Lys Gln Glu Asp Pro Lys Lys Glu Ile Leu Leu Ala Met Leu
 180 185 190
 Met Val Asp Lys Glu Lys Lys Gly Tyr Val Met Ala Ser Asp Leu Arg
 195 200 205
 Ser Lys Leu Thr Ser Gly Glu Lys Leu Thr His Lys Glu Val Asp Asp
 210 215 220
 Leu Phe Arg Glu Ala Asp Ile Glu Pro Asn Gly Lys Val Lys Tyr Asp
 225 230 235 240
 Glu Phe Ile His Lys Ile Thr Leu
 245

<210> 47

<211> 177

<212> PRT

<213> Homo Sapiens

<400> 47

Leu Cys Cys Met His Tyr Cys Cys Lys Ser Cys Trp Asn Glu Tyr Leu
 1 5 10 15
 Thr Thr Arg Ile Glu Gln Asn Leu Val Leu Asn Cys Thr Cys Pro Ile
 20 25 30
 Ala Asp Cys Pro Ala Gln Pro Thr Gly Ala Phe Ile Arg Ala Ile Val
 35 40 45
 Ser Ser Pro Glu Val Ile Ser Lys Tyr Lys Ala Leu Leu Arg Gly Tyr
 50 55 60
 Val Glu Ser Cys Ser Asn Leu Thr Trp Cys Thr Asn Pro Gln Gly Cys
 65 70 75 80
 Asp Arg Ile Leu Cys Arg Gln Gly Leu Gly Cys Gly Thr Thr Cys Ser
 85 90 95
 Lys Cys Gly Trp Ala Ser Cys Phe Asn Cys Ser Phe Pro Glu Ala His
 100 105 110
 Tyr Pro Ala Ser Cys Gly His Met Ser Gln Trp Val Asp Asp Gly Gly

```

      115      120      125
Tyr Tyr Asp Gly Met Ser Val Glu Ala Lys His Leu Ala Lys Leu Ile
      130      135      140
Ser Lys Arg Cys Pro Ser Cys Gln Ala Pro Ile Glu Asn Glu Gly Cys
145      150      155      160
Leu His Met Thr Cys Ala Lys Cys Asn His Gly Phe Cys Trp Arg Cys
      165      170      175
Leu

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<210> 48
 <211> 102
 <212> PRT
 <213> Homo Sapiens

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      <400> 48
Glu Lys Gly Leu His Ile Asp Gln Leu Val Cys Leu Val Leu Glu Ala
 1      5      10      15
Gln Lys Gly Pro Asn Pro Pro Gly Thr Leu Gly His Thr Val Ala Gly
      20      25      30
Gly Val Ala Cys Thr Thr Thr Val Leu Ser Cys Leu His Leu Leu Ser
      35      40      45
Gln Gly Tyr Lys Arg Asp Arg Pro Gln Ile Leu Met Tyr Ala Ala Pro
      50      55      60
Pro Met Gly Pro Cys Arg Gly Ala His Phe Cys Gly Ser Ser Gln Thr
      65      70      75      80
Ser Pro Pro Lys Pro Val Ala Thr Leu Ser Leu Leu Pro Cys Pro Leu
      85      90      95
Pro Pro Leu Lys Asn Gly
      100

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<210> 49
 <211> 179
 <212> PRT
 <213> Homo Sapiens

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      <400> 49
His Lys Pro Cys Asn Pro Arg Glu Lys Glu Arg Ile Gln Asn Ala Gly
 1      5      10      15
Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala Val Ser Arg
      20      25      30
Ala Leu Gly Asp Tyr Asp Tyr Lys Cys Val Asp Gly Lys Gly Pro Thr
      35      40      45
Glu Gln Leu Val Ser Pro Glu Pro Glu Val Tyr Glu Ile Leu Arg Ala
      50      55      60
Glu Glu Asp Glu Phe Ile Ile Leu Ala Cys Asp Gly Ile Trp Asp Val
      65      70      75      80
Met Ser Asn Glu Glu Leu Cys Glu Tyr Val Lys Ser Arg Leu Glu Val
      85      90      95
Ser Asp Asp Leu Glu Asn Val Cys Asn Trp Val Val Asp Thr Cys Leu
      100      105      110
His Lys Gly Ser Arg Asp Asn Met Ser Ile Val Leu Val Cys Phe Ser
      115      120      125
Asn Ala Pro Lys Val Ser Asp Glu Ala Val Lys Lys Asp Ser Glu Leu
      130      135      140

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Asp Lys His Leu Glu Ser Ile Met Glu Asn Leu Ala Lys Glu Cys Leu
 145 150 155 160
 Ile Leu Pro Met Ser Cys Ala Ser Cys Leu Gln Lys Ile Ser Gln Ile
 165 170 175
 Cys Leu Leu

<210> 50
 <211> 163
 <212> PRT
 <213> Homo Sapiens

<400> 50
 Asp Leu Pro Thr Leu Glu Asp His Gln Lys Gln Ser Gln Gln Leu Lys
 1 5 10 15
 Asp Ser Glu Leu Lys Ser Thr Glu Leu Gln Glu Lys Val Thr Glu Leu
 20 25 30
 Glu Ser Leu Leu Glu Glu Thr Gln Ala Ile Cys Arg Glu Lys Glu Ile
 35 40 45
 Gln Leu Glu Ser Leu Arg Gln Arg Glu Ala Glu Phe Ser Ser Ala Gly
 50 55 60
 His Ser Leu Gln Asp Lys Gln Ser Val Glu Glu Thr Ser Gly Glu Gly
 65 70 75 80
 Pro Glu Val Glu Met Glu Ser Trp Gln Lys Arg Tyr Asp Ser Leu Gln
 85 90 95
 Lys Ile Val Glu Lys Gln Gln Gln Lys Met Asp Gln Leu Arg Ser Gln
 100 105 110
 Val Gln Ser Leu Glu Gln Glu Val Ala Glu Glu Gly Thr Ser Gln Ala
 115 120 125
 Leu Arg Glu Glu Ala Gln Arg Arg Asp Ser Ala Leu Gln Gln Leu Arg
 130 135 140
 Thr Ala Val Lys Leu Ser Val Asn Gln Asp Leu Ile Glu Lys Asn Leu
 145 150 155 160
 Thr Leu Gln

<210> 51
 <211> 164
 <212> PRT
 <213> Homo Sapiens

<400> 51
 Phe Gly Asp Ser Val Asp Cys Ser Asp Cys Trp Leu Pro Val Val Lys
 1 5 10 15
 Phe Ile Glu Glu Gln Phe Glu Gln Tyr Leu Arg Asp Glu Ser Gly Leu
 20 25 30
 Asn Arg Lys Asn Ile Gln Asp Ser Arg Val His Cys Cys Leu Tyr Phe
 35 40 45
 Ile Ser Pro Phe Gly Arg Gly Leu Arg Pro Leu Ala Phe Leu Arg Ala
 50 55 60
 Val His Lys Val Asn Ile Ile Pro Val Ile Gly Lys Ala Asp Ala Leu
 65 70 75 80
 Met Pro Gln Glu Thr Gln Ala Leu Lys Gln Lys Ile Arg Asp Gln Leu
 85 90 95
 Lys Glu Glu Glu Ile His Ile Tyr Gln Phe Pro Glu Cys Asp Ser Asp

```

      100      105      110
Glu Asp Glu Asp Phe Lys Arg Gln Asp Ala Met Lys Glu Ser Ile Pro
      115      120      125
Phe Ala Val Val Gly Ser Cys Gln Val Val Arg Asp Gly Gly Asn Arg
      130      135      140
Pro Val Arg Gly Arg Arg Tyr Ser Trp Gly Asn Val Glu Val Asn His
      145      150      155      160
Ile Ala Ile Ser

```

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<210> 52
<211> 600
<212> PRT
<213> Homo Sapiens

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```

      <400> 52
Met Cys Pro Arg Gln Val Asp Arg Ala Lys Glu Lys Gly Ile Gly Thr
  1              5              10              15
Pro Gln Pro Asp Val Ala Lys Asp Ser Trp Ala Glu Leu Glu Asn Ser
      20              25              30
Ser Lys Glu Asn Glu Val Ile Glu Val Lys Ser Met Gly Glu Ser Gln
      35              40              45
Ser Lys Lys Leu Gln Gly Gly Tyr Glu Cys Lys Tyr Cys Pro Tyr Ser
      50              55              60
Thr Gln Asn Leu Asn Glu Phe Thr Glu His Val Asp Met Gln His Pro
      65              70              75              80
Asn Val Ile Leu Asn Pro Leu Tyr Val Cys Ala Glu Cys Asn Phe Thr
      85              90              95
Thr Lys Lys Tyr Asp Ser Leu Ser Asp His Asn Ser Lys Phe His Pro
      100              105              110
Gly Glu Ala Asn Phe Lys Leu Lys Leu Ile Lys Arg Asn Asn Gln Thr
      115              120              125
Val Leu Glu Gln Ser Ile Glu Thr Thr Asn His Val Val Ser Ile Thr
      130              135              140
Thr Ser Gly Pro Gly Thr Gly Asp Ser Asp Ser Gly Ile Ser Val Ser
      145              150              155              160
Lys Thr Pro Ile Met Lys Pro Gly Lys Pro Lys Ala Asp Ala Lys Lys
      165              170              175
Val Pro Lys Lys Pro Glu Glu Ile Thr Pro Glu Asn His Val Glu Gly
      180              185              190
Thr Ala Arg Leu Val Thr Asp Thr Ala Glu Ile Leu Ser Arg Leu Gly
      195              200              205
Gly Val Glu Leu Leu Gln Asp Thr Leu Gly His Val Met Pro Ser Val
      210              215              220
Gln Leu Pro Pro Asn Ile Asn Leu Val Pro Lys Val Pro Val Pro Leu
      225              230              235              240
Asn Thr Thr Lys Tyr Asn Ser Ala Leu Asp Thr Asn Ala Thr Met Ile
      245              250              255
Asn Ser Phe Asn Lys Phe Pro Tyr Pro Thr Gln Ala Glu Leu Ser Trp
      260              265              270
Leu Thr Ala Ala Ser Lys His Pro Glu Glu His Ile Arg Ile Trp Phe
      275              280              285
Ala Thr Gln Arg Leu Lys His Gly Ile Ser Trp Ser Pro Glu Glu Val
      290              295              300
Glu Glu Ala Arg Lys Lys Met Phe Asn Gly Thr Ile Gln Ser Val Pro

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305 310 315 320
 Pro-Thr Ile Thr Val Leu Pro Ala Gln Leu Ala Pro Thr Lys Met Thr
 325 330 335
 Gln Pro Ile Leu Gln Thr Ala Leu Pro Cys Gln Ile Leu Gly Gln Thr
 340 345 350
 Ser Leu Val Leu Thr Gln Val Thr Ser Gly Ser Thr Thr Val Ser Cys
 355 360 365
 Ser Pro Ile Thr Leu Ala Val Ala Gly Val Thr Asn His Gly Gln Lys
 370 375 380
 Arg Pro Leu Val Thr Pro Gln Ala Ala Pro Glu Pro Lys Arg Pro His
 385 390 395 400
 Ile Ala Gln Val Pro Glu Pro Pro Pro Lys Val Ala Asn Pro Pro Leu
 405 410 415
 Thr Pro Ala Ser Asp Arg Lys Lys Thr Lys Glu Gln Ile Ala His Leu
 420 425 430
 Lys Ala Ser Phe Leu Gln Ser Gln Phe Pro Asp Asp Ala Glu Val Tyr
 435 440 445
 Arg Leu Ile Glu Val Thr Gly Leu Ala Arg Ser Glu Ile Lys Lys Trp
 450 455 460
 Phe Ser Asp His Arg Tyr Arg Cys Gln Arg Gly Ile Val His Ile Thr
 465 470 475 480
 Ser Glu Ser Leu Ala Lys Asp Gln Leu Ala Ile Ala Ala Ser Arg His
 485 490 495
 Gly Arg Thr Tyr His Ala Tyr Pro Asp Phe Ala Pro Gln Lys Phe Lys
 500 505 510
 Glu Lys Thr Gln Gly Gln Val Lys Ile Leu Glu Asp Ser Phe Leu Lys
 515 520 525
 Ser Ser Phe Pro Thr Gln Ala Glu Leu Asp Arg Leu Arg Val Glu Thr
 530 535 540
 Lys Leu Ser Arg Arg Glu Ile Asp Ser Trp Phe Ser Glu Arg Arg Lys
 545 550 555 560
 Leu Arg Asp Ser Met Glu Gln Ala Val Leu Asp Ser Met Gly Ser Gly
 565 570 575
 Gln Lys Arg Pro Arg Cys Gly Lys Pro Pro Met Val Leu Cys Leu Asp
 580 585 590
 Ser Asn Ser Ser Pro Val Pro Ser
 595 600

<210> 53
 <211> 163
 <212> PRT
 <213> Homo Sapiens

<400> 53
 Arg Lys Ser Trp Glu His Lys Glu Glu Ile Ser Glu Ala Glu Pro Gly
 1 5 10 15
 Gly Gly Ser Leu Gly Asp Gly Arg Pro Pro Glu Glu Ser Ala His Glu
 20 25 30
 Met Met Glu Glu Glu Glu Ile Pro Lys Pro Lys Ser Val Val Ala
 35 40 45
 Pro Pro Gly Ala Pro Lys Lys Glu His Val Asn His Val Ala Gly Lys
 50 55 60
 Ser Thr Ile Gly Gly Gln Ile Met Tyr Leu Thr Gly Met Val Asp Lys
 65 70 75 80
 Arg Thr Leu Glu Lys Tyr Glu Arg Glu Ala Lys Glu Lys Asn Arg Glu

```

      85              90              95
Thr Trp Tyr Leu Ser Trp Ala Leu Asp Thr Asn Gln Glu Glu Arg Asp
      100              105              110
Lys Gly Lys Thr Val Glu Val Gly Arg Ala Tyr Phe Glu Thr Glu Lys
      115              120              125
Lys His Phe Thr Ile Leu Asp Met Asn Pro Arg Thr Leu Ser Ser Lys
      130              135              140
Pro Lys Ala Gln Asn Leu Lys Leu Lys Val Pro Asn Ser Lys Val Arg
145              150              155              160
Arg Cys Phe

```

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<210> 54
<211> 155
<212> PRT
<213> Homo Sapiens

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```

<400> 54
Glu Arg Trp Pro Glu Glu Gly Thr Ala Asp Leu Ala Gln Ser Gly Leu
 1              5              10              15
Glu Gly Gly Thr Thr Arg Ala Ser Val Ser Trp Cys Cys Leu Glu Gly
      20              25              30
Ser Trp Leu Leu Ser Gly Tyr Leu Thr Phe Leu Lys Thr Cys Ser His
      35              40              45
Thr Ala Ser Leu Ala Val Ser Ser Ser Ser Cys Arg Ile Arg His Glu
      50              55              60
Leu Val Pro Asn Ser Ala Arg Gly Lys His Tyr Ser Gln Arg Trp Ala
65              70              75              80
Gln Glu Asp Leu Leu Glu Glu Gln Lys Asp Gly Ala Arg Ala Ala Ala
      85              90              95
Val Ala Asp Lys Lys Lys Gly Leu Met Gly Pro Leu Thr Glu Leu Asp
      100              105              110
Thr Lys Asp Val Asp Ala Leu Leu Lys Lys Ser Glu Ala Gln His Glu
      115              120              125
Gln Pro Glu Asp Gly Cys Pro Phe Gly Ala Leu Thr Gln Arg Leu Leu
      130              135              140
Gln Ala Leu Val Glu Glu Asn Ile Ile Phe Ser
145              150              155

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<210> 55
<211> 112
<212> PRT
<213> Homo Sapiens

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<400> 55
Ser Glu Arg Ala Leu Ala Pro Arg Thr Tyr Arg Met Glu Thr Ala Arg
 1              5              10              15
Ser Ala Pro Tyr Met Arg Ser Met Met Gln Ser Leu Ser Gln Asn Pro
      20              25              30
Asp Leu Ala Ala Gln Met Met Leu Asn Ser Pro Leu Phe Thr Ala Asn
      35              40              45
Pro Gln Leu Gln Glu Gln Met Arg Pro Gln Leu Pro Ala Phe Leu Gln
      50              55              60
Gln Met Gln Asn Pro Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala
65              70              75              80

```

Met Gln Ala Leu Met Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr
 85 90 95
 Glu Ala Pro Gly Leu Ile Pro Ser Phe Thr Pro Gly Val Gly Val Gly
 100 105 110

<210> 56
 <211> 151
 <212> PRT
 <213> Homo Sapiens

<400> 56
 Lys Phe Gly Met Pro Ile Asp Cys Gly Leu Pro Pro His Ile Asp Phe
 1 5 10 15
 Gly Asp Cys Thr Lys Leu Lys Asp Asp Gln Gly Tyr Phe Glu Gln Glu
 20 25 30
 Asp Asp Met Met Glu Val Pro Tyr Val Thr Pro His Pro Pro Tyr His
 35 40 45
 Leu Gly Ala Val Ala Lys Thr Trp Glu Asn Thr Lys Glu Ser Pro Ala
 50 55 60
 Thr His Ser Ser Asn Phe Leu Tyr Gly Thr Met Val Ser Tyr Thr Cys
 65 70 75 80
 Asn Pro Gly Tyr Glu Leu Leu Gly Asn Pro Val Leu Ile Cys Gln Glu
 85 90 95
 Asp Gly Thr Trp Asn Gly Ser Ala Pro Ser Cys Ile Ser Ile Glu Cys
 100 105 110
 Asp Leu Pro Thr Ala Pro Glu Asn Gly Phe Leu Arg Phe Thr Glu Thr
 115 120 125
 Ser Met Gly Ser Ala Val Gln Tyr Ser Cys Lys Pro Gly His Ile Leu
 130 135 140
 Ala Gly Ser Asp Leu Arg Leu
 145 150

<210> 57
 <211> 220
 <212> PRT
 <213> Homo Sapiens

<400> 57
 Ala Ala Phe Val Ser Glu Val Thr Ser Phe Pro Val Val Gln Leu His
 1 5 10 15
 Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser
 20 25 30
 Ile Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys
 35 40 45
 Leu Lys Leu Tyr Ala Leu Tyr Lys Lys Gln Ala Thr Glu Gly Pro Cys Asn
 50 55 60
 Met Pro Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp
 65 70 75 80
 Ala Trp Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn
 85 90 95
 Tyr Val Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser
 100 105 110
 Gln Val Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu
 115 120 125
 Val Val Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro

```

      130              135              140
Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg
145              150              155              160
Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr
      165              170              175
Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr
      180              185              190
Asp Ile Pro Pro Gly Gly Val Glu Lys Ala Lys Asn Asn Ala Val Leu
      195              200              205
Leu Lys Gly Ile Cys Gly Leu Phe Tyr Arg Ile Ser
      210              215              220

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<210> 58
<211> 101
<212> PRT
<213> Homo Sapiens

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      <400> 58
Trp Pro Asp Leu Val His Thr Trp Ser Ser Glu Glu Ala Met Gly Ser
 1              5              10              15
Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn His Arg Asn
      20              25              30
Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu Leu Gly Ser
      35              40              45
Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr Thr Arg Lys
      50              55              60
Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg Tyr Gly Tyr
65              70              75              80
Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Pro Arg Cys Gln Thr Gly
      85              90              95
Thr Arg Asn Leu Cys
      100

```

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<210> 59
<211> 43
<212> PRT
<213> Homo Sapiens

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      <400> 59
Ala His Gly Pro Gly Val Glu Pro Thr Ser Arg His Gln Lys Asn Asn
 1              5              10              15
Leu Ser Ser Ser His Thr Val Arg Leu Glu Thr Arg Gly Gln Thr Glu
      20              25              30
Asn Gln Glu Cys Leu Leu Cys Pro His Glu Glu
      35              40

```

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<210> 60
<211> 210
<212> PRT
<213> Homo Sapiens

```

```

      <400> 60
Leu Asn Gln Trp Thr Tyr Gln Ala Met Val His Glu Leu Leu Gly Ile
 1              5              10              15
Asn Asn Asn Arg Ile Asp Leu Ser Arg Val Pro Gly Ile Ser Lys Asp

```

20 25 30
 Leu Arg Glu Val Val Leu Ser Ala Glu Asn Asp Glu Phe Tyr Ala Asn
 35 40 45
 Asn Met Tyr Leu Asn Phe Ala Glu Ile Gly Ser Asn Ile Lys Asn Leu
 50 55 60
 Met Glu Asp Phe Gln Lys Lys Lys Pro Lys Glu Gln Gln Lys Leu Glu
 65 70 75 80
 Ser Ile Ala Asp Met Lys Ala Phe Val Glu Asn Tyr Pro Gln Phe Lys
 85 90 95
 Lys Met Ser Gly Thr Val Ser Lys His Val Thr Val Val Gly Glu Leu
 100 105 110
 Ser Arg Leu Val Ser Glu Arg Asn Leu Leu Glu Val Ser Glu Val Glu
 115 120 125
 Gln Glu Leu Ala Cys Gln Asn Asp His Ser Ser Ala Leu Gln Asn Ile
 130 135 140
 Lys Arg Leu Leu Gln Asn Pro Lys Val Thr Glu Phe Asp Ala Ala Arg
 145 150 155 160
 Leu Val Met Leu Tyr Ala Leu His Tyr Glu Arg His Ser Ser Asn Ser
 165 170 175
 Leu Pro Gly Leu Met Met Leu Arg Asn Lys Gly Val Ser Glu Lys Tyr
 180 185 190
 Arg Lys Leu Val Ser Ala Val Val Glu Tyr Gly Gly Lys Thr Ser Gln
 195 200 205
 Arg Lys
 210

<210> 61
 <211> 40
 <212> PRT
 <213> Homo Sapiens

<400> 61
 Thr Pro Gly Pro Gly Ala Gly Phe Tyr Ala Cys Pro Ala Arg Pro Leu
 1 5 10 15
 Val Ser Gly Ile Tyr Ser Phe Arg Trp Val Arg Gly Leu Ala Asp Gln
 20 25 30
 Glu Arg Asn Trp Gly Leu Ser Gln
 35 40

<210> 62
 <211> 238
 <212> PRT
 <213> Homo Sapiens

<400> 62
 His Glu Ala Arg Leu Lys Arg Ala Ser Ala Pro Thr Phe Asp Asn Asp
 1 5 10 15
 Tyr Ser Leu Ser Glu Leu Leu Ser Gln Leu Asp Ser Gly Val Ser Gln
 20 25 30
 Ala Val Glu Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Ser Lys
 35 40 45
 Leu Pro Ser Ser Gly Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val
 50 55 60
 Asp Ser Ala Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg
 65 70 75 80

Glu Pro Ser Thr Ser Asp Leu Gly Thr Thr Asp Val Gln Lys Lys Lys
 85 90 95
 Leu Val Asp Ala Ile Val Ser Gly Asp Thr Ser Lys Leu Met Lys Ile
 100 105 110
 Leu Gln Pro Gln Asp Val Asp Leu Ala Leu Asp Ser Gly Ala Ser Leu
 115 120 125
 Leu His Leu Ala Val Glu Ala Gly Gln Glu Glu Cys Ala Lys Trp Leu
 130 135 140
 Leu Leu Asn Asn Ala Asn Pro Asn Leu Ser Asn Arg Arg Gly Ser Thr
 145 150 155 160
 Pro Leu His Met Ala Val Glu Arg Arg Val Arg Gly Val Val Glu Leu
 165 170 175
 Leu Leu Ala Arg Ile Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr
 180 185 190
 Ala Leu His Phe Ala Asn Gly Gly Val His Thr Ala Ala Val Gly Glu
 195 200 205
 Arg Leu Gly Gln Thr Lys Val Asp Phe Glu Gly Arg Thr Pro Met Gln
 210 215 220
 Val Gly Leu Pro Thr Thr Gly Lys Asn Ile Leu Arg Ile Leu
 225 230 235

<210> 63
 <211> 146
 <212> PRT
 <213> Homo Sapiens

<400> 63
 Arg Leu Gly Ala Ala Met Met Glu Gly Leu Asp Asp Gly Pro Asp Phe
 1 5 10 15
 Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val Asp Leu Gln
 20 25 30
 Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu Ser Glu Arg
 35 40 45
 Asp Lys Val Lys Phe Thr Val His Thr Lys Ile Pro Pro Ala Pro Pro
 50 55 60
 Arg Pro Asp Phe Asp Ala Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu
 65 70 75 80
 Gly Glu Gly Ser Met Thr Lys Glu Glu Phe Thr Lys Met Lys Gln Glu
 85 90 95
 Leu Glu Ala Glu Tyr Leu Ala Ile Phe Lys Lys Thr Val Ala Met His
 100 105 110
 Glu Val Phe Leu Cys Arg Val Ala Ala His Pro Ile Leu Arg Arg Asp
 115 120 125
 Leu Asn Phe His Val Phe Leu Glu Tyr Asn Gln Asp Leu Ser Val Arg
 130 135 140
 Gly Lys
 145

<210> 64
 <211> 63
 <212> PRT
 <213> Homo Sapiens

<400> 64
 Glu Arg Gly His Ser Ile Lys Asp Phe Val Ser Phe Ala Arg His Phe

1 5 10 15
 Ser Pro Asn Pro Arg Ile Val Ser Val Asn Ala Ser Tyr Ser Leu Ser
 20 25 30
 Asn Glu Ser Ser Leu Glu Gln Val Tyr Thr Leu Lys Met Ser Phe Ile
 35 40 45
 Ala Ser Asn Thr Tyr His Asn Gln Leu Tyr Lys Glu Gly Phe Leu
 50 55 60

<210> 65
 <211> 199
 <212> PRT
 <213> Homo Sapiens

<400> 65
 Glu Ala Pro Asp Ser Ala Glu Gly Thr Thr Leu Thr Val Leu Pro Glu
 1 5 10 15
 Gly Glu Glu Leu Pro Leu Cys Val Ser Glu Ser Asn Gly Leu Glu Leu
 20 25 30
 Pro Pro Ser Ala Ala Ser Asp Glu Pro Leu Gln Glu Pro Leu Glu Ala
 35 40 45
 Asp Arg Thr Ser Glu Glu Leu Thr Glu Ala Lys Thr Pro Thr Ser Ser
 50 55 60
 Pro Glu Lys Pro Gln Glu Leu Val Thr Ala Glu Val Ala Ala Pro Ser
 65 70 75 80
 Thr Ser Ser Ser Ala Thr Ser Ser Pro Glu Gly Pro Ser Pro Ala Arg
 85 90 95
 Pro Pro Arg Arg Arg Thr Ser Ala Asp Val Glu Ile Arg Gly Gln Gly
 100 105 110
 Thr Gly Arg Pro Gly Gln Pro Pro Gly Pro Lys Val Leu Arg Lys Leu
 115 120 125
 Pro Gly Arg Leu Val Thr Val Val Glu Glu Lys Glu Leu Val Arg Arg
 130 135 140
 Arg Arg Gln Gln Arg Gly Ala Ala Ser Thr Leu Val Pro Gly Val Ser
 145 150 155 160
 Glu Thr Ser Ala Ser Pro Gly Ser Pro Ser Val Arg Ser Met Ser Gly
 165 170 175
 Pro Glu Ser Ser Pro Pro Ile Gly Gly Pro Cys Glu Ala Ala Pro Ser
 180 185 190
 Ser Ser Leu Pro Thr Pro Pro
 195

<210> 66
 <211> 1599
 <212> DNA
 <213> Homo Sapiens

<400> 66
 ttctttgaaa cattattatt cagaacgaag gagaatgata .cagatacact ggctgaggtg 60
 ttttgaggtg cattgaaatg ttccatgctg ttacttaggt taacatgttc ttgaggtacc 120
 atgccatgga ttaaaaggaa atttggtgaag tggcttcac ctaaagcact tactagggaa 180
 gctatgcgaa attattttaa agggtaaggg gatcaaatag tacttatcct tcatgcaaaa 240
 gttgtacaga agtcatatgg caatcaaaaa attttttttt gccctcccc ttgtgtatat 300
 cttatgggca gtggatggaa gaaaaaaaaa gaacaaatga aatgcgatgg ttgttctgaa 360
 cacagctctc atccatgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag 420
 ctaaacttgg aaggaaagaa ctattgcaca gccaaaacat tgtacatatc tgattcagac 480

```

aagcaaaagc acttcatttt ttctgtaaag gtgttctatg gcaacgggtga tgacattggt      540
gtgttctctca gcaagtagat aaaagtcata tccaaacctt ccaaaaagaa gcagtcattg      600
aaaaatgctg acttatgcat tgtctcagga acaaagggtg ctctgtttta tcgactacga      660
tcccagacag ttagtaccag atacttgcat gtagaaggag gtaattttca tgccagttca      720
cagcagtggg gagcatttta cattcaattc ttggatgatg atggatcaga aggagaagaa      780
ttcacagtct gagatgccta cattcattat ggacaaacat gcaaacttgt gtgctcagtt      840
actggcatgg cactcccaag attgataatt atgaaagttg ataagcatac cgcattattg      900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat ttaccttaa ggatacagaa      960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca     1020
agagaaccaa ataaagagat gataaatgat ggcgcttcct ggacaatcat tagcacagat     1080
aaggcagggg atacatttta tgagggaatg ggccttctcc ttgccccagt cactcctgtg     1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca     1200
ggacagaatt tcaactccaa tttacgagtg tggtttgggg gggtagaagc tgaaactatg     1260
tacaggtgtg gagagagtat gctctgtgtc gtcccagaca tttctgcatt ccgagaaggt     1320
tggagatggg tccggcaacc agtccaggtt ccagtaactt tgggtccgaa tgatggaatc     1380
atttattcca ccagccttac ctttacctac acaccagaac cagggccgcg gccacattgc     1440
agtgcagcag gagcaatcct tctagccaat tcaagccagg tgccccctaa cgaatcaaac     1500
acaaacagcg aggggaagtta cacaacgcc agcacaaatt caaccagtg cacaatcatc     1560
acagccacag tggatccta actaccgtct ttttgctag                               1599

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<210> 67

<211> 729

<212> PRT

<213> Homo Sapiens

<400> 67

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Met Gly Lys Lys Tyr Lys Asn Ile Val Leu Leu Lys Gly Leu Glu Val
 1           5           10          15
Ile Asn Asp Tyr His Phe Arg Met Val Lys Ser Leu Leu Ser Asn Asp
      20           25           30
Leu Lys Leu Asn Leu Lys Met Arg Glu Glu Tyr Asp Lys Ile Gln Ile
      35           40           45
Ala Asp Leu Met Glu Glu Lys Phe Arg Gly Asp Ala Gly Leu Gly Lys
      50           55           60
Leu Ile Lys Ile Phe Glu Asp Ile Pro Thr Leu Glu Asp Leu Ala Glu
65           70           75           80
Thr Leu Lys Lys Glu Lys Leu Lys Val Lys Gly Pro Ala Leu Ser Arg
      85           90           95
Lys Arg Lys Lys Glu Val His Ala Thr Ser Pro Ala Pro Ser Thr Ser
      100          105          110
Ser Thr Val Lys Thr Glu Gly Ala Glu Ala Thr Pro Gly Ala Gln Lys
      115          120          125
Arg Lys Lys Ser Thr Lys Glu Lys Ala Gly Pro Lys Gly Ser Lys Val
      130          135          140
Ser Glu Glu Gln Thr Gln Pro Pro Ser Pro Ala Gly Ala Gly Met Ser
145          150          155          160
Thr Ala Met Gly Arg Ser Pro Ser Pro Lys Thr Ser Leu Ser Ala Pro
      165          170          175
Pro Asn Ser Ser Ser Thr Glu Asn Pro Lys Thr Val Ala Lys Cys Gln
      180          185          190
Val Thr Pro Arg Arg Asn Val Leu Gln Lys Arg Pro Val Ile Val Lys
      195          200          205
Val Leu Ser Thr Thr Lys Pro Phe Glu Tyr Glu Thr Pro Glu Met Glu
      210          215          220
Lys Lys Ile Met Phe His Ala Thr Val Ala Thr Gln Thr Gln Phe Phe

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225          230          235          240
His Val Lys Val Leu Asn Thr Ser Leu Lys Glu Lys Phe Asn Gly Lys
          245          250          255
Lys Ile Ile Ile Ile Ser Asp Tyr Leu Glu Tyr Asp Ser Leu Leu Glu
          260          265          270
Val Asn Glu Glu Ser Thr Val Ser Glu Ala Gly Pro Asn Gln Thr Phe
          275          280          285
Glu Val Pro Asn Lys Ile Ile Asn Arg Ala Lys Glu Thr Leu Lys Ile
          290          295          300
Asp Ile Leu His Lys Lys Gln Ala Ser Gly Asn Ile Val Tyr Gly Val Phe
305          310          315          320
Met Leu His Lys Lys Thr Val Asn Gln Lys Thr Thr Ile Tyr Glu Ile
          325          330          335
Gln Asp Asp Arg Gly Lys Met Asp Val Val Gly Thr Gly Gln Cys His
          340          345          350
Asn Ile Pro Cys Glu Glu Gly Asp Lys Leu Gln Leu Phe Cys Phe Arg
          355          360          365
Leu Arg Lys Lys Asn Gln Met Ser Lys Leu Ile Ser Glu Met His Ser
          370          375          380
Phe Ile Gln Ile Lys Lys Lys Thr Asn Pro Arg Asn Asn Asp Pro Lys
385          390          395          400
Ser Met Lys Leu Pro Gln Glu Gln Arg Gln Leu Pro Tyr Pro Ser Glu
          405          410          415
Ala Ser Thr Thr Phe Pro Glu Ser His Leu Arg Thr Pro Gln Met Pro
          420          425          430
Pro Thr Thr Pro Ser Ser Ser Phe Thr Lys Lys Ser Glu Asp Thr
          435          440          445
Ile Ser Lys Met Asn Asp Phe Met Arg Met Gln Ile Leu Lys Glu Gly
          450          455          460
Ser His Phe Pro Gly Pro Phe Met Thr Ser Ile Gly Pro Ala Glu Ser
465          470          475          480
His Pro His Thr Pro Gln Met Pro Pro Ser Thr Pro Ser Ser Ser Phe
          485          490          495
Leu Thr Thr Leu Lys Pro Arg Leu Lys Thr Glu Pro Glu Glu Val Ser
          500          505          510
Ile Glu Asp Ser Ala Gln Ser Asp Leu Lys Glu Val Met Val Leu Asn
          515          520          525
Ala Thr Glu Ser Phe Val Tyr Glu Pro Lys Glu Gln Lys Lys Met Phe
          530          535          540
His Ala Thr Val Ala Thr Glu Asn Glu Val Phe Arg Val Lys Val Phe
545          550          555          560
Asn Ile Asp Leu Lys Glu Lys Phe Thr Pro Lys Lys Ile Ile Ala Ile
          565          570          575
Ala Asn Tyr Val Cys Arg Asn Gly Phe Leu Glu Val Tyr Pro Phe Thr
          580          585          590
Leu Val Ala Asp Val Asn Ala Asp Ala Asn Met Glu Ile Pro Lys Gly
          595          600          605
Leu Ile Arg Ser Ala Ser Val Thr Pro Lys Ile Asn Gln Leu Cys Ser
          610          615          620
Gln Thr Lys Gly Ser Phe Val Asn Gly Val Phe Glu Val His Lys Lys
625          630          635          640
Asn Val Arg Gly Glu Phe Thr Tyr Tyr Glu Ile Gln Asp Asn Thr Gly
          645          650          655
Lys Met Glu Val Val Val His Gly Arg Leu Asn Thr Ile Asn Cys Glu
          660          665          670

```

Glu Gly Asp Lys Leu Lys Leu Thr Ser Phe Glu Leu Ala Pro Lys Ser
 675 680 685
 Gly Asn Thr Gly Glu Leu Arg Ser Val Ile His Ser His Ile Lys Val
 690 695 700
 Ile Lys Thr Lys Lys Asn Lys Lys Asp Ile Leu Asn Pro Asp Ser Ser
 705 710 715 720
 Met Glu Thr Ser Pro Asp Phe Phe Phe
 725

<210> 68
 <211> 754
 <212> PRT
 <213> Homo Sapiens

<400> 68
 Met Ala Ser Val Pro Ala Leu Gln Leu Thr Pro Ala Asn Pro Pro Pro
 1 5 10 15
 Pro Glu Val Ser Asn Pro Lys Lys Pro Gly Arg Val Thr Asn Gln Leu
 20 25 30
 Gln Tyr Leu His Lys Val Val Met Lys Ala Leu Trp Lys His Gln Phe
 35 40 45
 Ala Trp Pro Phe Arg Gln Pro Val Asp Ala Val Lys Leu Gly Leu Pro
 50 55 60
 Asp Tyr His Lys Ile Ile Lys Gln Pro Met Asp Met Gly Thr Ile Lys
 65 70 75 80
 Arg Arg Leu Glu Asn Asn Tyr Tyr Trp Ala Ala Ser Glu Cys Met Gln
 85 90 95
 Asp Phe Asn Thr Met Phe Thr Asn Cys Tyr Ile Tyr Asn Lys Pro Thr
 100 105 110
 Asp Asp Ile Val Leu Met Ala Gln Thr Leu Glu Lys Ile Phe Leu Gln
 115 120 125
 Lys Val Ala Ser Met Pro Gln Glu Glu Gln Glu Leu Val Val Thr Ile
 130 135 140
 Pro Lys Asn Ser His Lys Lys Gly Ala Lys Leu Ala Ala Leu Gln Gly
 145 150 155 160
 Ser Val Thr Ser Ala His Gln Val Pro Ala Val Ser Ser Val Ser His
 165 170 175
 Thr Ala Leu Tyr Thr Pro Pro Pro Glu Ile Pro Thr Thr Val Leu Asn
 180 185 190
 Ile Pro His Pro Ser Val Ile Ser Ser Pro Leu Leu Lys Ser Leu His
 195 200 205
 Ser Ala Gly Pro Pro Leu Leu Ala Val Thr Ala Ala Pro Pro Ala Gln
 210 215 220
 Pro Leu Ala Lys Lys Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr
 225 230 235 240
 Pro Thr Pro Thr Ala Ile Leu Ala Pro Gly Ser Pro Ala Ser Pro Pro
 245 250 255
 Gly Ser Leu Glu Pro Lys Ala Ala Arg Leu Pro Pro Met Arg Arg Glu
 260 265 270
 Ser Gly Arg Pro Ile Lys Pro Pro Arg Lys Asp Leu Pro Asp Ser Gln
 275 280 285
 Gln Gln His Gln Ser Ser Lys Lys Gly Lys Leu Ser Glu Gln Leu Lys
 290 295 300
 His Cys Asn Gly Ile Leu Lys Glu Leu Leu Ser Lys Lys His Ala Ala
 305 310 315 320

Tyr	Ala	Trp	Pro	Phe	Tyr	Lys	Pro	Val	Asp	Ala	Ser	Ala	Leu	Gly	Leu
				325					330					335	
His	Asp	Tyr	His	Asp	Ile	Ile	Lys	His	Pro	Met	Asp	Leu	Ser	Thr	Val
			340					345					350		
Lys	Arg	Lys	Met	Glu	Asn	Arg	Asp	Tyr	Arg	Asp	Ala	Gln	Glu	Phe	Ala
		355					360					365			
Ala	Asp	Val	Arg	Leu	Met	Phe	Ser	Asn	Cys	Tyr	Lys	Tyr	Asn	Pro	Pro
	370					375					380				
Asp	His	Asp	Val	Val	Ala	Met	Ala	Arg	Lys	Leu	Gln	Asp	Val	Phe	Glu
385					390					395					400
Phe	Arg	Tyr	Ala	Lys	Met	Pro	Asp	Glu	Pro	Leu	Glu	Pro	Gly	Pro	Leu
				405					410					415	
Pro	Val	Ser	Thr	Ala	Met	Pro	Pro	Gly	Leu	Ala	Lys	Ser	Ser	Ser	Glu
			420					425					430		
Ser	Ser	Ser	Glu	Glu	Ser	Ser	Ser	Glu	Ser	Ser	Ser	Glu	Glu	Glu	Glu
		435					440					445			
Glu	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Ser	Glu	Ser	Ser	Asp
	450					455					460				
Ser	Glu	Glu	Glu	Arg	Ala	His	Arg	Leu	Ala	Glu	Leu	Gln	Glu	Gln	Leu
465					470					475					480
Arg	Ala	Val	His	Glu	Gln	Leu	Ala	Ala	Leu	Ser	Gln	Gly	Pro	Ile	Ser
				485					490					495	
Lys	Pro	Lys	Arg	Lys	Arg	Glu	Lys	Lys	Glu	Lys	Lys	Lys	Lys	Arg	Lys
			500					505					510		
Ala	Glu	Lys	His	Arg	Gly	Arg	Ala	Gly	Ala	Asp	Glu	Asp	Asp	Lys	Gly
		515					520					525			
Pro	Arg	Ala	Pro	Arg	Pro	Pro	Gln	Pro	Lys	Lys	Ser	Lys	Lys	Ala	Ser
		530				535					540				
Gly	Ser	Gly	Gly	Gly	Ser	Ala	Ala	Leu	Gly	Pro	Ser	Gly	Phe	Gly	Pro
545					550					555					560
Ser	Gly	Gly	Ser	Gly	Thr	Lys	Leu	Pro	Lys	Lys	Ala	Thr	Lys	Thr	Ala
				565					570					575	
Pro	Pro	Ala	Leu	Pro	Thr	Gly	Tyr	Asp	Ser	Glu	Glu	Glu	Glu	Glu	Ser
			580					585					590		
Arg	Pro	Met	Ser	Tyr	Asp	Glu	Lys	Arg	Gln	Leu	Ser	Leu	Asp	Ile	Asn
		595					600					605			
Lys	Leu	Pro	Gly	Glu	Lys	Leu	Gly	Arg	Val	Val	His	Ile	Ile	Gln	Ala
	610					615					620				
Arg	Glu	Pro	Ser	Leu	Arg	Asp	Ser	Asn	Pro	Glu	Glu	Ile	Glu	Ile	Asp
625					630					635					640
Phe	Glu	Thr	Leu	Lys	Pro	Ser	Thr	Leu	Arg	Glu	Leu	Glu	Arg	Tyr	Val
			645						650					655	
Leu	Ser	Cys	Leu	Arg	Lys	Lys	Pro	Arg	Lys	Pro	Tyr	Thr	Ile	Lys	Lys
			660					665					670		
Pro	Val	Gly	Lys	Thr	Lys										

<210> 69
 <211> 210
 <212> PRT
 <213> Homo Sapiens

<400> 69
 Met Asp Asp Glu Glu Glu Thr Tyr Arg Leu Trp Lys Ile Arg Lys Thr
 1 5 10 15
 Ile Met Gln Leu Cys His Asp Arg Gly Tyr Leu Val Thr Gln Asp Glu
 20 25 30
 Leu Asp Gln Thr Leu Glu Glu Phe Lys Ala Gln Phe Gly Asp Lys Pro
 35 40 45
 Ser Glu Gly Arg Pro Arg Arg Thr Asp Leu Thr Val Leu Val Ala His
 50 55 60
 Asn Asp Asp Pro Thr Asp Gln Met Phe Val Phe Phe Pro Glu Glu Pro
 65 70 75 80
 Lys Val Gly Ile Lys Thr Ile Lys Val Tyr Cys Gln Arg Met Gln Glu
 85 90 95
 Glu Asn Ile Thr Arg Ala Leu Ile Val Val Gln Gln Gly Met Thr Pro
 100 105 110
 Ser Ala Lys Gln Ser Leu Val Asp Met Ala Pro Lys Tyr Ile Leu Glu
 115 120 125
 Gln Phe Leu Gln Gln Glu Leu Ile Asn Ile Thr Glu His Glu Leu
 130 135 140
 Val Pro Glu His Val Val Met Thr Lys Glu Glu Val Thr Glu Leu Leu
 145 150 155 160
 Ala Arg Tyr Lys Leu Arg Glu Asn Gln Leu Pro Arg Ile Gln Ala Gly
 165 170 175
 Asp Pro Val Ala Arg Tyr Phe Gly Ile Lys Arg Gly Gln Val Val Lys
 180 185 190
 Ile Ile Arg Pro Ser Glu Thr Ala Gly Arg Tyr Ile Thr Tyr Arg Leu
 195 200 205
 Val Gln
 210

<210> 70
 <211> 621
 <212> PRT
 <213> Homo Sapiens

<400> 70
 Met Leu Leu Leu Pro Ser Ala Ala Glu Gly Gln Gly Thr Ala Ile Thr
 1 5 10 15
 His Ala Leu Thr Ser Ala Ser Ser Val Cys Gln Val Glu Pro Val Gly
 20 25 30
 Arg Trp Phe Glu Ala Phe Val Lys Arg Arg Asn Arg Asn Ala Ser Thr
 35 40 45
 Ser Phe Gln Glu Leu Glu Asp Lys Lys Glu Leu Ser Glu Glu Ser Glu
 50 55 60
 Asp Glu Glu Leu Gln Leu Glu Glu Phe Pro Met Leu Lys Thr Leu Asp
 65 70 75 80
 Pro Lys Asp Trp Lys Asn Gln Asp His Tyr Ala Val Leu Gly Leu Gly
 85 90 95

His Val Arg Tyr Thr Ala Thr Gln Arg Gln Ile Lys Ala Ala His Lys
 100 105 110
 Ala Met Val Leu Lys His His Pro Asp Lys Arg Lys Ala Ala Gly Glu
 115 120 125
 Pro Ile Lys Glu Gly Asp Asn Asp Tyr Phe Thr Cys Ile Thr Lys Ala
 130 135 140
 Tyr Glu Met Leu Ser Asp Pro Val Lys Arg Arg Ala Phe Asn Ser Val
 145 150 155 160
 Asp Pro Thr Phe Asp Asn Ser Val Pro Ser Lys Ser Glu Ala Lys Asp
 165 170 175
 Asn Phe Phe Gln Val Phe Ser Pro Val Phe Glu Arg Asn Ser Arg Trp
 180 185 190
 Ser Asn Lys Lys Asn Val Pro Lys Leu Gly Asp Met Asn Ser Ser Phe
 195 200 205
 Glu Asp Val Asp Ala Phe Tyr Ser Phe Trp Tyr Asn Phe Asp Ser Trp
 210 215 220
 Arg Glu Phe Ser Tyr Leu Asp Glu Glu Glu Lys Glu Lys Ala Glu Cys
 225 230 235 240
 Arg Asp Glu Arg Lys Trp Ile Glu Lys Gln Asn Arg Ala Thr Arg Ala
 245 250 255
 Gln Arg Lys Lys Glu Glu Met Asn Arg Ile Arg Thr Leu Val Asp Asn
 260 265 270
 Ala Tyr Ser Cys Asp Pro Arg Ile Lys Lys Phe Lys Glu Glu Glu Lys
 275 280 285
 Ala Lys Lys Glu Ala Glu Lys Lys Ala Lys Ala Glu Ala Arg Arg Lys
 290 295 300
 Glu Gln Glu Ala Lys Glu Lys Gln Arg Gln Ala Glu Leu Glu Ala Val
 305 310 315 320
 Arg Leu Ala Lys Glu Lys Glu Glu Glu Glu Val Arg Gln Gln Ala Leu
 325 330 335
 Leu Ala Lys Lys Glu Lys Asp Ile Gln Lys Lys Ala Ile Lys Lys Glu
 340 345 350
 Arg Gln Lys Leu Arg Asn Ser Cys Lys Ser Trp Asn His Phe Ser Asp
 355 360 365
 Asn Glu Ala Asp Arg Val Lys Met Met Glu Glu Val Glu Lys Leu Cys
 370 375 380
 Asp Arg Leu Glu Leu Ala Ser Leu Gln Gly Leu Asn Glu Ile Leu Ala
 385 390 395 400
 Ser Ser Thr Arg Glu Val Gly Lys Ala Ala Leu Glu Lys Gln Ile Glu
 405 410 415
 Glu Val Asn Glu Gln Met Arg Arg Glu Lys Glu Glu Ala Asp Ala Arg
 420 425 430
 Met Arg Gln Ala Ser Lys Asn Ala Glu Lys Ser Thr Gly Gly Ser Gly
 435 440 445
 Ser Gly Ser Lys Asn Trp Ser Glu Asp Asp Leu Gln Leu Leu Ile Lys
 450 455 460
 Ala Val Asn Leu Phe Pro Ala Gly Thr Asn Ser Arg Trp Glu Val Ile
 465 470 475 480
 Ala Asn Tyr Met Asn Ile His Ser Ser Ser Gly Val Lys Arg Thr Ala
 485 490 495
 Lys Asp Val Ile Ser Lys Ala Lys Ser Leu Gln Lys Leu Asp Pro His
 500 505 510
 Gln Lys Asp Asp Ile Asn Lys Lys Ala Phe Asp Lys Phe Lys Lys Glu
 515 520 525
 His Gly Val Ala Ser Gln Ala Asp Ser Ala Ala Pro Ser Glu Arg Phe

530 535 540
 Glu Gly Pro Cys Ile Asp Ser Thr Pro Trp Thr Thr Glu Glu Gln Lys
 545 550 555 560
 Leu Leu Glu Gln Ala Leu Lys Thr Tyr Pro Val Asn Thr Pro Glu Arg
 565 570 575
 Trp Glu Lys Ile Ala Glu Ala Val Pro Gly Arg Thr Lys Lys Asp Cys
 580 585 590
 Met Arg Arg Tyr Lys Glu Leu Val Glu Met Val Lys Ala Lys Lys Ala
 595 600 605
 Ala Gln Glu Gln Val Leu Asn Ala Ser Arg Ala Arg Lys
 610 615 620

<210> 71
 <211> 267
 <212> PRT
 <213> Homo Sapiens

<400> 71
 Met Ala Ser Leu Leu Lys Val Asp Gln Glu Val Lys Leu Lys Val Asp
 1 5 10 15
 Ser Phe Arg Glu Arg Ile Thr Ser Lys Ala Glu Asp Leu Val Ala Asn
 20 25 30
 Phe Phe Pro Lys Lys Leu Leu Glu Leu Asp Ser Phe Leu Lys Glu Pro
 35 40 45
 Ile Leu Asn Ile His Asp Leu Thr Gln Ile His Ser Asp Met Asn Leu
 50 55 60
 Pro Val Pro Asp Pro Ile Leu Leu Thr Asn Ser His Asp Gly Leu Asp
 65 70 75 80
 Gly Pro Thr Tyr Lys Lys Arg Arg Leu Asp Glu Cys Glu Glu Ala Phe
 85 90 95
 Gln Gly Thr Lys Val Phe Val Met Pro Asn Gly Met Leu Lys Ser Asn
 100 105 110
 Gln Gln Leu Val Asp Ile Ile Glu Lys Val Lys Pro Glu Ile Arg Leu
 115 120 125
 Leu Ile Glu Lys Cys Asn Thr Pro Ser Gly Lys Gly Pro His Ile Cys
 130 135 140
 Phe Asp Leu Gln Val Lys Met Trp Val Gln Leu Leu Ile Pro Arg Ile
 145 150 155 160
 Glu Asp Gly Asn Asn Phe Gly Val Ser Ile Gln Glu Glu Thr Val Ala
 165 170 175
 Glu Leu Arg Thr Val Glu Ser Glu Ala Ala Ser Tyr Leu Asp Gln Ile
 180 185 190
 Ser Arg Tyr Tyr Ile Thr Arg Ala Lys Leu Val Ser Lys Ile Ala Lys
 195 200 205
 Tyr Pro His Val Glu Asp Tyr Arg Arg Thr Val Thr Glu Ile Asp Glu
 210 215 220
 Lys Glu Tyr Ile Ser Leu Arg Leu Ile Ile Ser Glu Leu Arg Asn Gln
 225 230 235 240
 Tyr Val Thr Leu His Asp Met Ile Leu Lys Asn Ile Glu Lys Ile Lys
 245 250 255
 Arg Pro Arg Ser Ser Asn Ala Glu Thr Leu Tyr
 260 265

<210> 72
 <211> 1752

<212> PRT

<213> Homo Sapiens

<400> 72

Arg Glu Lys Arg Arg Arg Lys Ser Val Glu Asp Arg Phe Asp Gln Gln
 1 5 10 15
 Lys Asn Asp Tyr Asp Gln Leu Gln Lys Ala Arg Gln Cys Glu Lys Glu
 20 25 30
 Asn Leu Gly Trp Gln Lys Leu Glu Ser Glu Lys Ala Ile Lys Glu Lys
 35 40 45
 Glu Tyr Glu Ile Glu Arg Leu Arg Val Leu Leu Gln Glu Glu Gly Thr
 50 55 60
 Arg Lys Arg Glu Tyr Glu Asn Glu Leu Ala Lys Val Arg Asn His Tyr
 65 70 75 80
 Asn Glu Glu Met Ser Asn Leu Arg Asn Lys Tyr Glu Thr Glu Ile Asn
 85 90 95
 Ile Thr Lys Thr Thr Ile Lys Glu Ile Ser Met Gln Lys Glu Asp Asp
 100 105 110
 Ser Lys Asn Leu Arg Asn Gln Leu Asp Arg Leu Ser Arg Glu Asn Arg
 115 120 125
 Asp Leu Lys Asp Glu Ile Val Arg Leu Asn Asp Ser Ile Leu Gln Ala
 130 135 140
 Thr Glu Gln Arg Arg Arg Ala Glu Glu Asn Ala Leu Gln Gln Lys Ala
 145 150 155 160
 Cys Gly Ser Glu Ile Met Gln Lys Lys Gln His Leu Glu Ile Glu Leu
 165 170 175
 Lys Gln Val Met Gln Gln Arg Ser Glu Asp Asn Ala Arg His Lys Gln
 180 185 190
 Ser Leu Glu Glu Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile
 195 200 205
 Glu Arg Leu Lys Ala Glu Phe Gln Glu Glu Ala Lys Arg Arg Trp Glu
 210 215 220
 Tyr Glu Asn Glu Leu Ser Lys Val Arg Asn Asn Tyr Asp Glu Glu Ile
 225 230 235 240
 Ile Ser Leu Lys Asn Gln Phe Glu Thr Glu Ile Asn Ile Thr Lys Thr
 245 250 255
 Thr Ile His Gln Leu Thr Met Gln Lys Glu Glu Asp Thr Ser Gly Tyr
 260 265 270
 Arg Ala Gln Ile Asp Asn Leu Thr Arg Glu Asn Arg Ser Leu Ser Glu
 275 280 285
 Glu Ile Lys Arg Leu Lys Asn Thr Leu Thr Gln Thr Thr Glu Asn Leu
 290 295 300
 Arg Arg Val Glu Glu Asp Ile Gln Gln Gln Lys Ala Thr Gly Ser Glu
 305 310 315 320
 Val Ser Gln Arg Lys Gln Gln Leu Glu Val Glu Leu Arg Gln Val Thr
 325 330 335
 Gln Met Arg Thr Glu Glu Ser Val Arg Tyr Lys Gln Ser Leu Asp Asp
 340 345 350
 Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile Glu Arg Leu Lys
 355 360 365
 Gln Leu Ile Asp Lys Glu Thr Asn Asp Arg Lys Cys Leu Glu Asp Glu
 370 375 380
 Asn Ala Arg Leu Gln Arg Val Gln Tyr Asp Leu Gln Lys Ala Asn Ser
 385 390 395 400
 Ser Ala Thr Glu Thr Ile Asn Lys Leu Lys Val Gln Glu Gln Glu Leu

405 410 415
 Thr Arg Leu Arg Ile Asp Tyr Glu Arg Val Ser Gln Glu Arg Thr Val
 420 425 430
 Lys Asp Gln Asp Ile Thr Arg Phe Gln Asn Ser Leu Lys Glu Leu Gln
 435 440 445
 Leu Gln Lys Gln Lys Val Glu Glu Glu Leu Asn Arg Leu Lys Arg Thr
 450 455 460
 Ala Ser Glu Asp Ser Cys Lys Arg Lys Lys Leu Glu Glu Leu Glu
 465 470 475 480
 Gly Met Arg Arg Ser Leu Lys Glu Gln Ala Ile Lys Ile Thr Asn Leu
 485 490 495
 Thr Gln Gln Leu Glu Gln Ala Ser Ile Val Lys Lys Arg Ser Glu Asp
 500 505 510
 Asp Leu Arg Gln Gln Arg Asp Val Leu Asp Gly His Leu Arg Glu Lys
 515 520 525
 Gln Arg Thr Gln Glu Glu Leu Arg Arg Leu Ser Ser Glu Val Glu Ala
 530 535 540
 Leu Arg Arg Gln Leu Leu Gln Glu Gln Glu Ser Val Lys Gln Ala His
 545 550 555 560
 Leu Arg Asn Glu His Phe Gln Lys Ala Ile Glu Asp Lys Ser Arg Ser
 565 570 575
 Leu Asn Glu Ser Lys Ile Glu Ile Glu Arg Leu Gln Ser Leu Thr Glu
 580 585 590
 Asn Leu Thr Lys Glu His Leu Met Leu Glu Glu Glu Leu Arg Asn Leu
 595 600 605
 Arg Leu Glu Tyr Asp Asp Leu Arg Arg Gly Arg Ser Glu Ala Asp Ser
 610 615 620
 Asp Lys Asn Ala Thr Ile Leu Glu Leu Arg Ser Gln Leu Gln Ile Ser
 625 630 635 640
 Asn Asn Arg Thr Leu Glu Leu Gln Gly Leu Ile Asn Asp Leu Gln Arg
 645 650 655
 Glu Arg Glu Asn Leu Arg Gln Glu Ile Glu Lys Phe Gln Lys Gln Ala
 660 665 670
 Leu Glu Ala Ser Asn Arg Ile Gln Glu Ser Lys Asn Gln Cys Thr Gln
 675 680 685
 Val Val Gln Glu Arg Glu Ser Leu Leu Val Lys Ile Lys Val Leu Glu
 690 695 700
 Gln Asp Lys Ala Arg Leu Gln Arg Leu Glu Asp Glu Leu Asn Arg Ala
 705 710 715 720
 Lys Ser Thr Leu Glu Ala Glu Thr Arg Val Lys Gln Arg Leu Glu Cys
 725 730 735
 Glu Lys Gln Gln Ile Gln Asn Asp Leu Asn Gln Trp Lys Thr Gln Tyr
 740 745 750
 Ser Arg Lys Glu Glu Ala Ile Arg Lys Ile Glu Ser Glu Arg Glu Lys
 755 760 765
 Ser Glu Arg Glu Lys Asn Ser Leu Arg Ser Glu Ile Glu Arg Leu Gln
 770 775 780
 Ala Glu Ile Lys Arg Ile Glu Glu Arg Cys Arg Arg Lys Leu Glu Asp
 785 790 795 800
 Ser Thr Arg Glu Thr Gln Ser Gln Leu Glu Thr Glu Arg Ser Arg Tyr
 805 810 815
 Gln Arg Glu Ile Asp Lys Leu Arg Gln Arg Pro Tyr Gly Ser His Arg
 820 825 830
 Glu Thr Gln Thr Glu Cys Glu Trp Thr Val Asp Thr Ser Lys Leu Val
 835 840 845

Phe Asp Gly Leu Arg Lys Lys Val Thr Ala Met Gln Leu Tyr Glu Cys
 850 855 860
 Gln Leu Ile Asp Lys Thr Thr Leu Asp Lys Leu Leu Lys Gly Lys Lys
 865 870 875 880
 Ser Val Glu Glu Val Ala Ser Glu Ile Gln Pro Phe Leu Arg Gly Ala
 885 890 895
 Gly Ser Ile Ala Gly Ala Ser Ala Ser Pro Lys Glu Lys Tyr Ser Leu
 900 905 910
 Val Glu Ala Lys Arg Lys Lys Leu Ile Ser Pro Glu Ser Thr Val Met
 915 920 925
 Leu Leu Glu Ala Gln Ala Ala Thr Gly Gly Ile Ile Asp Pro His Arg
 930 935 940
 Asn Glu Lys Leu Thr Val Asp Ser Ala Ile Ala Arg Asp Leu Ile Asp
 945 950 955 960
 Phe Asp Asp Arg Gln Gln Ile Tyr Ala Ala Glu Lys Ala Ile Thr Gly
 965 970 975
 Phe Asp Asp Pro Phe Ser Gly Lys Thr Val Ser Val Ser Glu Ala Ile
 980 985 990
 Lys Lys Asn Leu Ile Asp Arg Glu Thr Gly Met Arg Leu Leu Glu Ala
 995 1000 1005
 Gln Ile Ala Ser Gly Gly Val Val Asp Pro Val Asn Ser Val Phe Leu
 1010 1015 1020
 Pro Lys Asp Val Ala Leu Ala Arg Gly Leu Ile Asp Arg Asp Leu Tyr
 1025 1030 1035 104
 Arg Ser Leu Asn Asp Pro Arg Asp Ser Gln Lys Asn Phe Val Asp Pro
 1045 1050 1055
 Val Thr Lys Lys Lys Val Ser Tyr Val Gln Leu Lys Glu Arg Cys Arg
 1060 1065 1070
 Ile Glu Pro His Thr Gly Leu Leu Leu Leu Ser Val Gln Lys Arg Ser
 1075 1080 1085
 Met Ser Phe Gln Gly Ile Arg Gln Pro Val Thr Val Thr Glu Leu Val
 1090 1095 1100
 Asp Ser Gly Ile Leu Arg Pro Ser Thr Val Asn Glu Leu Glu Ser Gly
 1105 1110 1115 112
 Gln Ile Ser Tyr Asp Glu Val Gly Glu Arg Ile Lys Asp Phe Leu Gln
 1125 1130 1135
 Gly Ser Ser Cys Ile Ala Gly Ile Tyr Asn Glu Thr Thr Lys Gln Lys
 1140 1145 1150
 Leu Gly Ile Tyr Glu Ala Met Lys Ile Gly Leu Val Arg Pro Gly Thr
 1155 1160 1165
 Ala Leu Glu Leu Leu Glu Ala Gln Ala Ala Thr Gly Phe Ile Val Asp
 1170 1175 1180
 Pro Val Ser Asn Leu Arg Leu Pro Val Glu Glu Ala Tyr Lys Arg Gly
 1185 1190 1195 120
 Leu Val Gly Ile Glu Phe Lys Glu Lys Leu Leu Ser Ala Glu Arg Ala
 1205 1210 1215
 Val Thr Gly Tyr Asn Asp Pro Glu Thr Gly Asn Ile Ile Ser Leu Phe
 1220 1225 1230
 Gln Ala Met Asn Lys Glu Leu Ile Glu Lys Gly His Gly Ile Arg Leu
 1235 1240 1245
 Leu Glu Ala Gln Ile Ala Thr Gly Gly Ile Ile Asp Pro Lys Glu Ser
 1250 1255 1260
 His Arg Leu Pro Val Asp Ile Ala Tyr Lys Arg Gly Tyr Phe Asn Glu
 1265 1270 1275 128
 Glu Leu Ser Glu Ile Leu Ser Asp Pro Ser Asp Asp Thr Lys Gly Phe

	1285	1290	1295
Phe Asp Pro Asn Thr Glu Glu Asn Leu Thr Tyr Leu Gln Leu Lys Glu			
	1300	1305	1310
Arg Cys Ile Lys Asp Glu Glu Thr Gly Leu Cys Leu Leu Pro Leu Lys			
	1315	1320	1325
Glu Lys Lys Lys Gln Val Gln Thr Ser Gln Lys Asn Thr Leu Arg Lys			
	1330	1335	1340
Arg Arg Val Val Ile Val Asp Pro Glu Thr Asn Lys Glu Met Ser Val			
	1345	1350	1355
Gln Glu Ala Tyr Lys Lys Gly Leu Ile Asp Tyr Glu Thr Phe Lys Glu			
	1365	1370	1375
Leu Cys Glu Gln Glu Cys Glu Trp Glu Glu Ile Thr Ile Thr Gly Ser			
	1380	1385	1390
Asp Gly Ser Thr Arg Val Val Leu Val Asp Arg Lys Thr Gly Ser Gln			
	1395	1400	1405
Tyr Asp Ile Gln Asp Ala Ile Asp Lys Gly Leu Val Asp Arg Lys Phe			
	1410	1415	1420
Phe Asp Gln Tyr Arg Ser Gly Ser Leu Ser Leu Thr Gln Phe Ala Asp			
	1425	1430	1435
Met Ile Ser Leu Lys Asn Gly Val Gly Thr Ser Ser Ser Met Gly Ser			
	1445	1450	1455
Gly Val Ser Asp Asp Val Phe Ser Ser Ser Arg His Glu Ser Val Ser			
	1460	1465	1470
Lys Ile Ser Thr Ile Ser Ser Val Arg Asn Leu Thr Ile Arg Ser Ser			
	1475	1480	1485
Ser Phe Ser Asp Thr Leu Glu Glu Ser Ser Pro Ile Ala Ala Ile Phe			
	1490	1495	1500
Asp Thr Glu Asn Leu Glu Lys Ile Ser Ile Thr Glu Gly Ile Glu Arg			
	1505	1510	1515
Gly Ile Val Asp Ser Ile Thr Gly Gln Arg Leu Leu Glu Ala Gln Ala			
	1525	1530	1535
Cys Thr Gly Gly Ile Ile His Pro Thr Thr Gly Gln Lys Leu Ser Leu			
	1540	1545	1550
Gln Asp Ala Val Ser Gln Gly Val Ile Asp Gln Asp Met Ala Thr Ser			
	1555	1560	1565
Val Lys Pro Ala Gln Lys Ala Phe Ile Gly Phe Glu Gly Val Lys Gly			
	1570	1575	1580
Lys Lys Lys Met Ser Ala Ala Glu Ala Val Lys Glu Lys Trp Leu Pro			
	1585	1590	1595
Tyr Glu Ala Gly Gln Arg Phe Leu Glu Phe Gln Tyr Leu Thr Gly Gly			
	1605	1610	1615
Leu Val Asp Pro Glu Val His Gly Arg Ile Ser Thr Glu Glu Ala Ile			
	1620	1625	1630
Arg Lys Gly Phe Ile Asp Gly Arg Ala Ala Gln Arg Leu Gln Asp Thr			
	1635	1640	1645
Ser Ser Tyr Ala Lys Ile Leu Thr Cys Pro Lys Thr Lys Leu Lys Ile			
	1650	1655	1660
Ser Tyr Lys Asp Ala Ile Asn Arg Ser Met Val Glu Asp Ile Thr Gly			
	1665	1670	1675
Leu Arg Leu Leu Glu Ala Ala Ser Val Ser Ser Lys Gly Leu Pro Ser			
	1685	1690	1695
Pro Tyr Asn Met Ser Ser Ala Pro Gly Ser Arg Ser Gly Ser Arg Ser			
	1700	1705	1710
Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Arg			
	1715	1720	1725

Gly Ser Phe Asp Ala Thr Gly Asn Ser Ser Tyr Ser Tyr Ser Tyr Ser
 1730 1735 1740
 Phe Ser Ser Ser Ser Ile Gly His
 1745 1750

<210> 73
 <211> 1978
 <212> PRT
 <213> Homo Sapiens

<400> 73
 Met Ser Arg Pro Arg Phe Asn Pro Arg Gly Asp Phe Pro Leu Gln Arg
 1 5 10 15
 Pro Arg Ala Pro Asn Pro Ser Gly Met Arg Pro Pro Gly Pro Phe Met
 20 25 30
 Arg Pro Gly Ser Met Gly Leu Pro Arg Phe Tyr Pro Ala Gly Arg Ala
 35 40 45
 Arg Gly Ile Pro His Arg Phe Ala Gly Leu Glu Ser Tyr Gln Asn Met
 50 55 60
 Gly Pro Gln Arg Met Asn Val Gln Val Thr Gln His Arg Thr Asp Pro
 65 70 75 80
 Arg Leu Thr Lys Glu Lys Leu Asp Phe His Glu Ala Gln Gln Lys Lys
 85 90 95
 Gly Lys Pro His Gly Ser Arg Trp Asp Asp Glu Pro His Ile Ser Ala
 100 105 110
 Ser Val Ala Val Lys Gln Ser Ser Val Thr Gln Val Thr Glu Gln Ser
 115 120 125
 Pro Lys Val Gln Ser Arg Tyr Thr Lys Glu Ser Ala Ser Ser Ile Leu
 130 135 140
 Ala Ser Phe Gly Leu Ser Asn Glu Asp Leu Glu Glu Leu Ser Arg Tyr
 145 150 155 160
 Pro Asp Glu Gln Leu Thr Pro Glu Asn Met Pro Leu Ile Leu Arg Asp
 165 170 175
 Ile Arg Met Arg Lys Met Gly Arg Arg Leu Pro Asn Leu Pro Ser Gln
 180 185 190
 Ser Arg Asn Lys Glu Thr Leu Gly Ser Glu Ala Val Ser Ser Asn Val
 195 200 205
 Ile Asp Tyr Gly His Ala Ser Lys Tyr Gly Tyr Thr Glu Asp Pro Leu
 210 215 220
 Glu Val Arg Ile Tyr Asp Pro Glu Ile Pro Thr Asp Glu Val Glu Asn
 225 230 235 240
 Glu Phe Gln Ser Gln Gln Asn Ile Ser Ala Ser Val Pro Asn Pro Asn
 245 250 255
 Val Ile Cys Asn Ser Met Phe Pro Val Glu Asp Val Phe Arg Gln Met
 260 265 270
 Asp Phe Pro Gly Glu Ser Ser Asn Asn Arg Ser Phe Phe Ser Val Glu
 275 280 285
 Ser Gly Thr Lys Met Ser Gly Leu His Ile Ser Gly Gly Gln Ser Val
 290 295 300
 Leu Glu Pro Ile Lys Ser Val Asn Gln Ser Ile Asn Gln Thr Val Ser
 305 310 315 320
 Gln Thr Met Ser Gln Ser Leu Ile Pro Pro Ser Met Asn Gln Gln Pro
 325 330 335
 Phe Ser Ser Glu Leu Ile Ser Ser Val Ser Gln Gln Glu Arg Ile Pro
 340 345 350

His Glu Pro Val Ile Asn Ser Ser Asn Val His Val Gly Ser Arg Gly
 355 360 365
 Ser Lys Lys Asn Tyr Gln Ser Gln Ala Asp Ile Pro Ile Arg Ser Pro
 370 375 380
 Phe Gly Ile Val Lys Ala Ser Trp Leu Pro Lys Phe Ser His Ala Asp
 385 390 395 400
 Ala Gln Lys Met Lys Arg Leu Pro Thr Pro Ser Met Met Asn Asp Tyr
 405 410 415
 Tyr Ala Ala Ser Pro Arg Ile Phe Pro His Leu Cys Ser Leu Cys Asn
 420 425 430
 Val Glu Cys Ser His Leu Lys Asp Trp Ile Gln His Gln Asn Thr Ser
 435 440 445
 Thr His Ile Glu Ser Cys Arg Gln Leu Arg Gln Gln Tyr Pro Asp Trp
 450 455 460
 Asn Pro Glu Ile Leu Pro Ser Arg Arg Asn Glu Gly Asn Arg Lys Glu
 465 470 475 480
 Asn Glu Thr Pro Arg Arg Arg Ser His Ser Pro Ser Pro Arg Arg Ser
 485 490 495
 Arg Arg Ser Ser Ser Ser His Arg Phe Arg Arg Ser Arg Ser Pro Met
 500 505 510
 His Tyr Met Tyr Arg Pro Arg Ser Arg Ser Pro Arg Ile Cys His Arg
 515 520 525
 Phe Ile Ser Arg Tyr Arg Ser Arg Ser Arg Ser Arg Ser Pro Tyr Arg
 530 535 540
 Ile Arg Asn Pro Phe Arg Gly Ser Pro Lys Cys Phe Arg Ser Val Ser
 545 550 555 560
 Pro Glu Arg Met Ser Arg Arg Ser Val Arg Ser Ser Asp Arg Lys Lys
 565 570 575
 Ala Leu Glu Asp Val Val Gln Arg Ser Gly His Gly Thr Glu Phe Asn
 580 585 590
 Lys Gln Lys His Leu Glu Ala Ala Asp Lys Gly His Ser Pro Ala Gln
 595 600 605
 Lys Pro Lys Thr Ser Ser Gly Thr Lys Pro Ser Val Lys Pro Thr Ser
 610 615 620
 Ala Thr Lys Ser Asp Ser Asn Leu Gly Gly His Ser Ile Arg Cys Lys
 625 630 635 640
 Ser Lys Asn Leu Glu Asp Asp Thr Leu Ser Glu Cys Lys Gln Val Ser
 645 650 655
 Asp Lys Ala Val Ser Leu Gln Arg Lys Leu Arg Lys Glu Gln Ser Leu
 660 665 670
 His Tyr Gly Ser Val Leu Leu Ile Thr Glu Leu Pro Glu Asp Gly Cys
 675 680 685
 Thr Glu Glu Asp Val Arg Lys Leu Phe Gln Pro Phe Gly Lys Val Asn
 690 695 700
 Asp Val Leu Ile Val Pro Tyr Arg Lys Glu Ala Tyr Leu Glu Met Glu
 705 710 715 720
 Phe Lys Glu Ala Ile Thr Ala Ile Met Lys Tyr Ile Glu Thr Thr Pro
 725 730 735
 Leu Thr Ile Lys Gly Lys Ser Val Lys Ile Cys Val Pro Gly Lys Lys
 740 745 750
 Lys Ala Gln Asn Lys Glu Val Lys Lys Lys Thr Leu Glu Ser Lys Lys
 755 760 765
 Val Ser Ala Ser Thr Leu Lys Arg Asp Ala Asp Ala Ser Lys Ala Val
 770 775 780
 Glu Ile Val Thr Ser Thr Ser Ala Ala Lys Thr Gly Gln Ala Lys Ala

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Glu Arg Asn Leu Lys Gly Ile Leu Glu Glu Ser Pro Ser Glu Ala Glu
 1235 1240 1245
 Asp Phe Ile Ser Gly Ile Thr Gln Thr Met Val Glu Ala Val Ala Glu
 1250 1255 1260
 Val Glu Lys Asn Glu Thr Val Ser Glu Ile Leu Pro Ser Thr Cys Ile
 1265 1270 1275 128
 Val Thr Leu Val Pro Gly Ile Pro Thr Gly Asp Glu Lys Thr Val Asp
 1285 1290 1295
 Lys Lys Asn Ile Ser Glu Lys Lys Gly Asn Met Asp Glu Lys Glu Glu
 1300 1305 1310
 Lys Glu Phe Asn Thr Lys Glu Thr Arg Met Asp Leu Gln Ile Gly Thr
 1315 1320 1325
 Glu Lys Ala Glu Lys Asn Glu Gly Arg Met Asp Ala Glu Lys Val Glu
 1330 1335 1340
 Lys Met Ala Ala Met Lys Glu Lys Pro Ala Glu Asn Thr Leu Phe Lys
 1345 1350 1355 136
 Ala Tyr Pro Asn Lys Gly Val Gly Gln Ala Asn Lys Pro Asp Glu Thr
 1365 1370 1375
 Ser Lys Thr Ser Ile Leu Ala Val Ser Asp Val Ser Ser Ser Lys Pro
 1380 1385 1390
 Ser Ile Lys Ala Val Ile Val Ser Ser Pro Lys Ala Lys Ala Thr Val
 1395 1400 1405
 Ser Lys Thr Glu Asn Gln Lys Ser Phe Pro Lys Ser Val Pro Arg Asp
 1410 1415 1420
 Gln Ile Asn Ala Glu Lys Lys Leu Ser Ala Lys Glu Phe Gly Leu Leu
 1425 1430 1435 144
 Lys Pro Thr Ser Ala Arg Ser Gly Leu Ala Glu Ser Ser Ser Lys Phe
 1445 1450 1455
 Lys Pro Thr Gln Ser Ser Leu Thr Arg Gly Gly Ser Gly Arg Ile Ser
 1460 1465 1470
 Ala Leu Gln Gly Lys Leu Ser Lys Leu Asp Tyr Arg Asp Ile Thr Lys
 1475 1480 1485
 Gln Ser Gln Glu Thr Glu Ala Arg Pro Ser Ile Met Lys Arg Asp Asp
 1490 1495 1500
 Ser Asn Asn Lys Thr Leu Ala Glu Gln Asn Thr Lys Asn Pro Lys Ser
 1505 1510 1515 152
 Thr Thr Gly Arg Ser Ser Lys Ser Lys Glu Glu Pro Leu Phe Pro Phe
 1525 1530 1535
 Asn Leu Asp Glu Phe Val Thr Val Asp Glu Val Ile Glu Glu Val Asn
 1540 1545 1550
 Pro Ser Gln Ala Lys Gln Asn Pro Leu Lys Gly Lys Arg Lys Glu Thr
 1555 1560 1565
 Leu Lys Asn Val Pro Phe Ser Glu Leu Asn Leu Lys Lys Lys Gly
 1570 1575 1580
 Lys Thr Ser Thr Pro Arg Gly Val Glu Gly Glu Leu Ser Phe Val Thr
 1585 1590 1595 160
 Leu Asp Glu Ile Gly Glu Glu Asp Ala Ala Ala His Leu Ala Gln
 1605 1610 1615
 Ala Leu Val Thr Val Asp Glu Val Ile Asp Glu Glu Glu Leu Asn Met
 1620 1625 1630
 Glu Glu Met Val Lys Asn Ser Asn Ser Leu Phe Thr Leu Asp Glu Leu
 1635 1640 1645
 Ile Asp Gln Asp Asp Cys Ile Ser His Ser Glu Pro Lys Asp Val Thr
 1650 1655 1660
 Val Leu Ser Val Ala Glu Glu Gln Asp Leu Leu Lys Gln Glu Arg Leu

1665 1670 1675 168
 Val Thr Val Asp Glu Ile Gly Glu Val Glu Glu Leu Pro Leu Asn Glu
 1685 1690 1695
 Ser Ala Asp Ile Thr Phe Ala Thr Leu Asn Thr Lys Gly Asn Glu Gly
 1700 1705 1710
 Asp Ile Val Arg Asp Ser Ile Gly Phe Ile Ser Ser Gln Val Pro Glu
 1715 1720 1725
 Asp Pro Ser Thr Leu Val Thr Val Asp Glu Ile Gln Asp Asp Ser Ser
 1730 1735 1740
 Asp Leu His Leu Val Thr Leu Asp Glu Val Thr Glu Glu Asp Glu Asp
 1745 1750 1755 176
 Ser Leu Ala Asp Phe Asn Asn Leu Lys Glu Glu Leu Asn Phe Val Thr
 1765 1770 1775
 Val Asp Glu Val Gly Glu Glu Glu Asp Gly Asp Asn Asp Leu Lys Val
 1780 1785 1790
 Glu Leu Ala Gln Ser Lys Asn Asp His Pro Thr Asp Lys Lys Gly Asn
 1795 1800 1805
 Arg Lys Lys Arg Ala Val Asp Thr Lys Lys Thr Lys Leu Glu Ser Leu
 1810 1815 1820
 Ser Gln Val Gly Pro Val Asn Glu Asn Val Met Glu Glu Asp Leu Lys
 1825 1830 1835 184
 Thr Met Ile Glu Arg His Leu Thr Ala Lys Thr Pro Thr Lys Arg Val
 1845 1850 1855
 Arg Ile Gly Lys Thr Leu Pro Ser Glu Lys Ala Val Val Thr Glu Pro
 1860 1865 1870
 Ala Lys Gly Glu Glu Ala Phe Gln Met Ser Glu Val Asp Glu Glu Ser
 1875 1880 1885
 Gly Leu Lys Asp Ser Glu Pro Glu Arg Lys Arg Lys Lys Thr Glu Asp
 1890 1895 1900
 Ser Ser Ser Gly Lys Ser Val Ala Ser Asp Val Pro Glu Glu Leu Asp
 1905 1910 1915 192
 Phe Leu Val Pro Lys Ala Gly Phe Phe Cys Pro Ile Cys Ser Leu Phe
 1925 1930 1935
 Tyr Ser Gly Glu Lys Ala Met Thr Asn His Cys Lys Ser Thr Arg His
 1940 1945 1950
 Lys Gln Asn Thr Glu Lys Phe Met Ala Lys Gln Arg Lys Glu Lys Glu
 1955 1960 1965
 Gln Asn Glu Ala Glu Glu Arg Ser Ser Arg
 1970 1975

<210> 74

<211> 366

<212> PRT

<213> Homo Sapiens

<400> 74

Met Arg Val Met Ala Pro Arg Thr Leu Ile Leu Leu Ser Gly Ala
 1 5 10 15
 Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe
 20 25 30
 Tyr Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro His Phe Ile Ala
 35 40 45
 Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
 50 55 60
 Ala Ser Pro Arg Gly Glu Pro Arg Ala Pro Trp Val Glu Gln Glu Gly

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65          70          75          80
Pro Glu Tyr Trp Asp Arg Glu Thr Gln Lys Tyr Lys Arg Gln Ala Gln
      85          90          95
Thr Asp Arg Val Ser Leu Arg Asn Leu Arg Gly Tyr Tyr Asn Gln Ser
      100         105         110
Glu Ala Gly Ser His Ile Ile Gln Arg Met Tyr Gly Cys Asp Val Gly
      115         120         125
Pro Asp Gly Arg Leu Leu Arg Gly Tyr Asp Gln Tyr Ala Tyr Asp Gly
      130         135         140
Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala
      145         150         155         160
Asp Thr Ala Ala Gln Ile Thr Gln Arg Lys Trp Glu Ala Ala Arg Glu
      165         170         175
Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Leu Cys Val Glu Trp Leu
      180         185         190
Arg Arg Tyr Leu Lys Asn Gly Lys Glu Thr Leu Gln Arg Ala Glu His
      195         200         205
Pro Lys Thr His Val Thr His His Pro Val Ser Asp His Glu Ala Thr
      210         215         220
Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr
      225         230         235         240
Trp Gln Trp Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
      245         250         255
Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Val Val
      260         265         270
Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
      275         280         285
Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro
      290         295         300
Thr Ile Pro Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val
      305         310         315         320
Leu Ala Val Leu Gly Ala Val Val Ala Val Val Met Cys Arg Arg Lys
      325         330         335
Ser Ser Gly Gly Lys Gly Gly Ser Cys Ser Gln Ala Ala Ser Ser Asn
      340         345         350
Ser Ala Gln Gly Ser Asp Glu Ser Leu Ile Ala Cys Lys Ala
      355         360         365

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<210> 75

<211> 240

<212> PRT

<213> Homo Sapiens

<400> 75

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Met Gly Leu Glu Leu Tyr Leu Asp Leu Leu Ser Gln Pro Cys Arg Ala
1          5          10          15
Val Tyr Ile Phe Ala Lys Lys Asn Asp Ile Pro Phe Glu Leu Arg Ile
      20          25          30
Val Asp Leu Ile Lys Gly Gln His Leu Ser Asp Ala Phe Ala Gln Val
      35          40          45
Asn Pro Leu Lys Lys Val Pro Ala Leu Lys Asp Gly Asp Phe Thr Leu
      50          55          60
Thr Glu Ser Val Ala Ile Leu Leu Tyr Leu Thr Arg Lys Tyr Lys Val
65          70          75          80
Pro Asp Tyr Trp Tyr Pro Gln Asp Leu Gln Ala Arg Ala Arg Val Asp

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      85              90              95
Glu Tyr Leu Ala Trp Gln His Thr Thr Leu Arg Arg Ser Cys Leu Arg
      100              105              110
Ala Leu Trp His Lys Val Met Phe Pro Val Phe Leu Gly Gly Pro Val
      115              120              125
Ser Pro Gln Thr Leu Ala Ala Thr Leu Ala Glu Leu Asp Val Thr Leu
      130              135              140
Gln Leu Leu Glu Asp Lys Phe Leu Gln Asn Lys Ala Phe Leu Thr Gly
      145              150              155              160
Pro His Ile Ser Leu Ala Asp Leu Val Ala Ile Thr Glu Leu Met His
      165              170              175
Pro Val Gly Ala Gly Cys Gln Val Phe Glu Gly Arg Pro Lys Leu Ala
      180              185              190
Thr Trp Arg Gln Arg Val Glu Ala Val Gly Glu Asp Leu Phe Gln
      195              200              205
Glu Ala His Glu Val Ile Leu Lys Ala Lys Asp Phe Pro Pro Ala Asp
      210              215              220
Pro Thr Ile Lys Gln Lys Leu Met Pro Trp Val Leu Ala Met Ile Arg
      225              230              235              240

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<210> 76
 <211> 953
 <212> PRT
 <213> Homo Sapiens

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      <400> 76
Met Ile Thr Ser Ala Ala Gly Ile Ile Ser Leu Leu Asp Glu Asp Glu
  1              5              10              15
Pro Gln Leu Lys Glu Phe Ala Leu His Lys Leu Asn Ala Val Val Asn
      20              25              30
Asp Phe Trp Ala Glu Ile Ser Glu Ser Val Asp Lys Ile Glu Val Leu
      35              40              45
Tyr Glu Asp Glu Gly Phe Arg Ser Arg Gln Phe Ala Ala Leu Val Ala
      50              55              60
Ser Lys Val Phe Tyr His Leu Gly Ala Phe Glu Glu Ser Leu Asn Tyr
      65              70              75              80
Ala Leu Gly Ala Arg Asp Leu Phe Asn Val Asn Asp Asn Ser Glu Tyr
      85              90              95
Val Glu Thr Ile Ile Ala Lys Cys Ile Asp His Tyr Thr Lys Gln Cys
      100              105              110
Val Glu Asn Ala Asp Leu Pro Glu Gly Glu Lys Lys Pro Ile Asp Gln
      115              120              125
Arg Leu Glu Gly Ile Val Asn Lys Met Phe Gln Arg Cys Leu Asp Asp
      130              135              140
His Lys Tyr Lys Gln Ala Ile Gly Ile Ala Leu Glu Thr Arg Arg Leu
      145              150              155              160
Asp Val Phe Glu Lys Thr Ile Leu Glu Ser Asn Asp Val Pro Gly Met
      165              170              175
Leu Ala Tyr Ser Leu Lys Leu Cys Met Ser Leu Met Gln Asn Lys Gln
      180              185              190
Phe Arg Asn Lys Val Leu Arg Val Leu Val Lys Ile Tyr Met Asn Leu
      195              200              205
Glu Lys Pro Asp Phe Ile Asn Val Cys Gln Cys Leu Ile Phe Leu Asp
      210              215              220
Asp Pro Gln Ala Val Ser Asp Ile Leu Glu Lys Leu Val Lys Glu Asp

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225          230          235          240
Asn Leu Leu Met Ala Tyr Gln Ile Cys Phe Asp Leu Tyr Glu Ser Ala
          245          250          255
Ser Gln Gln Phe Leu Ser Ser Val Ile Gln Asn Leu Arg Thr Val Gly
          260          265          270
Thr Pro Ile Ala Ser Val Pro Gly Ser Thr Asn Thr Gly Thr Val Pro
          275          280          285
Gly Ser Glu Lys Asp Ser Asp Ser Met Glu Thr Glu Glu Lys Thr Ser
          290          295          300
Ser Ala Phe Val Gly Lys Thr Pro Glu Ala Ser Pro Glu Pro Lys Asp
305          310          315          320
Gln Thr Leu Lys Met Ile Lys Ile Leu Ser Gly Glu Met Ala Ile Glu
          325          330          335
Leu His Leu Gln Phe Leu Ile Arg Asn Asn Thr Asp Leu Met Ile
          340          345          350
Leu Lys Asn Thr Lys Asp Ala Val Arg Asn Ser Val Cys His Thr Ala
          355          360          365
Thr Val Ile Ala Asn Ser Phe Met His Cys Gly Thr Thr Ser Asp Gln
          370          375          380
Phe Leu Arg Asp Asn Leu Glu Trp Leu Ala Arg Ala Thr Asn Trp Ala
385          390          395          400
Lys Phe Thr Ala Thr Ala Ser Leu Gly Val Ile His Lys Gly His Glu
          405          410          415
Lys Glu Ala Leu Gln Leu Met Ala Thr Tyr Leu Pro Lys Asp Thr Ser
          420          425          430
Pro Gly Ser Ala Tyr Gln Glu Gly Gly Leu Tyr Ala Leu Gly Leu
          435          440          445
Ile His Ala Asn His Gly Gly Asp Ile Ile Asp Tyr Leu Leu Asn Gln
          450          455          460
Leu Lys Asn Ala Ser Asn Asp Ile Val Arg His Gly Gly Ser Leu Gly
465          470          475          480
Leu Gly Leu Ala Ala Met Gly Thr Ala Arg Gln Asp Val Tyr Asp Leu
          485          490          495
Leu Lys Thr Asn Leu Tyr Gln Asp Asp Ala Val Thr Gly Glu Ala Ala
          500          505          510
Gly Leu Ala Leu Gly Leu Val Met Leu Gly Ser Lys Asn Ala Gln Ala
          515          520          525
Ile Glu Asp Met Val Gly Tyr Ala Gln Glu Thr Gln His Glu Lys Ile
          530          535          540
Leu Arg Gly Leu Ala Val Gly Ile Ala Leu Val Met Tyr Gly Arg Met
545          550          555          560
Glu Glu Ala Asp Ala Leu Ile Glu Ser Leu Cys Arg Asp Lys Asp Pro
          565          570          575
Ile Leu Arg Arg Ser Gly Met Tyr Thr Val Ala Met Ala Tyr Cys Gly
          580          585          590
Ser Gly Asn Asn Lys Ala Ile Arg Arg Leu Leu His Val Ala Val Ser
          595          600          605
Asp Val Asn Asp Asp Val Arg Ser Ala Ala Val Glu Ser Leu Gly Phe
          610          615          620
Ile Leu Phe Arg Thr Pro Glu Gln Cys Pro Ser Val Val Ser Leu Leu
625          630          635          640
Ser Glu Ser Tyr Asn Pro His Val Arg Tyr Gly Ala Ala Met Ala Leu
          645          650          655
Gly Ile Cys Cys Ala Gly Thr Gly Asn Lys Glu Ala Ile Asn Leu Leu
          660          665          670

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Glu Pro Met Thr Asn Asp Pro Val Asn Tyr Val Arg Gln Gly Ala Leu
 675 680 685
 Ile Ala Ser Ala Leu Ile Met Ile Gln Gln Thr Glu Ile Thr Cys Pro
 690 695 700
 Lys Val Asn Gln Phe Arg Gln Leu Tyr Ser Lys Val Ile Asn Asp Lys
 705 710 715 720
 His Asp Asp Val Met Ala Lys Phe Gly Ala Ile Leu Ala Gln Gly Ile
 725 730 735
 Leu Asp Ala Gly Gly His Asn Val Thr Ile Ser Leu Gln Ser Arg Thr
 740 745 750
 Gly His Thr His Met Pro Ser Val Val Gly Val Leu Val Phe Thr Gln
 755 760 765
 Phe Trp Phe Trp Phe Pro Leu Ser His Phe Leu Ser Leu Ala Tyr Thr
 770 775 780
 Pro Thr Cys Val Ile Gly Leu Asn Lys Asp Leu Lys Met Pro Lys Val
 785 790 795 800
 Gln Tyr Lys Ser Asn Cys Lys Pro Ser Thr Phe Ala Tyr Pro Ala Pro
 805 810 815
 Leu Glu Val Pro Lys Glu Lys Glu Lys Glu Lys Val Ser Thr Ala Val
 820 825 830
 Leu Ser Ile Thr Ala Lys Ala Lys Lys Lys Glu Lys Glu Lys Glu Lys
 835 840 845
 Lys Glu Glu Glu Lys Met Glu Val Asp Glu Ala Glu Lys Lys Glu Glu
 850 855 860
 Lys Glu Lys Lys Lys Glu Pro Glu Pro Asn Phe Gln Leu Leu Asp Asn
 865 870 875 880
 Pro Ala Arg Val Met Pro Ala Gln Leu Lys Val Leu Thr Met Pro Glu
 885 890 895
 Thr Cys Arg Tyr Gln Pro Phe Lys Pro Leu Ser Ile Gly Gly Ile Ile
 900 905 910
 Ile Leu Lys Asp Thr Ser Glu Asp Ile Glu Glu Leu Val Glu Pro Val
 915 920 925
 Ala Ala His Gly Pro Lys Ile Glu Glu Glu Glu Gln Glu Pro Glu Pro
 930 935 940
 Pro Glu Pro Phe Glu Tyr Ile Asp Asp
 945 950

<210> 77

<211> 335

<212> PRT

<213> Homo Sapiens

<400> 77

Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg
 1 5 10 15
 Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala
 20 25 30
 Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
 35 40 45
 Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn
 50 55 60
 Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg
 65 70 75 80
 Asp Pro Ser Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val
 85 90 95

Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu
 100 105 110
 Gln Gly Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala
 115 120 125
 Pro Met Phe Val Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu
 130 135 140
 Lys Ile Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu
 145 150 155 160
 Ala Lys Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr
 165 170 175
 Thr Val His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser
 180 185 190
 Gly Lys Leu Trp Arg Asp Gly Arg Gly Ala Leu Gln Asn Ile Ile Pro
 195 200 205
 Ala Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu
 210 215 220
 Asn Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val
 225 230 235 240
 Ser Val Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp
 245 250 255
 Asp Ile Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly
 260 265 270
 Ile Leu Gly Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser
 275 280 285
 Asp Thr His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn
 290 295 300
 Asp His Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr
 305 310 315 320
 Ser Asn Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu
 325 330 335

<210> 78
 <211> 117
 <212> PRT
 <213> Homo Sapiens

<400> 78
 Met Val Gln Arg Leu Thr Tyr Arg Arg Arg Leu Ser Tyr Asn Thr Ala
 1 5 10 15
 Ser Asn Lys Thr Arg Leu Ser Arg Thr Pro Gly Asn Arg Ile Val Tyr
 20 25 30
 Leu Tyr Thr Lys Lys Val Gly Lys Ala Pro Lys Ser Ala Cys Gly Val
 35 40 45
 Cys Pro Gly Lys Leu Arg Gly Val Arg Pro Val Arg Pro Lys Val Leu
 50 55 60
 Met Arg Leu Ser Lys Thr Lys Lys His Val Ser Arg Ala Tyr Gly Gly
 65 70 75 80
 Ser Met Cys Ala Lys Cys Val Arg Asp Arg Ile Lys Arg Ala Phe Leu
 85 90 95
 Ile Glu Glu Gln Lys Ile Ile Val Lys Val Leu Lys Ala Gln Ala Gln
 100 105 110
 Ser Gln Lys Ala Lys
 115

<210> 79

<211> 614
 <212> PRT
 <213> Homo Sapiens

<400> 79
 Arg Ser Gly Gln Pro Arg Ala Glu Gly Leu Gly Ala Gly Ala Ala Gly
 1 5 10 15
 Pro Leu Arg Ala Met Ala Ala Pro Val Lys Gly Asn Arg Lys Gln Ser
 20 25 30
 Thr Glu Gly Asp Ala Leu Asp Pro Pro Ala Ser Pro Lys Pro Ala Gly
 35 40 45
 Lys Gln Asn Gly Ile Gln Asn Pro Ile Ser Leu Glu Asp Ser Pro Glu
 50 55 60
 Ala Gly Gly Glu Arg Glu Glu Glu Gln Glu Arg Glu Glu Gln Ala
 65 70 75 80
 Phe Leu Val Ser Leu Tyr Lys Phe Met Lys Glu Arg His Thr Pro Ile
 85 90 95
 Glu Arg Val Pro His Leu Gly Phe Lys Gln Ile Asn Leu Trp Lys Ile
 100 105 110
 Tyr Lys Ala Val Glu Lys Leu Gly Ala Tyr Glu Leu Val Thr Gly Arg
 115 120 125
 Arg Leu Trp Lys Asn Val Tyr Asp Glu Leu Gly Gly Ser Pro Gly Ser
 130 135 140
 Thr Ser Ala Ala Thr Cys Thr Arg Arg His Tyr Glu Arg Leu Val Leu
 145 150 155 160
 Pro Tyr Val Arg His Leu Lys Gly Glu Asp Asp Lys Pro Leu Pro Thr
 165 170 175
 Ser Lys Pro Arg Lys Gln Tyr Lys Met Ala Lys Glu Asn Arg Gly Asp
 180 185 190
 Asp Gly Ala Thr Glu Arg Pro Lys Lys Ala Lys Glu Glu Arg Arg Met
 195 200 205
 Asp Gln Met Met Pro Gly Lys Thr Lys Ala Asp Ala Ala Asp Pro Ala
 210 215 220
 Pro Leu Pro Ser Gln Glu Pro Pro Arg Asn Ser Thr Glu Gln Gln Gly
 225 230 235 240
 Leu Ala Ser Gly Ser Ser Val Ser Phe Val Gly Ala Ser Gly Cys Pro
 245 250 255
 Glu Ala Tyr Lys Arg Leu Leu Ser Ser Phe Tyr Cys Lys Gly Thr His
 260 265 270
 Gly Ile Met Ser Pro Leu Ala Lys Lys Lys Leu Leu Ala Gln Val Ser
 275 280 285
 Lys Val Glu Ala Leu Gln Cys Gln Glu Glu Gly Cys Arg His Gly Ala
 290 295 300
 Glu Pro Gln Ala Ser Pro Ala Val His Leu Pro Glu Ser Pro Gln Ser
 305 310 315 320
 Pro Lys Gly Leu Thr Glu Asn Ser Arg His Arg Leu Thr Pro Gln Glu
 325 330 335
 Gly Leu Gln Ala Pro Gly Gly Ser Leu Arg Glu Glu Ala Gln Ala Gly
 340 345 350
 Pro Cys Pro Ala Ala Pro Ile Phe Lys Gly Cys Phe Tyr Thr His Pro
 355 360 365
 Thr Glu Val Leu Lys Pro Val Ser Gln His Pro Arg Asp Phe Phe Ser
 370 375 380
 Arg Leu Lys Asp Gly Val Leu Leu Gly Pro Pro Gly Lys Glu Gly Leu
 385 390 395 400

Ser Val Lys Glu Pro Gln Leu Val Trp Gly Gly Asp Ala Asn Arg Pro
 405 410 415
 Ser Ala Phe His Lys Gly Gly Ser Arg Lys Gly Ile Leu Tyr Pro Lys
 420 425 430
 Pro Lys Ala Cys Trp Val Ser Pro Met Ala Lys Val Pro Ala Glu Ser
 435 440 445
 Pro Thr Leu Pro Pro Thr Phe Pro Ser Ser Pro Gly Leu Gly Ser Lys
 450 455 460
 Arg Ser Leu Glu Glu Glu Gly Ala Ala His Ser Gly Lys Arg Leu Arg
 465 470 475 480
 Ala Val Ser Pro Phe Leu Lys Glu Ala Asp Ala Lys Lys Cys Gly Ala
 485 490 495
 Lys Pro Ala Gly Ser Gly Leu Val Ser Cys Leu Leu Gly Pro Ala Leu
 500 505 510
 Gly Pro Val Pro Pro Glu Ala Tyr Arg Gly Thr Met Leu His Cys Pro
 515 520 525
 Leu Asn Phe Thr Gly Thr Pro Gly Pro Leu Lys Gly Gln Ala Ala Leu
 530 535 540
 Pro Phe Ser Pro Leu Val Ile Pro Ala Phe Pro Ala His Phe Leu Ala
 545 550 555 560
 Thr Ala Gly Pro Ser Pro Met Ala Ala Gly Leu Met His Phe Pro Pro
 565 570 575
 Thr Ser Phe Asp Ser Ala Leu Arg His Arg Leu Cys Pro Ala Ser Ser
 580 585 590
 Ala Trp His Ala Pro Pro Val Thr Thr Tyr Ala Ala Pro His Phe Phe
 595 600 605
 His Leu Asn Thr Lys Leu
 610

<210> 80
 <211> 114
 <212> PRT
 <213> Homo Sapiens

<400> 80
 Met Ala Ser Val Ser Glu Leu Ala Cys Ile Tyr Ser Ala Leu Ile Leu
 1 5 10 15
 His Asp Asp Glu Val Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile
 20 25 30
 Lys Ala Ala Gly Val Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala
 35 40 45
 Lys Ala Leu Ala Asn Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly
 50 55 60
 Ala Gly Gly Pro Ala Pro Ala Ala Gly Ala Ala Pro Ala Gly Gly Pro
 65 70 75 80
 Ala Pro Ser Thr Ala Ala Ala Pro Ala Glu Glu Lys Lys Val Glu Ala
 85 90 95
 Lys Lys Glu Glu Ser Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu
 100 105 110
 Phe Asp

<210> 81
 <211> 596
 <212> PRT

<213> Homo Sapiens

<400> 81

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Met Arg Arg Ala His Glu Gly Arg Glu Ile Pro Ser Leu Gly Gly Ala
 1              5              10              15
Arg Arg Arg Glu Val Leu Gln Ala Gly Arg Ser Gln Arg Ala Ala Gly
      20              25              30
Arg Arg Arg Arg Arg Gln Glu Leu Glu Leu Gly Val Gly Ser Gly Arg
      35              40              45
Pro Gly Gly Pro Pro Pro Gly Pro Gly Arg Arg Gly Thr Cys Ala Ala
      50              55              60
Ala Leu Pro Pro Glu Trp Pro Arg Arg Arg Thr Gly Leu Pro Arg Arg
      65              70              75              80
Gly Pro Arg Pro Pro Leu Ala Met Ala Lys Trp Leu Asn Lys Tyr Phe
      85              90              95
Ser Leu Gly Asn Ser Lys Thr Lys Ser Pro Pro Gln Pro Pro Arg Pro
      100             105             110
Asp Tyr Arg Glu Gln Arg Arg Arg Gly Glu Arg Pro Ser Gln Pro Pro
      115             120             125
Gln Ala Val Pro Gln Ala Ser Ser Ala Ala Ser Ala Ser Cys Gly Pro
      130             135             140
Ala Thr Ala Ser Cys Phe Ser Ala Ser Ser Gly Ser Leu Pro Asp Asp
      145             150             155             160
Ser Gly Ser Thr Ser Asp Leu Ile Arg Ala Tyr Arg Ala Gln Lys Glu
      165             170             175
Arg His Phe Gln Asp Pro Tyr Asn Gly Pro Gly Ser Ser Leu Arg Lys
      180             185             190
Leu Arg Ala Met Cys Arg Leu Asp Tyr Cys Gly Gly Ser Gly Glu Pro
      195             200             205
Gly Gly Val Gln Arg Ala Phe Ser Ala Ser Ser Ala Ser Gly Ala Ala
      210             215             220
Gly Cys Cys Cys Ala Ser Ser Gly Ala Gly Ala Ala Ala Ser Ser Ser
      225             230             235             240
Ser Ser Ser Gly Ser Pro His Leu Tyr Arg Ser Ser Ser Glu Arg Arg
      245             250             255
Pro Ala Thr Pro Ala Glu Val Arg Tyr Ile Ser Pro Lys His Arg Leu
      260             265             270
Ile Lys Val Glu Ser Ala Ala Gly Gly Gly Ala Gly Asp Pro Leu Gly
      275             280             285
Gly Ala Cys Ala Gly Gly Arg Thr Trp Ser Pro Thr Ala Cys Gly Gly
      290             295             300
Lys Lys Leu Leu Asn Lys Cys Ala Ala Ser Ala Ala Glu Glu Ser Gly
      305             310             315             320
Ala Gly Lys Lys Asp Lys Val Thr Ile Ala Asp Asp Tyr Ser Asp Pro
      325             330             335
Phe Asp Ala Lys Asn Asp Leu Lys Ser Lys Ala Gly Lys Gly Glu Ser
      340             345             350
Ala Gly Tyr Met Glu Pro Tyr Glu Ala Gln Arg Ile Met Thr Glu Phe
      355             360             365
Gln Arg Gln Glu Ser Val Arg Ser Gln His Lys Gly Ile Gln Leu Tyr
      370             375             380
Asp Thr Pro Tyr Glu Pro Glu Gly Gln Ser Val Asp Ser Asp Ser Glu
      385             390             395             400
Ser Thr Val Ser Pro Arg Leu Arg Glu Ser Lys Leu Pro Gln Asp Asp
      405             410             415

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Asp Arg Pro Ala Asp Glu Tyr Asp Gln Pro Trp Glu Trp Asn Arg Val
 420 425 430
 Thr Ser Pro Ala Leu Ala Ala Gln Phe Asn Gly Asn Glu Lys Arg Gln
 435 440 445
 Ser Ser Pro Ser Pro Ser Arg Asp Arg Arg Gln Leu Arg Ala Pro
 450 455 460
 Gly Gly Gly Phe Lys Pro Ile Lys His Gly Ser Pro Glu Phe Cys Gly
 465 470 475 480
 Ile Leu Gly Glu Arg Val Asp Pro Ala Val Pro Leu Glu Lys Gln Ile
 485 490 495
 Trp Tyr His Gly Ala Ile Ser Arg Gly Asp Ala Glu Asn Leu Leu Arg
 500 505 510
 Leu Cys Lys Glu Cys Ser Tyr Leu Val Arg Asn Ser Gln Thr Ser Lys
 515 520 525
 His Asp Tyr Pro Leu Ser Leu Arg Ser Asn Gln Gly Phe Met His Met
 530 535 540
 Lys Leu Ala Lys Thr Lys Glu Lys Tyr Val Leu Gly Gln Asn Ser Pro
 545 550 555 560
 Pro Phe Asp Ser Val Pro Glu Val Ile His Tyr Tyr Thr Thr Arg Lys
 565 570 575
 Leu Pro Ile Lys Gly Ala Glu His Leu Ser Leu Leu Tyr Pro Val Ala
 580 585 590
 Val Arg Thr Leu
 595

<210> 82

<211> 207

<212> PRT

<213> Homo Sapiens

<400> 82

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15
 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 130 135 140
 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
 145 150 155 160
 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
 165 170 175
 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
 180 185 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 195 200 205

<210> 83
 <211> 429
 <212> PRT
 <213> Homo Sapiens

<400> 83
 Glu Cys Asp Val Met Thr Tyr Val Arg Glu Thr Cys Gly Cys Cys Asp
 1 5 10 15
 Cys Glu Lys Arg Cys Gly Ala Leu Asp Val Val Phe Val Ile Asp Ser
 20 25 30
 Ser Glu Ser Ile Gly Tyr Thr Asn Phe Thr Leu Glu Lys Asn Phe Val
 35 40 45
 Ile Asn Val Val Asn Arg Leu Gly Ala Ile Ala Lys Asp Pro Lys Ser
 50 55 60
 Glu Thr Gly Thr Arg Val Gly Val Val Gln Tyr Ser His Glu Gly Thr
 65 70 75 80
 Phe Glu Ala Ile Gln Leu Asp Asp Glu His Ile Asp Ser Leu Ser Ser
 85 90 95
 Phe Lys Glu Ala Val Lys Asn Leu Glu Trp Ile Ala Gly Gly Thr Trp
 100 105 110
 Thr Pro Ser Ala Leu Lys Phe Ala Tyr Asp Arg Leu Ile Lys Glu Ser
 115 120 125
 Arg Arg Gln Lys Thr Arg Val Phe Ala Val Val Ile Thr Asp Gly Arg
 130 135 140
 His Asp Pro Arg Asp Asp Leu Asn Leu Arg Ala Leu Cys Asp Arg
 145 150 155 160
 Asp Val Thr Val Thr Ala Ile Gly Ile Gly Asp Met Phe His Glu Lys
 165 170 175
 His Glu Ser Glu Asn Leu Tyr Ser Ile Ala Cys Asp Lys Pro Gln Gln
 180 185 190
 Val Arg Asn Met Thr Leu Phe Ser Asp Leu Val Ala Glu Lys Phe Ile
 195 200 205
 Asp Asp Met Glu Asp Val Leu Cys Pro Asp Pro Gln Ile Val Cys Pro
 210 215 220
 Asp Leu Pro Cys Gln Thr Glu Leu Ser Val Ala Gln Cys Thr Gln Arg
 225 230 235 240
 Pro Val Asp Ile Val Phe Leu Leu Asp Gly Ser Glu Arg Leu Gly Glu
 245 250 255
 Gln Asn Phe His Lys Ala Arg Arg Phe Val Glu Gln Val Ala Arg Arg
 260 265 270
 Leu Thr Leu Ala Arg Arg Asp Asp Asp Pro Leu Asn Ala Arg Val Ala
 275 280 285
 Leu Leu Gln Phe Gly Gly Pro Gly Glu Gln Gln Val Ala Phe Pro Leu
 290 295 300
 Ser His Asn Leu Thr Ala Ile His Glu Ala Leu Glu Thr Thr Gln Tyr
 305 310 315 320
 Leu Asn Ser Phe Ser His Val Gly Ala Gly Val Val His Ala Ile Asn
 325 330 335
 Ala Ile Val Arg Ser Pro Arg Gly Gly Ala Arg Arg His Ala Glu Leu
 340 345 350
 Ser Phe Val Phe Leu Thr Asp Gly Val Thr Gly Asn Asp Ser Leu His
 355 360 365

Glu Ser Ala His Ser Met Arg Asn Glu Asn Val Val Pro Thr Val Leu
 370 375 380
 Ala Leu Gly Ser Asp Val Asp Met Asp Val Leu Thr Thr Leu Ser Leu
 385 390 395 400
 Gly Asp Arg Ala Ala Val Phe His Glu Lys Asp Tyr Asp Ser Leu Ala
 405 410 415
 Gln Pro Gly Phe Phe Asp Arg Phe Ile Arg Trp Ile Cys
 420 425

<210> 84
 <211> 113
 <212> PRT
 <213> Homo Sapiens

<400> 84
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
 1 5 10 15
 Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
 20 25 30
 Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
 35 40 45
 Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
 50 55 60
 Gly Ser Phe Ile Leu Ala Val Cys Leu Arg Ile Gln Ile Asn Pro Gln
 65 70 75 80
 Asn Lys Ala Asp Phe Gln Gly Ile Ser Pro Glu Arg Ala Phe Ala Asp
 85 90 95
 Phe Leu Phe Ala Ser Thr Ile Leu His Leu Val Val Met Asn Phe Val
 100 105 110
 Gly

<210> 85
 <211> 258
 <212> PRT
 <213> Homo Sapiens

<400> 85
 Met Ile Asn Ile Glu Ser Met Asp Thr Asp Lys Asp Asp Pro His Gly
 1 5 10 15
 Arg Leu Glu Tyr Thr Glu His Gln Gly Arg Ile Lys Asn Ala Arg Glu
 20 25 30
 Ala His Ser Gln Ile Glu Lys Arg Arg Arg Asp Lys Met Asn Ser Phe
 35 40 45
 Ile Asp Glu Leu Ala Ser Leu Val Pro Thr Cys Asn Ala Met Ser Arg
 50 55 60
 Lys Leu Asp Lys Leu Thr Val Leu Arg Met Ala Val Gln His Met Lys
 65 70 75 80
 Thr Leu Arg Gly Ala Thr Asn Pro Tyr Thr Glu Ala Asn Tyr Lys Pro
 85 90 95
 Thr Phe Leu Ser Asp Asp Glu Leu Lys His Leu Ile Leu Arg Ala Ala
 100 105 110
 Asp Gly Phe Leu Phe Val Val Gly Cys Asp Arg Gly Lys Ile Leu Phe
 115 120 125
 Val Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr Ser Gln Asn Asp Leu

130 135 140
 Ile Gly Gln Ser Leu Phe Asp Tyr Leu His Pro Lys Asp Ile Ala Lys
 145 150 155 160
 Val Lys Glu Gln Leu Ser Ser Ser Asp Thr Ala Pro Arg Glu Arg Leu
 165 170 175
 Ile Asp Ala Lys Thr Gly Leu Pro Val Lys Thr Asp Ile Thr Pro Gly
 180 185 190
 Pro Ser Arg Leu Cys Ser Gly Ala Arg Arg Ser Phe Phe Cys Arg Met
 195 200 205
 Lys Cys Asn Arg Pro Ser Val Asn Val Glu Asp Lys Asn Phe Pro Ser
 210 215 220
 Thr Cys Ser Lys Lys Lys Ala Asp Arg Lys Ala Phe Cys Thr Ile His
 225 230 235 240
 Ser Thr Gly Tyr Phe Gly Ile Phe Thr Thr Arg Thr Ser Arg His Ile
 245 250 255
 Val Leu

<210> 86
 <211> 569
 <212> PRT
 <213> Homo Sapiens

<400> 86
 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
 1 5 10 15
 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
 20 25 30
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
 35 40 45
 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
 50 55 60
 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
 65 70 75 80
 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
 85 90 95
 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
 100 105 110
 Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln
 115 120 125
 Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu
 130 135 140
 Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser
 145 150 155 160
 Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe
 165 170 175
 Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser
 180 185 190
 Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg
 195 200 205
 Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg
 210 215 220
 Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu
 225 230 235 240
 Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile

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                245                250                255
Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Ala Asn
                260                265                270
Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp
                275                280                285
His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly
                290                295                300
Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu
305                310                315                320
Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys
                325                330                335
Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu
                340                345                350
Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys
                355                360                365
Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala
370                375                380
Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr
385                390                395                400
Lys Glu Ile Leu Thr Arg Ala His Glu Arg Glu Phe Gly Ser Val Asp
                405                410                415
Asp Glu Asn Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Cys
                420                425                430
Lys Gly Lys Gln Lys Asp Gly Thr Ser Phe Gly Glu Tyr Gly Gly Trp
                435                440                445
Tyr Lys Ala Cys Lys Val Asp Ser Pro Thr Val Thr Thr Thr Leu Lys
450                455                460
Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Phe Glu Ala Ala Glu
465                470                475                480
Thr Leu Glu Glu Ala Ala Met Arg Ser Arg Lys Gln Gly Leu Asp Asn
                485                490                495
Val His Lys Gln Arg Val Ala Glu Val Leu Asn Asp Pro Glu Asn Met
500                505                510
Glu Lys Arg Arg Ser Arg Glu Ser Leu Asn Val Asp Val Val Lys Tyr
515                520                525
Glu Ser Gly Pro Asp Gly Gly Glu Glu Val Ser Met Ser Val Glu Trp
530                535                540
Asn Gly Gly Val Ser Gly Arg Ala Ser Phe Cys Gly Lys Arg Gln Gln
545                550                555                560
Gln Gln Trp Pro Gly Arg Arg His Arg
                565

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<210> 87

<211> 736

<212> PRT

<213> Homo Sapiens

<400> 87

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Met Glu Ala Leu Ile Pro Val Ile Asn Lys Leu Gln Asp Val Phe Asn
1                5                10                15
Thr Val Gly Ala Asp Ile Ile Gln Leu Pro Gln Ile Val Val Val Gly
                20                25                30
Thr Gln Ser Ser Gly Lys Ser Ser Val Leu Glu Ser Leu Val Gly Arg
35                40                45
Asp Leu Leu Pro Arg Gly Thr Gly Ile Val Thr Arg Arg Pro Leu Ile

```

50. 55 60
 Leu Gln Leu Val His Val Thr Gln Glu Asp Lys Arg Lys Thr Thr Gly
 65 70 75 80
 Glu Glu Asn Gly Val Glu Ala Glu Glu Trp Gly Lys Phe Leu His Thr
 85 90 95
 Lys Asn Lys Leu Tyr Thr Asp Phe Asp Glu Ile Arg Gln Glu Ile Glu
 100 105 110
 Asn Glu Thr Glu Arg Ile Ser Gly Asn Asn Lys Gly Val Ser Pro Glu
 115 120 125
 Pro Ile His Leu Lys Ile Phe Ser Pro Asn Val Val Asn Leu Thr Leu
 130 135 140
 Val Asp Leu Pro Gly Met Thr Lys Val Pro Val Gly Asp Gln Pro Lys
 145 150 155 160
 Asp Ile Glu Leu Gln Ile Arg Glu Leu Ile Leu Arg Phe Ile Ser Asn
 165 170 175
 Pro Asn Ser Ile Ile Leu Ala Val Thr Ala Ala Asn Thr Asp Met Ala
 180 185 190
 Thr Ser Glu Ala Leu Lys Ile Ser Arg Glu Val Asp Pro Asp Gly Arg
 195 200 205
 Arg Thr Leu Ala Val Ile Thr Lys Leu Asp Leu Met Asp Ala Gly Thr
 210 215 220
 Asp Ala Met Asp Val Leu Met Gly Arg Val Ile Pro Val Lys Leu Gly
 225 230 235 240
 Ile Ile Gly Val Val Asn Arg Ser Gln Leu Asp Ile Asn Asn Lys Lys
 245 250 255
 Ser Val Thr Asp Ser Ile Arg Asp Glu Tyr Ala Phe Leu Gln Lys Lys
 260 265 270
 Tyr Pro Ser Leu Ala Asn Arg Asn Gly Thr Lys Tyr Leu Ala Arg Thr
 275 280 285
 Leu Asn Arg Leu Leu Met His His Ile Arg Asp Cys Leu Pro Glu Leu
 290 295 300
 Lys Thr Arg Ile Asn Val Leu Ala Ala Gln Tyr Gln Ser Leu Leu Asn
 305 310 315 320
 Ser Tyr Gly Glu Pro Val Asp Asp Lys Ser Ala Thr Leu Leu Gln Leu
 325 330 335
 Ile Thr Lys Phe Ala Thr Glu Tyr Cys Asn Thr Ile Glu Gly Thr Ala
 340 345 350
 Lys Tyr Ile Glu Thr Ser Glu Leu Cys Gly Gly Ala Arg Ile Cys Tyr
 355 360 365
 Ile Phe His Glu Thr Phe Gly Arg Thr Leu Glu Ser Val Asp Pro Leu
 370 375 380
 Gly Gly Leu Asn Thr Ile Asp Ile Leu Thr Ala Ile Arg Asn Ala Thr
 385 390 395 400
 Gly Pro Arg Pro Ala Leu Phe Val Pro Glu Val Ser Phe Glu Leu Leu
 405 410 415
 Val Lys Arg Gln Ile Lys Arg Leu Glu Glu Pro Ser Leu Arg Cys Val
 420 425 430
 Glu Leu Val His Glu Glu Met Gln Arg Ile Ile Gln His Cys Ser Asn
 435 440 445
 Tyr Ser Thr Gln Glu Leu Leu Arg Phe Pro Lys Leu His Asp Ala Ile
 450 455 460
 Val Glu Val Val Thr Cys Leu Leu Arg Lys Arg Leu Pro Val Thr Asn
 465 470 475 480
 Glu Met Val His Asn Leu Val Ala Ile Glu Leu Ala Tyr Ile Asn Thr
 485 490 495

Lys His Pro Asp Phe Ala Asp Ala Cys Gly Leu Met Asn Asn Asn Ile
 500 505 510
 Glu Glu Gln Arg Arg Asn Arg Leu Ala Arg Glu Leu Pro Ser Ala Val
 515 520 525
 Ser Arg Asp Lys Ser Ser Lys Val Pro Ser Ala Leu Ala Pro Ala Ser
 530 535 540
 Gln Glu Pro Ser Pro Ala Ala Ser Ala Glu Ala Asp Gly Lys Leu Ile
 545 550 555 560
 Gln Asp Ser Arg Arg Glu Thr Lys Asn Val Ala Ser Gly Gly Gly Gly
 565 570 575
 Val Gly Asp Gly Val Gln Glu Pro Thr Thr Gly Asn Trp Arg Gly Met
 580 585 590
 Leu Lys Thr Ser Lys Ala Glu Glu Leu Leu Ala Glu Glu Lys Ser Lys
 595 600 605
 Pro Ile Pro Ile Met Pro Ala Ser Pro Gln Lys Gly His Ala Val Asn
 610 615 620
 Leu Leu Asp Val Pro Val Pro Val Ala Arg Lys Leu Ser Ala Arg Glu
 625 630 635 640
 Gln Arg Asp Cys Glu Val Ile Glu Arg Leu Ile Lys Ser Tyr Phe Leu
 645 650 655
 Ile Val Arg Lys Asn Ile Gln Asp Ser Val Pro Lys Ala Val Met His
 660 665 670
 Phe Leu Val Asn His Val Lys Asp Thr Leu Gln Ser Glu Leu Val Gly
 675 680 685
 Gln Leu Tyr Lys Ser Ser Leu Leu Asp Asp Leu Leu Thr Glu Ser Glu
 690 695 700
 Asp Met Ala Gln Arg Arg Lys Glu Ala Ala Asp Met Leu Lys Ala Leu
 705 710 715 720
 Gln Gly Ala Ser Gln Ile Ile Ala Glu Ile Arg Glu Thr His Leu Trp
 725 730 735

<210> 88
 <211> 37
 <212> PRT
 <213> Homo Sapiens

<400> 88
 Met Gly Asp His Ala Trp Ser Phe Leu Lys Asp Phe Leu Ala Gly Gly
 1 5 10 15
 Val Ala Ala Ala Val Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val
 20 25 30
 Lys Leu Leu Leu Gln
 35

<210> 89
 <211> 1381
 <212> DNA
 <213> Homo Sapiens

<400> 89
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 gcgttcgtgt ccgagttctc tgcaggtcnc tantttccc gtagttcanc tgcncatgaa 120
 tanaacagca atgagagccn ctncaaaaga ctttgaaaat tcaactgaatc nagtgaaact 180
 ctngaaaaag gatccangaa acgaaatgaa nctnaaaactc tncgcgctat atnancangc 240
 cncctgaanga cttgtntcat gcccnaacca ngtgtntttg acttgatcna caaggggcca 300


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atgggacaca tggaaatgcc ttggcancct gccnaagaa ctgccaggca naactatgtg 360
gatttgggtg ccannttgat tccntccttg gaatectcna atcnngtgga ncctggaaca 420
nacaggaaat ccaactgggt tgaaactctg gtggtgacct ccgaagatgg catcacaag 480
atcatgttca accggcccaa aaagaaaaat gccataaaca ctgagatgta tcatgaaatt 540
atgcgtgcac ttaaagctgc cagcaaggat gactcaatca tcaactgttt aacaggaaat 600
ggtgactatt acagtagtgg gaatgatctg actaacttca ctgatattcc ccctgggtgga 660
gtagaggaga aagctaaaaa taatgccgtt ttactgaggg aatttgtggg ctgttttata 720
gattttccta agcctctgat tgcagtggtc aatgggtccag ctgtgggcat ctccgtcacc 780
ctccttgggc tattcgatgc cgtgtatgca tctgacaggg caacatttca tacaccattt 840
agtcacctag gccaaagtcc ggaaggatgc tcctcttaca cttttccgaa gataatgagc 900
ccagccaagg caacagagat gcttattttt ggaaagaagt taacagcggg agaggcatgt 960
gctcaaggac ttgttactga agttttccct gatagcactt ttcagaaaga agtctggacc 1020
aggctgaagg catttgcaaa gcttccccc aatgccttga gaatttcaaa agaggtaatc 1080
aggaaaagag agagagaaaa actacacgct gttaatgctg aagaatgcaa tgccttcag 1140
ggaagatggc tatcagatga atgcacaaat gctgtggtga acttcttacc cagaaaatca 1200
aaactgtgat gaccactaca gcagagtaaa gcatgtccaa ggaaggatgt gctgttacct 1260
ctgatttcca gtactggaac taaataagct tcattgtgcc tttttagtg ctagaatatc 1320
aattacaatg atgatatttc actacagctc tgatgaataa aaagttttgt aaaacaagaa 1380
a 1381

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<210> 90
 <211> 298
 <212> PRT
 <213> Homo Sapiens

<400> 90

Thr	Cys	Met	Pro	Val	Phe	Asp	Leu	Ile	Lys	Gly	Pro	Met	Gly	His	
1			5				10					15			
Met	Glu	Cys	Pro	Trp	Pro	Ala	Arg	Thr	Ala	Arg	Asn	Tyr	Val	Asp	Leu
			20				25					30			
Val	Ser	Leu	Pro	Ser	Leu	Glu	Ser	Ser	Asn	Val	Pro	Gly	Thr	Arg	Lys
			35				40					45			
Ser	Thr	Gly	Phe	Glu	Thr	Leu	Val	Val	Thr	Ser	Glu	Asp	Gly	Ile	Thr
			50				55					60			
Lys	Ile	Met	Phe	Asn	Arg	Pro	Lys	Lys	Lys	Asn	Ala	Ile	Asn	Thr	Glu
							70				75				80
Met	Tyr	His	Glu	Ile	Met	Arg	Ala	Leu	Lys	Ala	Ala	Ser	Lys	Asp	Asp
							85				90				95
Ser	Ile	Ile	Thr	Val	Leu	Thr	Gly	Asn	Gly	Asp	Tyr	Tyr	Ser	Ser	Gly
							100								110
Asn	Asp	Leu	Thr	Asn	Phe	Thr	Asp	Ile	Pro	Pro	Gly	Gly	Val	Glu	Glu
							115					125			
Lys	Ala	Lys	Asn	Asn	Ala	Val	Leu	Leu	Arg	Glu	Phe	Val	Gly	Cys	Phe
							130					140			
Ile	Asp	Phe	Pro	Lys	Pro	Leu	Ile	Ala	Val	Val	Asn	Gly	Pro	Ala	Val
							145								160
Gly	Ile	Ser	Val	Thr	Leu	Leu	Gly	Leu	Phe	Asp	Ala	Val	Tyr	Ala	Ser
							165								175
Asp	Arg	Ala	Thr	Phe	His	Thr	Pro	Phe	Ser	His	Leu	Gly	Gln	Ser	Pro
							180								190
Glu	Gly	Cys	Ser	Ser	Tyr	Thr	Phe	Pro	Lys	Ile	Met	Ser	Pro	Ala	Lys
							195								205
Ala	Thr	Glu	Met	Leu	Ile	Phe	Gly	Lys	Lys	Leu	Thr	Ala	Gly	Glu	Ala
							210								220
Cys	Ala	Gln	Leu	Val	Thr	Glu	Val	Phe	Pro	Asp	Ser	Thr	Phe	Gln	Lys

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225          230          235          240
Glu Val Trp Thr Lys Leu Lys Ala Phe Ala Lys Ala Ser Pro Lys Cys
          245          250          255
Leu Glu Asn Phe Lys Arg Gly Asn Gln Gly Lys Glu Arg Glu Lys Asn
          260          265          270
Tyr Thr Pro Leu Met Leu Lys Lys Cys Asn Val Pro Ser Arg Lys Gly
          275          280          285
Tyr Gln Asp Glu Cys Thr Lys Cys Leu Trp
          290          295

```

<210> 91
 <211> 1514
 <212> DNA
 <213> Homo Sapiens

```

<400> 91
gccgcgcgct gtgtctccgc tgcgtccgcc gagggccccc agtgtcaggg acaaaagcct      60
ccgcctgtct ccgcagccgg ggctcatctg ccgcgcgcgc cgcgctgagg agagttcgcc      120
gccgtcgccg cccgtgagga tctgagagcc atgtcggcca gcagcctctt ggagcagaga      180
ccaaaagggtc aaggaaacaa agtacaaaat ggatctgtac atcaaaagga tggattaaac      240
gatgatgatt ttgaacctta cttgagtcca caggcaaggc ccaataatgc atatactgcc      300
atgtcagatt cctacttacc cagttactac agtcctcca ttggcttctc ctattctttg      360
ggtgaagctg cttggtctac ggggggtgac acagccatgc cctacttaac ttcttatgga      420
cagctgagca acggagagcc ccacttecta ccagatgcaa tgtttgggca accaggagcc      480
ctaggtagca ctccatttct tggtcagcat ggttttaatt tctttcccag tgggattgac      540
ttctcagcat ggggaaataa cagttctcag ggacagtcta ctacagagctc tggatatagt      600
agcaattatg cttatgcacc tagctcctta ggtggagcca tgattgatgg acagtcagct      660
tttgccaatg agaccctcaa taaggctcct ggcatagaata ctatagacca agggatggca      720
gcactgaagt tgggtagcac agaagttgca agcaatgttc caaaagttgt aggttctgct      780
gttggttagcg ggtccattac tagtaacatc gtggcttcca atagtttgcc tccagccacc      840
attgtccttc caaaaccagc atcttgggct gatattgcta gcaagcctgc aaaacagcaa      900
cctaaactga agaccaagaa tggcattgca ggggtcaagtc ttccgccacc cccgataaag      960
cataacatgg atattggaac ttgggataac aagggtcccc ttgcaaaagc cccctcacag     1020
gctttgggtc agaatatagg tcagccaacc cagggtctc ctcagcctgt aggtcagcag     1080
gctaacaata gccaccagt ggctcaggca tcagtagggc aacagacaca gccattgcct     1140
ccacctccac cacagcctgc ccagcttcca gtccagcaac aggcagctca gccaacccgc     1200
tgggtagcac ctcggaaccg tggcagtggt ttcggtcata atgggggtgga tggtaatgga     1260
gtaggacagt ctcaggctgg ttctggatct actccttcag aaccccaccc agtgttggag     1320
aagcttcggt ccattaataa ctataacccc aaagattttg actgggaaat ctgaaacatg     1380
ggcgggtttt catcattaaa gaactactct gangacgata ttcaccgttc catttaagtt     1440
ataatatttg gtggancaca anagcaatgg taacaagaga atgggatgcc ngcttatcgt     1500
ttccatgaac gggg                                     1514

```

<210> 92
 <211> 407
 <212> PRT
 <213> Homo Sapiens

```

<400> 92
Met Ser Ala Ser Ser Leu Leu Glu Gln Arg Pro Lys Gly Gln Gly Asn
  1          5          10          15
Lys Val Gln Asn Gly Ser Val His Gln Lys Asp Gly Leu Asn Asp Asp
          20          25          30
Asp Phe Glu Pro Tyr Leu Ser Pro Gln Ala Arg Pro Asn Asn Ala Tyr
          35          40          45

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```

Thr Ala Met Ser Asp Ser Tyr Leu Pro Ser Tyr Tyr Ser Pro Ser Ile
 50                      55                      60
Gly Phe Ser Tyr Ser Leu Gly Glu Ala Ala Trp Ser Thr Gly Gly Asp
65                      70                      75                      80
Thr Ala Met Pro Tyr Leu Thr Ser Tyr Gly Gln Leu Ser Asn Gly Glu
                      85                      90                      95
Pro His Phe Leu Pro Asp Ala Met Phe Gly Gln Pro Gly Ala Leu Gly
                      100                      105                      110
Ser Thr Pro Phe Leu Gly Gln His Gly Phe Asn Phe Phe Pro Ser Gly
                      115                      120                      125
Ile Asp Phe Ser Ala Trp Gly Asn Asn Ser Ser Gln Gly Gln Ser Thr
                      130                      135                      140
Gln Ser Ser Gly Tyr Ser Ser Asn Tyr Ala Tyr Ala Pro Ser Ser Leu
145                      150                      155                      160
Gly Gly Ala Met Ile Asp Gly Gln Ser Ala Phe Ala Asn Glu Thr Leu
                      165                      170                      175
Asn Lys Ala Pro Gly Met Asn Thr Ile Asp Gln Gly Met Ala Ala Leu
                      180                      185                      190
Lys Leu Gly Ser Thr Glu Val Ala Ser Asn Val Pro Lys Val Val Gly
                      195                      200                      205
Ser Ala Val Gly Ser Gly Ser Ile Thr Ser Asn Ile Val Ala Ser Asn
                      210                      215                      220
Ser Leu Pro Pro Ala Thr Ile Ala Pro Pro Lys Pro Ala Ser Trp Ala
225                      230                      235                      240
Asp Ile Ala Ser Lys Pro Ala Lys Gln Gln Pro Lys Leu Lys Thr Lys
                      245                      250                      255
Asn Gly Ile Ala Gly Ser Ser Leu Pro Pro Pro Pro Ile Lys His Asn
                      260                      265                      270
Met Asp Ile Gly Thr Trp Asp Asn Lys Gly Pro Val Ala Lys Ala Pro
                      275                      280                      285
Ser Gln Ala Leu Val Gln Asn Ile Gly Gln Pro Thr Gln Gly Ser Pro
                      290                      295                      300
Gln Pro Val Gly Gln Gln Ala Asn Asn Ser Pro Pro Val Ala Gln Ala
305                      310                      315                      320
Ser Val Gly Gln Gln Thr Gln Pro Leu Pro Pro Pro Pro Gln Pro
                      325                      330                      335
Ala Gln Leu Ser Val Gln Gln Gln Ala Ala Gln Pro Thr Arg Trp Val
                      340                      345                      350
Ala Pro Arg Asn Arg Gly Ser Gly Phe Gly His Asn Gly Val Asp Gly
                      355                      360                      365
Asn Gly Val Gly Gln Ser Gln Ala Gly Ser Gly Ser Thr Pro Ser Glu
                      370                      375                      380
Pro His Pro Val Leu Glu Lys Leu Arg Ser Ile Asn Asn Tyr Asn Pro
385                      390                      395                      400
Lys Asp Phe Asp Trp Glu Ile
                      405

```

<210> 93

<211> 2236

<212> DNA

<213> Homo Sapiens

<400> 93

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cctggcccggtcggtcgc ggctctttcc agctcctggc agccgggcac ccgaaggaaac      60
gggtcgtgca acgacgcagc tggacctggc ccagccatgg accgaaaagt ggccccgagaa      120

```

```

ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180
gtgctgcgaa tgtaccacca gaccatggac gtggcgtgc tcgtgggaga cctgaagctg 240
gtcatcaatg aaccagccg tctgcctctg tttgatgcca ttcggccgct gatccactg 300
aagcaccagg tggaatatga tcagctgacc ccccgcgct ccaggaagct gaaggaggtg 360
cgtctggacc gtctgcaccc cgaaggcctc ggctgagtg tgcgtggtgg cctggagttt 420
ggctgtgggc tcttcacatc ccacctcatc aaaggcggtc aggcagacag cgtcgggctc 480
caggtagggg acgagatcgt ccggatcaat ggatattcca tctcctcctg taccatgag 540
gaggtcatca acctattcg aaccaagaaa actgtgtcca tcaaagttag acacatcggc 600
ctgatccccg tgaaaagctc tcctgatgag cccctcactt ggcagtatgt ggatcagttt 660
gtgtcggaat ctggggcgct gcgaggcagc ctgggctccc ctggaaatcg ggaaaacaag 720
gagaagaagg tcttcacag cctggtaggc tcccgaggcc ttggctgcag cattccagc 780
ggccccatcc agaagcctgg catctttatc agccatgtga aacctggctc cctgtctgct 840
gaggtgggat tggagatagg ggaccagatt gtgcaagtca atggcgtcga cttctctaac 900
ctggatcaca aggagctgt aaatgtgctg aaaaatagcc gcagcctgac catctccatt 960
gtagctgcag ctggccggga gctgttcacg acagaccggg agcggctggc agaggcgagg 1020
cagcgtgagc tgcagcggca ggagcttctc atgcagaagc ggctggcgat ggagtccaac 1080
aagatcctcc aaaatgagca ggagatggag cggcaaagga gaaaagaaat tgcccagaag 1140
gcagcagagg aaaatgagag ataccggaag gagatggaac agattgtaga ggaggagag 1200
aagtttaaga agcaatggga agaagactgg ggctcaaagg aacagctact cttgcctaaa 1260
accatcactg ctgaggtaca ccagtagcc cttcgcaagc caaagtatga tcaggagtg 1320
gaacctgagc tcgagcccg agatgacctg gatggaggca cggaggagca gggagagcag 1380
gatttccgga aatatgagga aggccttgac ccctactcta tgttcacccc agagcagatc 1440
atggggaagg atgtccggct cctacgcac aagaaggagg gatccttaga cctggccctg 1500
gaaggcgggt tggactcccc cattgggaag gtggtcggtt ctgctgtgta tgagcgggga 1560
gctgctgagc ggcattggtg cattgtgaaa ggggacgaga tcatggcaat caacggcaag 1620
attgtgacag actacacctt ggctgaggct gacgtgccc tgcagaaggc ctggaatcag 1680
ggcggggact ggatcgacct tgtggttgcc gtctgcccc caaaggagta tgacgatgag 1740
ctgaccttct tgctgaagtc caaaagggga aaccaaattc acgcgttagg aaacagttag 1800
ctccggcccc acctcgtgaa caaaagcct cggaccagcc ttgagagagg ccacatgaca 1860
cacaccagat ggcattcctg ggacctgaat ctatcaccca ggaatctcaa actccctttg 1920
gccctgaacc agggccagat aaggaacagc tcgggccact tttttgaagg ccaatgtgga 1980
ggaaagggag cagccagccg tttgggagaa gatctcaagg atccagactc tcattccttt 2040
cctctggccc agtgaatttg gtctctccca gctttgggg actccttcct tgaaccctaa 2100
taagacccca ctggagtctc tctctctcca tccctctcct ctgccctctg ctctaattgc 2160
tgccaggatt gtcactccaa acctactct gagctcatta ataaaataaa cagatttatt 2220
ttccagctta aaaaaa 2236

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<210> 94

<211> 652

<212> PRT

<213> Homo Sapiens

<400> 94

```

Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
 1           5           10          15
Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
 20          25          30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
 35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
 50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
 65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
 85          90          95

```

Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
 100 105 110
 Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
 115 120 125
 Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
 130 135 140
 Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
 145 150 155 160
 Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
 165 170 175
 Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
 180 185 190
 Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
 195 200 205
 Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
 210 215 220
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
 370 375 380
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
 385 390 395 400
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
 405 410 415
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys
 420 425 430
 Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile
 435 440 445
 Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu
 450 455 460
 Asp Leu Ala Leu Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val
 465 470 475 480
 Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile
 485 490 495
 Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp
 500 505 510
 Tyr Thr Leu Ala Glu Ala Asp Ala Leu Gln Lys Ala Trp Asn Gln
 515 520 525
 Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu

530 535 540
 Tyr Asp Asp Glu Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln
 545 550 555 560
 Ile His Ala Leu Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr
 565 570 575
 Lys Pro Arg Thr Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp
 580 585 590
 His Pro Trp Asp Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu
 595 600 605
 Ala Leu Asn Gln Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu
 610 615 620
 Gly Gln Cys Gly Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu
 625 630 635 640
 Lys Asp Pro Asp Ser His Ser Phe Pro Leu Ala Gln
 645 650

<210> 95
 <211> 831
 <212> DNA
 <213> Homo Sapiens

<400> 95
 cataactggg actcgcgcgc ctgcaggtcg acactagtgg gatccaaaga attcggcacg 60
 agaaaccaca atgccagat ctcaagtaga tgaagagttt ttgaagcaaa gtttaaagga 120
 aaaacnattg cagaaaacat ttgattnta tgaaatatat aatnanancc aaaanccatt 180
 tgaanttaat nganccttac ctgtentcac taaatcaggg ttntctgcgc caccnaaggg 240
 cngcccancg cctgctgtgt tggttanta ggcctnagca tangggcagn tgcaatcctt 300
 tcctcctnng gcggcanatg ggcttctgga anaacccttn ccttatcccc ancgcaaggc 360
 ggccctccc ctgccctnaa aggaaacctc ntggacncag ggaatatang gccaccttga 420
 aggttgact ggctatcntg gaagatcaga taccaccaag caatttgag acagttcctg 480
 ttgagaataa ccacggtttc catgaaaaga cagcagcgct gaagcttgag gccgagggcg 540
 aggccatgga agatgcagcc gcgccagggg acgaccgagg cggcacacag gagccagccc 600
 cagtgcctgc tgagccgttt gacaacacta cctacaagaa cctgcagcat catgactaca 660
 gcacgtacac cttcttagac ctcaacctcg aactctcaaa attcaggatg cctcagccct 720
 cctcagggcg ggagtcacct cgacactgag ggccctcggt gtgaagatga acctccacc 780
 gtcttcactg catcctggag tgcaaaaata aaatccactc aagagtcaaa a 831

<210> 96
 <211> 184
 <212> PRT
 <213> Homo Sapiens

<400> 96
 Arg Lys Asn Cys Arg Lys His Leu Asp Met Lys Tyr Ile Lys His Leu
 1 5 10 15
 Leu Pro Tyr Leu Ser Ser Leu Asn Gln Gly Leu Arg His Arg Ala Ala
 20 25 30
 Arg Leu Leu Cys Trp Leu Arg Pro His Gly Cys Asn Pro Phe Leu Leu
 35 40 45
 Arg Met Gly Phe Trp Asn Pro Leu Ile Pro Ala Arg Arg Pro Leu Pro
 50 55 60
 Cys Pro Arg Lys Pro Gly Arg Glu Tyr Ala Thr Leu Lys Gly Gly Leu
 65 70 75 80
 Ala Ile Glu Asp Gln Ile Pro Pro Ser Asn Leu Glu Thr Val Pro Val
 85 90 95

Glu Asn Asn His Gly Phe His Glu Lys Thr Ala Ala Leu Lys Leu Glu
 100 105 110
 Ala Glu Gly Glu Ala Met Glu Asp Ala Ala Ala Pro Gly Asn Asp Arg
 115 120 125
 Gly Gly Thr Gln Glu Pro Ala Pro Val Pro Ala Glu Pro Phe Asp Asn
 130 135 140
 Thr Thr Tyr Lys Asn Leu Gln His His Asp Tyr Ser Thr Tyr Thr Phe
 145 150 155 160
 Leu Asp Leu Asn Leu Glu Leu Ser Lys Phe Arg Met Pro Gln Pro Ser
 165 170 175
 Ser Gly Arg Glu Ser Pro Arg His
 180

<210> 97
 <211> 1008
 <212> DNA
 <213> Homo Sapiens

<400> 97
 gcaaggtctc caagtcccag ctcaaggtcc tttcccataa cctgtgcacg gtgctgaagg 60
 ttccctcatga cccagttgcc cttgaagagc acttcaggga tgatgatgag ggtccagtgt 120
 ccaaccagggt ctacatgcct tatttaaaca gggtcatttt ggaaaagggtc caagacaact 180
 ttgacaagat tgaattcaat aggatgtgtt ggacctctctg tgtcaaaaaa aacctcacia 240
 agaatccctt gctcattaca gaagaanatg catttaaaat atgggttatt ttcaactttt 300
 tatctgagga caagtatcca ttaattattg tgcagaana gattgaatac ctgcttaaga 360
 agcttacaga agctatggga ggaggttggc agcaagaaca atttgaacat tataaaatca 420
 actttgatga cagtaaaaaat ggcctttctg catgggaact tattgagctt attggaaatg 480
 gacagtttag caaaggcatg gaccggcaga ctgtgtctat ggcaattaat gaagtcttta 540
 atgaacttat attagatgtg ttaaagcagg gttacatgat gaaaaagggtc cacagacgga 600
 aaaactggac tgaacgatgg tttgtactaa aaccaacat aatttcttac tatgtgagtg 660
 aggatctgaa ggataagaaa ggagacattc tcttgatga aaattgctgt gtagagtcct 720
 tgcctgacaa agatggaaaag aaatgccttt ttctcgtaaa atgttttgat aagacttttg 780
 aaatcagtgct ttcaagataag aanaanaaac aggagtggat tcaagccatt cattctacta 840
 ttcattctgtt gaagctgngc agccctccac canacaaaga agccnccag cttctnaaan 900
 aactccgna gaatcatctg gctgaacaag angaactgga gcgacaaatg aangaactcc 960
 aagcccgcga atgaaagcaa ncagcaagag ctggaaggcc ttncggaa 1008

<210> 98
 <211> 312
 <212> PRT
 <213> Homo Sapiens

<400> 98
 Lys Val Ser Lys Ser Gln Leu Lys Val Leu Ser His Asn Leu Cys Thr
 1 5 10 15
 Val Leu Lys Val Pro His Asp Pro Val Ala Leu Glu Glu His Phe Arg
 20 25 30
 Asp Asp Asp Glu Gly Pro Val Ser Asn Gln Gly Tyr Met Pro Tyr Leu
 35 40 45
 Asn Arg Phe Ile Leu Glu Lys Val Gln Asp Asn Phe Asp Lys Ile Glu
 50 55 60
 Phe Asn Arg Met Cys Trp Thr Leu Cys Val Lys Lys Asn Leu Thr Lys
 65 70 75 80
 Asn Pro Leu Leu Ile Thr Glu Glu Ala Phe Lys Ile Trp Val Ile Phe
 85 90 95

Asn Phe Leu Ser Glu Asp Lys Tyr Pro Leu Ile Ile Val Ser Glu Ile
 100 105 110
 Glu Tyr Leu Leu Lys Lys Leu Thr Glu Ala Met Gly Gly Gly Trp Gln
 115 120 125
 Gln Glu Gln Phe Glu His Tyr Lys Ile Asn Phe Asp Asp Ser Lys Asn
 130 135 140
 Gly Leu Ser Ala Trp Glu Leu Ile Glu Leu Ile Gly Asn Gly Gln Phe
 145 150 155 160
 Ser Lys Gly Met Asp Arg Gln Thr Val Ser Met Ala Ile Asn Glu Val
 165 170 175
 Phe Asn Glu Leu Ile Leu Asp Val Leu Lys Gln Gly Tyr Met Met Lys
 180 185 190
 Lys Gly His Arg Arg Lys Asn Trp Thr Glu Arg Trp Phe Val Leu Lys
 195 200 205
 Pro Asn Ile Ile Ser Tyr Tyr Val Ser Glu Asp Leu Lys Asp Lys Lys
 210 215 220
 Gly Asp Ile Leu Leu Asp Glu Asn Cys Cys Val Glu Ser Leu Pro Asp
 225 230 235 240
 Lys Asp Gly Lys Lys Cys Leu Phe Leu Val Lys Cys Phe Asp Lys Thr
 245 250 255
 Phe Glu Ile Ser Ala Ser Asp Lys Lys Gln Glu Trp Ile Gln Ala Ile
 260 265 270
 His Ser Thr Ile His Leu Leu Lys Leu Ser Pro Pro Pro Lys Glu Ala
 275 280 285
 Gln Leu Leu Lys Leu Arg Asn His Leu Ala Glu Gln Glu Leu Glu Arg
 290 295 300
 Gln Met Glu Leu Gln Ala Arg Gln
 305 310

<210> 99
 <211> 1009
 <212> DNA
 <213> Homo Sapiens

<400> 99
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 aacttttgca gaagatgagg agttacaaaa tatggacaaa gaagatgcat taatttgctt 120
 tgaagaacac attcgggctt tagaaaagga ggaagaagaa gaaaaacaga agagtttgct 180
 gagagaaagg agacgacagc gaaaaaatag ggaatctttc cagatatttt tagatgaatt 240
 acatgaacat ggacaactgc attctatgtc atcttggatg gaattgtatc caactattag 300
 ttctgatatt agattcacta atatgcttgg tcagcctgga tcaactgcac ttgatctttt 360
 caagttttat gttgaggatc ttaaagcacg ttatcatgac gagaagaaga taataaaaga 420
 cattctaaag gataaaggat ttgtagttga agtaaacact acttttgaag attttgtggc 480
 gataatcagt tcaactaaaa gatcaactac attagatgct ggaaatatca aattggcttt 540
 caatagttta ctagaaaagg cagaagcccc tgaacgtgaa agagaaaaag aagaggctcg 600
 gaagatgaaa cgaaaagaat ctgcatttaa gagtatgtta aaacaagctg ctctccgat 660
 agaattggat gctgtctggg aagatatccg tgagagattt gtaaaagagc cagcatttga 720
 ggacataact ctagaatctg aaagaaaacg aatattttaa gattttatgc atgtgcttga 780
 gcatgaatgt cagcatcatc attcaaagaa caagaaacat tctaagaaat ctaaaaaaca 840
 tcataggaaa cgttcccgct ctcgatcggt gtcagattca ngatgatgat gatagccatt 900
 caaagaaaaa aagacagcga tgagaagtct cgggtctgntt canaacattc ttccantngc 960
 agagtctgag agaagtntaa aaagtcaaaa nagcatagan aggaaagtt 1009

<210> 100
 <211> 292

<212> PRT

<213> Homo Sapiens

<400> 100

Ala Asn Val Thr Tyr Ser Thr Thr Trp Ser Glu Ala Gln Gln Tyr Leu
 1 5 10 15
 Met Asp Asn Pro Thr Phe Ala Glu Asp Glu Glu Leu Gln Asn Met Asp
 20 25 30
 Lys Glu Asp Ala Leu Ile Cys Phe Glu Glu His Ile Arg Ala Leu Glu
 35 40 45
 Lys Glu Glu Glu Glu Glu Lys Gln Lys Ser Leu Leu Arg Glu Arg Arg
 50 55 60
 Arg Gln Arg Lys Asn Arg Glu Ser Phe Gln Ile Phe Leu Asp Glu Leu
 65 70 75 80
 His Glu His Gly Gln Leu His Ser Met Ser Ser Trp Met Glu Leu Tyr
 85 90 95
 Pro Thr Ile Ser Ser Asp Ile Arg Phe Thr Asn Met Leu Gly Gln Pro
 100 105 110
 Gly Ser Thr Ala Leu Asp Leu Phe Lys Phe Tyr Val Glu Asp Leu Lys
 115 120 125
 Ala Arg Tyr His Asp Glu Lys Lys Ile Ile Lys Asp Ile Leu Lys Asp
 130 135 140
 Lys Gly Phe Val Val Glu Val Asn Thr Thr Phe Glu Asp Phe Val Ala
 145 150 155 160
 Ile Ile Ser Ser Thr Lys Arg Ser Thr Thr Leu Asp Ala Gly Asn Ile
 165 170 175
 Lys Leu Ala Phe Asn Ser Leu Leu Glu Lys Ala Glu Ala Arg Glu Arg
 180 185 190
 Glu Arg Glu Lys Glu Glu Ala Arg Lys Met Lys Arg Lys Glu Ser Ala
 195 200 205
 Phe Lys Ser Met Leu Lys Gln Ala Ala Pro Pro Ile Glu Leu Asp Ala
 210 215 220
 Val Trp Glu Asp Ile Arg Glu Arg Phe Val Lys Glu Pro Ala Phe Glu
 225 230 235 240
 Asp Ile Thr Leu Glu Ser Glu Arg Lys Arg Ile Phe Lys Asp Phe Met
 245 250 255
 His Val Leu Glu His Glu Cys Gln His His His Ser Lys Asn Lys Lys
 260 265 270
 His Ser Lys Lys Ser Lys Lys His His Arg Lys Arg Ser Arg Ser Arg
 275 280 285
 Ser Gly Ser Asp
 290

<210> 101

<211> 983

<212> DNA

<213> Homo Sapiens

<400> 101

aggtgacaat agatatagaa gtacgttgat gtgcgaagat gtattttggt ttagccagcg 60
 aggaaaaaag aatcagtttg attatacatt taccaaacat taagaattta atatggtaac 120
 ttttatttca gtattaaaaat agcaatttta tttattactt ttttatatat agaatttgac 180
 accaaatttt ggaacttaaa aagaagattc ttaaaactta caatccagat tacgatgagg 240
 acctggtgca ggaagcttca tctgaagatg tcctgggcgt tcatatggtg gacaaagaca 300
 cagagagaga cattgagatg aaacggcaac tacggcgact acgggagctc cacctataca 360

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gcacatggaa gaagtaccaa gaggcgatga agacatcctt gggagttcca caacgtgagc 420
gtgacgaagg ctcttgggc aagccattgt gtccaccgga gatactctcg gagacgttgc 480
caggctctgt gaagaaaagg gtatgctttc catcagaaga tcatctagag gagtttatag 540
cagaacatct ccctgaagca tccaatcaga gtctcctcac tgttgcccat gcagacgcag 600
gcacccaaac caacggtgac ctggaagacc tggaggagca tgggccaggg cagacagtct 660
ctgaggaagc cacagaagtt cacatgatgg agggggaccc agacacactg gccgaacttc 720
tgatcagga tgtacttcag gagctgtcca gttacaacgg cgaggaggag gacccanagg 780
aggtgaagac atccttggga gttccacaac gtggtgacct ggaagacctg gaggagcatg 840
tgncagggca gnnnttctct gaggaagcca caggggttca catgatgcag gtggaccag 900
ccacgctggc aaagagtgc ctggaagacc tggaggagca tgtgccagag cagacagtct 960
ctgaggaagc cacaggggtt cac 983

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<210> 102
 <211> 230
 <212> PRT
 <213> Homo Sapiens

<400> 102

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Met Val Asp Lys Asp Thr Glu Arg Asp Ile Glu Met Lys Arg Gln Leu
 1           5           10          15
Arg Arg Leu Arg Glu Leu His Leu Tyr Ser Thr Trp Lys Lys Tyr Gln
          20          25          30
Glu Ala Met Lys Thr Ser Leu Gly Val Pro Gln Arg Glu Arg Asp Glu
        35          40          45
Gly Ser Leu Gly Lys Pro Leu Cys Pro Pro Glu Ile Leu Ser Glu Thr
       50          55          60
Leu Pro Gly Ser Val Lys Lys Arg Val Cys Phe Pro Ser Glu Asp His
      65          70          75          80
Leu Glu Glu Phe Ile Ala Glu His Leu Pro Glu Ala Ser Asn Gln Ser
          85          90          95
Leu Leu Thr Val Ala His Ala Asp Ala Gly Thr Gln Thr Asn Gly Asp
        100         105         110
Leu Glu Asp Leu Glu Glu His Gly Pro Gly Gln Thr Val Ser Glu Glu
       115         120         125
Ala Thr Glu Val His Met Met Glu Gly Asp Pro Asp Thr Leu Ala Glu
      130         135         140
Leu Leu Ile Arg Asp Val Leu Gln Glu Leu Ser Ser Tyr Asn Gly Glu
     145         150         155         160
Glu Glu Asp Pro Glu Val Lys Thr Ser Leu Gly Val Pro Gln Arg Gly
        165         170         175
Asp Leu Glu Asp Leu Glu Glu His Val Gly Gln Phe Ser Glu Glu Ala
       180         185         190
Thr Gly Val His Met Met Gln Val Asp Pro Ala Thr Leu Ala Lys Ser
      195         200         205
Asp Leu Glu Asp Leu Glu Glu His Val Pro Glu Gln Thr Val Ser Glu
     210         215         220
Glu Ala Thr Gly Val His
    225         230

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<210> 103
 <211> 843
 <212> DNA
 <213> Homo Sapiens

<400> 103

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aatncccgct gcaggctcgac actagtggat ccaaagaatt cggcacgagg caagtctctgg      60
gagctggaca cggaccacga cctgctcatc gacgcggacg acctggcgcg gcacaatgac      120
cacgcccttt ctaccaagat gatagacagg atcttctcag gagcagtcac acgaggcaga      180
aaagtgcaga aggaaggga gatcagctat gccgactttg tctggttttt gatctctgag      240
gaagacaaaa aaacaccgac cagcatcgag tactggttcc gctgcatgga cctggacggg      300
gacggcgccc tgtccatggt cgagctcgag tacttctacg aggagcagtg ccgaaggctg      360
gacagcatgg ccatcgaggc cctgcccttc caggactgcc tctgccagat gctggacctg      420
gtcaagccga ggactgaagg gaagatcacg ctgcaggacc tgaagcgctg caagctggcc      480
aacgtcttct tcgacacctt cttcaacatc gagaagtncc tcgaccacga gcagaaagag      540
cagatctccc tgctcaggga cggtgacagc ggcgggcccc agctctcgga ctgggagaag      600
tnccggccga agagtncgac atcctggtgg ccgangaaac cgtggggana nccctgggga      660
agacgggttc naaggcgaac tcaccccnt ggancanaaa ctgantgcgc tgcgtcccc      720
gctgggcan aggccttctt ccaagcgct cccgctggg cgccgtggaa ctgttncaaa      780
ttccctcgcg gggacaagaa cttgaaaccg ctgtganncc cccncnana accnccccg      840
gnt                                                                    843

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<210> 104
 <211> 197
 <212> PRT
 <213> Homo Sapiens

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<400> 104
Arg Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser Ala Arg Gly Lys
 1          5          10          15
Phe Trp Glu Leu Asp Thr Asp His Asp Leu Leu Ile Asp Ala Asp Asp
 20          25          30
Leu Ala Arg His Asn Asp His Ala Leu Ser Thr Lys Met Ile Asp Arg
 35          40          45
Ile Phe Ser Gly Ala Val Thr Arg Gly Arg Lys Val Gln Lys Glu Gly
 50          55          60
Lys Ile Ser Tyr Ala Asp Phe Val Trp Phe Leu Ile Ser Glu Glu Asp
 65          70          75          80
Lys Lys Thr Pro Thr Ser Ile Glu Tyr Trp Phe Arg Cys Met Asp Leu
 85          90          95
Asp Gly Asp Gly Ala Leu Ser Met Phe Glu Leu Glu Tyr Phe Tyr Glu
100          105          110
Glu Gln Cys Arg Arg Leu Asp Ser Met Ala Ile Glu Ala Leu Pro Phe
115          120          125
Gln Asp Cys Leu Cys Gln Met Leu Asp Leu Val Lys Pro Arg Thr Glu
130          135          140
Gly Lys Ile Thr Leu Gln Asp Leu Lys Arg Cys Lys Leu Ala Asn Val
145          150          155          160
Phe Phe Asp Thr Phe Phe Asn Ile Glu Lys Leu Asp His Glu Gln Lys
165          170          175
Glu Gln Ile Ser Leu Leu Arg Asp Gly Asp Ser Gly Gly Pro Glu Leu
180          185          190
Ser Asp Trp Glu Lys
195

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<210> 105
 <211> 2264
 <212> DNA
 <213> Homo Sapiens

<400> 105

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ctagcacaag tacacaggcc ccagccgctt cccctactgg ttagttcct ggtaccaa 60
atgcagtacc tgacacgtcc acttaccagt atgatgaatc ttcaggatat tactatgatc 120
cgacaacagg gctctattat gaccccaact cgcaatacta ctataattcc ttgaccagc 180
agtaccttta ctgggatggg gaaaaagaga cctacgtgcc agctgcagag tctagctccc 240
accagcagtc gggcctgcct cctgcaaaaag aggggaaaga gaagaaggag aaaccaaga 300
gcaaaacagc ccagcagatt gccaaagaca tggaacgctg ggctaagagt ttgaataagc 360
agaaagaaaa ctttaaaaat agctttcagc ctgtcaattc cttgagggaa gaagaaagga 420
gagaatctgc tgcagcagac gctggccttg ctctctttga gaagaaggga gccttagctg 480
aaaggcagca gctcatccca gaattgggtg gaaatggaga tgaggagaat cccctcaaaa 540
ggggtctggg tgctgcttac agtggtgaca gtgacaatga ggaggagctg gtggagagac 600
ttgagagtga ggaagagaag ctagctgact ggaagaagat ggctgtctg ctctgccggc 660
gccagtcccc gaacaaagat gccctagtca ggcaccagca actctcagac cttcacaagc 720
aaaaatgga catctaccga cgatccaggc tgagcgagca ggagctggaa gccttgagc 780
taaggagag agagatgaaa taccgagacc gagctgcaga aagacgggag aagtagggca 840
ttccagaacc tccagagccc aagcgcaaga agcagtttga tgccggcact gtgaattacg 900
agcaaccac caaagatggc attgaccaca gtaacattgg caacaagatg ctgcaggcca 960
tgggctggcg ggaaggctct ggcttgggac gaaagtgtca aggcattacg gctcccattg 1020
aggctcaagt tcggctaaaag gagctgggcc taggagccaa aggcagcgca tatggtttgt 1080
cgggcgcgca ttcctacaaa gatgctgtcc ggaaagccat gtttgccegg ttcactgaga 1140
tggagtgaga gagagagaga gagagagatg acaaggagca caagaagtgg tccatctccc 1200
gaattcgctg ttaccgcctg tctctttaag ggcattgctt gtgctgttaa tagatcttag 1260
ggtgaaccac ttcattctgc agggttctcc ctcccacctt aaagaagttc cccttatgtg 1320
ggttgccctg tgaatggcct tccttcccgc cagagggctt gtgaacagac cggagaggac 1380
agtggattgt ttatactcca gtgtacatag tgtaatgtag cgtgtttaca tgtgtagcct 1440
atgttgtggg ccatcagccc ctacattcc taggggtttg agatgctgta ggtggtatgt 1500
gacaccaaag ccacctctgt catttggtgt gatgtctttt cttggcaaaa gccttggtgta 1560
tattgtata ttacacattt gtacagaatt ttggaagatt ttcaatccaa gttgccaaat 1620
ctggctcctt tacaaaagaa ataccttgag aaaaaaaann aannaaaaaa aannccnann 1680
nnntttttaa aanggnncgg gggccaannn ttttcnncg gggnggggna nnaagtaaan 1740
ngtcccaaat nccccaaaa nggagcccn ttaaaattaa angggccgcn nttttaaaan 1800
nttcngaata gggnaaaccc tnggggtttn ccaaatttaa cccctttgaa aaaaaanccc 1860
ctttcncaaa anngggnata tanccaaaaa gggcccccnn ccatttttgc cnttccaaa 1920
aaaatttgnc caancnnaa atgggnaaan ggggaatcca attttttaaa gggmnnaaan 1980
gggtttaaac nnacgggntt ccaaanntgn ttgggggaat ttttaaattc ccaannnccc 2040
aaggggggna atttagnggn cccnaatcc cccaaaaant gggtcnnggn tnaaanncngc 2100
cnnnnccnaa tttntanggg tttacttngn tttaaaaaac cncnccaaaa actccccnnc 2160
gaaccnaaaa aanaaaagga ngccattttt ngngnnaaac ttttttaann nncnnttaa 2220
angggttaaa aaannnnnnn tnncccnnaa tttttcaaan aang 2264

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<210> 106

<211> 381

<212> PRT

<213> Homo Sapiens

<400> 106

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Ser Thr Ser Thr Gln Ala Pro Ala Ala Ser Pro Thr Gly Val Val Pro
1          5          10          15
Gly Thr Lys Tyr Ala Val Pro Asp Thr Ser Thr Tyr Gln Tyr Asp Glu
20          25          30
Ser Ser Gly Tyr Tyr Tyr Asp Pro Thr Thr Gly Leu Tyr Tyr Asp Pro
35          40          45
Asn Ser Gln Tyr Tyr Tyr Asn Ser Leu Thr Gln Gln Tyr Leu Tyr Trp
50          55          60
Asp Gly Glu Lys Glu Thr Tyr Val Pro Ala Ala Glu Ser Ser Ser His
65          70          75          80

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Gln Gln Ser Gly Leu Pro Pro Ala Lys Glu Gly Lys Glu Lys Lys Glu
 85 90 95
 Lys Pro Lys Ser Lys Thr Ala Gln Gln Ile Ala Lys Asp Met Glu Arg
 100 105 110
 Trp Ala Lys Ser Leu Asn Lys Gln Lys Glu Asn Phe Lys Asn Ser Phe
 115 120 125
 Gln Pro Val Asn Ser Leu Arg Glu Glu Arg Arg Glu Ser Ala Ala
 130 135 140
 Ala Asp Ala Gly Phe Ala Leu Phe Glu Lys Lys Gly Ala Leu Ala Glu
 145 150 155 160
 Arg Gln Gln Leu Ile Pro Glu Leu Val Arg Asn Gly Asp Glu Glu Asn
 165 170 175
 Pro Leu Lys Arg Gly Leu Val Ala Ala Tyr Ser Gly Asp Ser Asp Asn
 180 185 190
 Glu Glu Glu Leu Val Glu Arg Leu Glu Ser Glu Glu Glu Lys Leu Ala
 195 200 205
 Asp Trp Lys Lys Met Ala Cys Leu Leu Cys Arg Arg Gln Phe Pro Asn
 210 215 220
 Lys Asp Ala Leu Val Arg His Gln Gln Leu Ser Asp Leu His Lys Gln
 225 230 235 240
 Asn Met Asp Ile Tyr Arg Arg Ser Arg Leu Ser Glu Gln Glu Leu Glu
 245 250 255
 Ala Leu Glu Leu Arg Glu Arg Glu Met Lys Tyr Arg Asp Arg Ala Ala
 260 265 270
 Glu Arg Arg Glu Lys Tyr Gly Ile Pro Glu Pro Pro Glu Pro Lys Arg
 275 280 285
 Lys Lys Gln Phe Asp Ala Gly Thr Val Asn Tyr Glu Gln Pro Thr Lys
 290 295 300
 Asp Gly Ile Asp His Ser Asn Ile Gly Asn Lys Met Leu Gln Ala Met
 305 310 315 320
 Gly Trp Arg Glu Gly Ser Gly Leu Gly Arg Lys Cys Gln Gly Ile Thr
 325 330 335
 Ala Pro Ile Glu Ala Gln Val Arg Leu Lys Gly Ala Gly Leu Gly Ala
 340 345 350
 Lys Gly Ser Ala Tyr Gly Leu Ser Gly Ala Asp Ser Tyr Lys Asp Ala
 355 360 365
 Val Arg Lys Ala Met Phe Ala Arg Phe Thr Glu Met Glu
 370 375 380

<210> 107

<211> 1367

<212> DNA

<213> Homo Sapiens

<400> 107

gcgacacagg cctcgaggct gtctctgaca agtgttcaca ggaggtgggg acgcctctgc	60
gcgaggaacg aggagctacg ggcctgggcc cggttattgc catgggcagc ggctgccgca	120
tcgaatgcat attcttcagc gagttccacc ccacgctggg acccaagatc acctatcagg	180
tccctgaaga cttcatctcc cgagagctgt ttgacacagt ccaagtgtac atcatcacca	240
agccagagct gcagaacaag cttatcactg tcacagctat ggaaaagaag ctgatcggt	300
gtcctgtgtg catcgaacac aagaagtaca gccgcaatgc tctcctcttc aacctgggct	360
tcgtgtgtga tgcccaggcc aagacctgcg ccctcgagcc cattgttaaa aagctggctg	420
gctatctgac cacactagag ctgagagca gcttcgtgtc catggaggag agcaagcaga	480
agttggtgcc catcatgacc atcttgctgg aggagctaaa tgcctcaggc cgggtgcactc	540
tgccattga tgagtccaac accatccact tgaaggtgat tgagcagcgg ccagaccctc	600

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cggtggccca ggagtatgat gtacctgtct ttaccaaaga caaggaggat ttcttcaact    660
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agaagatttc agcagaggca gatgtggagc tcaacctggt gcgcattgct atccagaacc    780
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caacgcccac ggtccaggac ctggtagatg acaagtccct gcaagaggca tgtctatcct    900
acgtgaccaa gcaagggcac aagagggcca gtctccggga tgtgttccag ctatactgca    960
gcctgagccc tggcactacc gtgagagacc tcattggccg ccacccccag cagctgcagc   1020
atgttgatga acggaagctg atccagttcg ggcttatgaa gaacctcatc aggcgactac   1080
agaagtatcc tgtgcgggtg actcgggaag agcagagcca ccctgcccgg ctttatacag   1140
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<210> 108

<211> 413

<212> PRT

<213> Homo Sapiens

<400> 108

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Asp Thr Gly Leu Glu Ala Val Ser Asp Lys Cys Ser Gln Glu Val Gly
 1           5           10          15
Thr Pro Leu Arg Glu Glu Arg Gly Ala Thr Gly Leu Gly Pro Val Ile
          20          25          30
Ala Met Gly Ser Gly Cys Arg Ile Glu Cys Ile Phe Phe Ser Glu Phe
          35          40          45
His Pro Thr Leu Gly Pro Lys Ile Thr Tyr Gln Val Pro Glu Asp Phe
          50          55          60
Ile Ser Arg Glu Leu Phe Asp Thr Val Gln Val Tyr Ile Ile Thr Lys
65          70          75          80
Pro Glu Leu Gln Asn Lys Leu Ile Thr Val Thr Ala Met Glu Lys Lys
          85          90          95
Leu Ile Gly Cys Pro Val Cys Ile Glu His Lys Lys Tyr Ser Arg Asn
          100         105         110
Ala Leu Leu Phe Asn Leu Gly Phe Val Cys Asp Ala Gln Ala Lys Thr
          115         120         125
Cys Ala Leu Glu Pro Ile Val Lys Lys Leu Ala Gly Tyr Leu Thr Thr
          130         135         140
Leu Glu Leu Glu Ser Ser Phe Val Ser Met Glu Glu Ser Lys Gln Lys
145          150         155         160
Leu Val Pro Ile Met Thr Ile Leu Leu Glu Glu Leu Asn Ala Ser Gly
          165         170         175
Arg Cys Thr Leu Pro Ile Asp Glu Ser Asn Thr Ile His Leu Lys Val
          180         185         190
Ile Glu Gln Arg Pro Asp Pro Pro Val Ala Gln Glu Tyr Asp Val Pro
          195         200         205
Val Phe Thr Lys Asp Lys Glu Asp Phe Phe Asn Ser Gln Trp Asp Leu
          210         215         220
Thr Thr Gln Gln Ile Leu Pro Tyr Ile Asp Gly Phe Arg His Ile Gln
225          230         235         240
Lys Ile Ser Ala Glu Ala Asp Val Glu Leu Asn Leu Val Arg Ile Ala
          245         250         255
Ile Gln Asn Leu Leu Tyr Tyr Gly Val Val Thr Leu Val Ser Ile Leu
          260         265         270
Gln Tyr Ser Asn Val Tyr Cys Pro Thr Pro Lys Val Gln Asp Leu Val

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275 280 285
 Asp Asp Lys Ser Leu Gln Glu Ala Cys Leu Ser Tyr Val Thr Lys Gln
 290 295 300
 Gly His Lys Arg Ala Ser Leu Arg Asp Val Phe Gln Leu Tyr Cys Ser
 305 310 315 320
 Leu Ser Pro Gly Thr Thr Val Arg Asp Leu Ile Gly Arg His Pro Gln
 325 330 335
 Gln Leu Gln His Val Asp Glu Arg Lys Leu Ile Gln Phe Gly Leu Met
 340 345 350
 Lys Asn Leu Ile Arg Arg Leu Gln Lys Tyr Pro Val Arg Val Thr Arg
 355 360 365
 Glu Glu Gln Ser His Pro Ala Arg Leu Tyr Thr Gly Cys His Ser Tyr
 370 375 380
 Asp Glu Ile Cys Cys Lys Thr Gly Met Ser Tyr His Glu Leu Asp Glu
 385 390 395 400
 Arg Leu Glu Asn Asp Pro Asn Ile Ile Ile Cys Trp Lys
 405 410

<210> 109
 <211> 2113
 <212> DNA
 <213> Homo Sapiens

<400> 109
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<210> 110

<211> 543

<212> PRT

<213> Homo Sapiens

<400> 110

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Val Gly Asn Ile Asp Asp Ala Leu Gln Cys Tyr Ser Glu Ala Ile Lys
           20           25           30
Leu Asp Pro His Asn His Val Leu Tyr Ser Asn Arg Ser Ala Ala Tyr
           35           40           45
Ala Lys Lys Gly Asp Tyr Gln Lys Ala Tyr Glu Asp Gly Cys Lys Thr
           50           55           60
Val Asp Leu Lys Pro Asp Trp Gly Lys Gly Tyr Ser Arg Lys Ala Ala
           65           70           75           80
Ala Leu Glu Phe Leu Asn Arg Phe Glu Glu Ala Lys Arg Thr Tyr Glu
           85           90           95
Glu Gly Leu Lys His Glu Ala Asn Asn Pro Gln Leu Lys Glu Gly Leu
           100          105          110
Gln Asn Met Glu Ala Arg Leu Ala Glu Arg Lys Phe Met Asn Pro Phe
           115          120          125
Asn Met Pro Asn Leu Tyr Gln Lys Leu Glu Ser Asp Pro Arg Thr Arg
           130          135          140
Thr Leu Leu Ser Asp Pro Thr Tyr Arg Glu Leu Ile Glu Gln Leu Arg
           145          150          155          160
Asn Lys Pro Ser Asp Leu Gly Thr Lys Leu Gln Asp Pro Arg Ile Met
           165          170          175
Thr Thr Leu Ser Val Leu Leu Gly Val Asp Leu Gly Ser Met Asp Glu
           180          185          190
Glu Glu Glu Ile Ala Thr Pro Pro Pro Pro Pro Pro Lys Lys Glu
           195          200          205
Thr Lys Pro Glu Pro Met Glu Glu Asp Leu Pro Glu Asn Lys Lys Gln
           210          215          220
Ala Leu Lys Glu Lys Glu Leu Gly Asn Asp Ala Tyr Lys Lys Lys Asp
           225          230          235          240
Phe Asp Thr Ala Leu Lys His Tyr Asp Lys Ala Lys Glu Leu Asp Pro
           245          250          255
Thr Asn Met Thr Tyr Ile Thr Asn Gln Ala Ala Val Tyr Phe Glu Lys
           260          265          270
Gly Asp Tyr Asn Lys Cys Arg Glu Leu Cys Glu Lys Ala Ile Glu Val
           275          280          285
Gly Arg Glu Asn Arg Glu Asp Tyr Arg Gln Ile Ala Lys Ala Tyr Ala
           290          295          300
Arg Ile Gly Asn Ser Tyr Phe Lys Glu Glu Lys Tyr Lys Asp Ala Ile
           305          310          315          320
His Phe Tyr Asn Lys Ser Leu Ala Glu His Arg Thr Pro Asp Val Leu
           325          330          335
Lys Lys Cys Gln Gln Ala Glu Lys Ile Leu Lys Glu Gln Glu Arg Leu

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340 345 350
 Ala Tyr Ile Asn Pro Asp Leu Ala Leu Glu Glu Lys Asn Lys Gly Asn
 355 360 365
 Glu Cys Phe Gln Lys Gly Asp Tyr Pro Gln Ala Met Lys His Tyr Thr
 370 375 380
 Glu Ala Ile Lys Arg Asn Pro Lys Asp Ala Lys Leu Tyr Ser Asn Arg
 385 390 395 400
 Ala Ala Cys Tyr Thr Lys Leu Leu Glu Phe Gln Leu Ala Leu Lys Asp
 405 410 415
 Cys Glu Glu Cys Ile Gln Leu Glu Pro Thr Phe Ile Lys Gly Tyr Thr
 420 425 430
 Arg Lys Ala Ala Ala Leu Glu Ala Met Lys Asp Tyr Thr Lys Ala Met
 435 440 445
 Asp Val Tyr Gln Lys Ala Leu Asp Leu Asp Ser Ser Cys Lys Glu Ala
 450 455 460
 Ala Asp Gly Tyr Gln Arg Cys Met Met Ala Gln Tyr Asn Arg His Asp
 465 470 475 480
 Ser Pro Glu Asp Val Lys Arg Arg Ala Met Ala Asp Pro Glu Val Gln
 485 490 495
 Gln Ile Met Ser Asp Pro Ala Met Arg Leu Ile Leu Glu Gln Met Gln
 500 505 510
 Lys Asp Pro Gln Ala Leu Ser Glu His Leu Lys Asn Pro Val Ile Ala
 515 520 525
 Gln Lys Ile Gln Lys Leu Met Asp Val Gly Leu Ile Ala Ile Arg
 530 535 540

<210> 111

<211> 2765

<212> DNA

<213> Homo Sapiens

<400> 111

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 caaccaccg ctgccgaaat gaagtataag aatcttatgg caagggcctt atatgacaat 180
 gtcccagagt gtgccgagga actggccttt cgcaagggag acatcctgac cgtcatagag 240
 cagaacacag ggggactgga aggatgggtg ctgtgtctgt tacacggctg gcaaggcatt 300
 gtcccaggca accgggtgaa gcttctgatt ggtcccatgc aggagactgc ctccagtcac 360
 gagcagcctg cctctggact gatgcagcag acctttggcc aacagaagct ctatcaagtg 420
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 caggggaattt accaagtccc cactggccac ggcacccaag aacaagaggt atatcagggtg 540
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<210> 112

<211> 834

<212> PRT

<213> Homo Sapiens

<400> 112

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Glu Cys Ala Glu Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val
      20             25             30
Ile Glu Gln Asn Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu
      35             40             45
His Gly Arg Gln Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile
      50             55             60
Gly Pro Met Gln Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly
      65             70             75             80
Leu Met Gln Gln Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn
      85             90             95
Pro Gln Ala Ala Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr
      100             105             110
Gln Asn Gln Gly Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu
      115             120             125
Gln Glu Val Tyr Gln Val Pro Ser Val Gln Arg Ser Ile Gly Gly
      130             135             140
Thr Ser Gly Pro His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr
      145             150             155             160
Gly His Gly Tyr Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val
      165             170             175
Tyr Asp Ile Pro Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro
      180             185             190

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Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile
 195 200 205
 Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala
 210 215 220
 Ile Pro Pro Ser Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp
 225 230 235 240
 Tyr Asp Phe Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg
 245 250 255
 Pro Glu Gly Val Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly
 260 265 270
 Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu
 275 280 285
 Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro
 290 295 300
 Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro
 305 310 315 320
 Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala
 325 330 335
 Asn Pro Gln Glu Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro
 340 345 350
 Pro Asp Ala Lys Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu
 355 360 365
 Ser Phe Ser Ser Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser
 370 375 380
 Thr Ser Ser Lys Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys
 385 390 395 400
 Arg Leu Phe Leu Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu
 405 410 415
 Gln Gln Ala Leu Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr
 420 425 430
 Thr Asp Trp Arg Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile
 435 440 445
 Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His
 450 455 460
 Phe Val Lys Gly Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile
 465 470 475 480
 Leu His Asn Lys Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His
 485 490 495
 Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser
 500 505 510
 Leu Asn Ile Leu Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu
 515 520 525
 Asp Arg Phe Val Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln
 530 535 540
 Leu Thr Thr Thr Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly
 545 550 555 560
 Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser
 565 570 575
 Thr Glu Tyr Pro His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly
 580 585 590
 Asp His Lys Ala Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser
 595 600 605
 Lys Glu Gln Ala Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser
 610 615 620
 Trp Met Asp Asp Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe

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<210> 113
<211> 3429
<212> DNA
<213> Homo Sapiens
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-80-

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<210> 114

<211> 906

<212> PRT

<213> Homo Sapiens

<400> 114

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Met Thr Ala Val His Ala Gly Asn Ile Asn Phe Lys Trp Asp Pro Lys
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20           25           30
Val Thr Gln Val Thr Thr Leu Val Asn Thr Asn Ser Lys Gly Pro Ser
35           40           45
Asn Lys Lys Arg Gly Arg Ser Lys Lys Ala His Val Leu Ala Ala Ser
50           55           60
Val Glu Gln Ala Thr Glu Asn Phe Leu Glu Lys Gly Asp Lys Ile Ala
65           70           75           80
Lys Glu Ser Gln Phe Leu Lys Glu Glu Leu Val Ala Ala Val Glu Asp

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Ala Leu Gln Glu Lys Asp Val Asp Gly Leu Asp Arg Thr Ala Gly Ala
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 Ile Arg Gly Arg Ala Ala Arg Val Ile His Val Val Thr Ser Glu Met
 545 550 555 560
 Asp Asn Tyr Glu Pro Gly Val Tyr Thr Glu Lys Val Leu Glu Ala Thr
 565 570 575
 Lys Leu Leu Ser Asn Thr Val Met Pro Arg Phe Thr Glu Gln Val Glu
 580 585 590
 Ala Ala Val Glu Ala Leu Ser Ser Asp Pro Ala Gln Pro Met Asp Glu
 595 600 605
 Asn Glu Phe Ile Asp Ala Ser Arg Leu Val Tyr Asp Gly Ile Arg Asp
 610 615 620
 Ile Arg Lys Ala Val Leu Met Ile Arg Thr Pro Glu Glu Leu Asp Asp
 625 630 635 640
 Ser Asp Phe Glu Thr Glu Asp Phe Asp Val Arg Ser Arg Thr Ser Val
 645 650 655
 Gln Thr Glu Asp Asp Gln Leu Ile Ala Gly Gln Ser Ala Arg Ala Ile
 660 665 670
 Met Ala Gln Leu Pro Gln Glu Gln Lys Ala Lys Ile Ala Glu Gln Val
 675 680 685
 Ala Ser Phe Gln Glu Glu Lys Ser Lys Leu Asp Ala Glu Val Ser Lys
 690 695 700
 Trp Asp Asp Ser Gly Asn Asp Ile Ile Val Leu Ala Lys Gln Met Cys
 705 710 715 720
 Met Ile Met Met Glu Met Thr Asp Phe Thr Arg Gly Lys Gly Pro Leu
 725 730 735
 Lys Asn Thr Ser Asp Val Ile Ser Ala Ala Lys Lys Ile Ala Glu Ala
 740 745 750
 Gly Ser Arg Met Asp Lys Leu Gly Arg Thr Ile Ala Asp His Cys Pro
 755 760 765
 Asp Ser Ala Cys Lys Gln Asp Leu Leu Ala Tyr Leu Gln Arg Ile Ala
 770 775 780
 Leu Tyr Cys His Gln Leu Asn Ile Cys Ser Lys Val Lys Ala Glu Val
 785 790 795 800
 Gln Asn Leu Gly Gly Glu Leu Val Val Ser Gly Val Asp Ser Ala Met
 805 810 815
 Ser Leu Ile Gln Ala Ala Lys Asn Leu Met Asn Ala Val Val Gln Thr
 820 825 830
 Val Lys Ala Ser Tyr Val Ala Ser Thr Lys Tyr Gln Lys Ser Gln Gly
 835 840 845
 Met Ala Ser Leu Asn Leu Pro Ala Val Ser Trp Lys Met Lys Ala Pro
 850 855 860
 Glu Lys Lys Pro Leu Val Lys Arg Glu Lys Gln Asp Glu Thr Gln Thr
 865 870 875 880
 Lys Ile Lys Arg Ala Ser Gln Lys Lys His Val Asn Pro Val Gln Ala
 885 890 895
 Leu Ser Glu Phe Lys Ala Met Asp Ser Ile
 900 905

<210> 115

<211> 1701

<212> DNA

<213> Homo Sapiens

<400> 115

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cctgataaga atcccaaaat gcaggagaca aactttaaag aaataagttt tgcatatgaa 180
gtactatcaa atcctgagaa gcgtgagtta tatgacagat acggagagca aggtcttcgg 240
gaaggcagcg gcggaggtgg gtggcatgga ttgatatttt ctctcacctg tttttgtggg 300
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gacatgatgc atccactcaa agtatcttta gaagatctgt ataatggcaa gacaaccaa 420
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gtaattaatg aaaaagaccg ctgtaaaaaa tgtgaaggga agaaggtgat taaagaagtc 660
aagattcttg aagtcacagt agacaaaggc atgaacatg gacagagaat tacattcact 720
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cctttcacac atggattatt ataagtttca atcctgggat ctgtgcttga tttttatcag 1560
ttttgtgtag atttttatgt ttcataatttt aaatttaaat cccacattgt aaagtttgta 1620
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agaatttcat agcctgtaaa a 1701

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<210> 116

<211> 415

<212> PRF

<213> Homo Sapiens

<400> 116

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Met Ala Asn Val Ala Asp Thr Lys Leu Tyr Asp Ile Leu Gly Val Pro
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Ala Gly Ala Ser Glu Asn Glu Leu Lys Lys Ala Tyr Arg Lys Leu Ala
 20             25             30
Lys Glu Tyr His Pro Asp Lys Asn Pro Gln Met Gln Glu Thr Asn Phe
 35             40             45
Lys Glu Ile Ser Phe Ala Tyr Glu Val Leu Ser Asn Pro Glu Lys Arg
 50             55             60
Glu Leu Tyr Asp Arg Tyr Gly Glu Gln Gly Leu Arg Glu Gly Ser Gly
 65             70             75             80
Gly Gly Gly Trp His Gly Leu Ile Phe Ser Leu Thr Val Phe Cys Gly
 85             90             95
Gly Leu Phe Gly Phe Met Gly Asn Gln Ser Arg Ser Arg Asn Gly Arg
100            105            110
Arg Arg Gly Glu Asp Met Met His Pro Leu Lys Val Ser Leu Glu Asp
115            120            125
Leu Tyr Asn Gly Lys Thr Thr Lys Leu Gln Leu Ser Lys Asn Val Leu
130            135            140
Cys Ser Ala Cys Ser Gly Gln Gly Gly Lys Ser Gly Ala Val Gln Lys

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145 150 155 160
 Cys Ser Ala Cys Arg Gly Arg Gly Val Arg Ile Met Ile Arg Gln Leu
 165 170 175
 Ala Pro Gly Met Val Gln Gln Met Gln Ser Val Cys Ser Asp Cys Asn
 180 185 190
 Gly Glu Gly Glu Val Ile Asn Glu Lys Asp Arg Cys Lys Lys Cys Glu
 195 200 205
 Gly Lys Lys Val Ile Lys Glu Val Lys Ile Leu Glu Val His Val Asp
 210 215 220
 Lys Gly Met Lys His Gly Gln Arg Ile Thr Phe Thr Gly Glu Ala Asp
 225 230 235 240
 Gln Ala Pro Glu Trp Asn Pro Glu Thr Leu Phe Phe Leu Leu Pro Gly
 245 250 255
 Glu Lys Asn Met Glu Val Phe Gln Arg Asp Gly Asn Asp Leu His Met
 260 265 270
 Thr Tyr Lys Ile Gly Leu Val Glu Ala Leu Cys Gly Phe Gln Phe Thr
 275 280 285
 Leu Ser His Leu Asp Gly Arg Gln Ile Val Val Lys Tyr Pro Pro Gly
 290 295 300
 Lys Val Ile Glu Pro Gly Cys Val Arg Val Val Arg Gly Glu Gly Met
 305 310 315 320
 Pro Gln Tyr Arg Asn Pro Phe Glu Lys Gly Gly Leu Tyr Ile Lys Phe
 325 330 335
 Asp Val Gln Phe Pro Glu Asn Asn Trp Ile Asn Pro Asp Lys Leu Ser
 340 345 350
 Glu Leu Glu Asp Leu Leu Pro Ser Arg Pro Glu Val Pro Asn Ile Ile
 355 360 365
 Gly Glu Thr Glu Glu Val Glu Leu Gln Glu Phe Asp Ser Thr Arg Gly
 370 375 380
 Ser Gly Gly Gly Gln Arg Arg Glu Ala Tyr Asn Asp Ser Ser Asp Glu
 385 390 395 400
 Glu Ser Ser Ser His His Gly Pro Gly Val Gln Cys Ala His Gln
 405 410 415

<210> 117

<211> 1821

<212> DNA

<213> Homo Sapiens

<400> 117

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 aaacatacaa gcttgcaagg agcttgccca aaccactcgt acagcatatg gaccaaagg 180
 aatgaacaaa atgggttatca accacttgga gaagttgttt gtgacaaacg atgcagcaac 240
 tattttaaga gaactagaag tacagcatcc tgctgcaaaa atgattgtaa tggcttctca 300
 tatgcaagag caagaagttg gagatggcac aaactttgtt ctggtatttg ctggagctct 360
 cctggaatta gctgaagaac ttctgaggat tggcctgtca gtttcagagg tcatagaagg 420
 ttatgaaata gcctgcagaa aagctcatga gattcttcct aatttggtat gttgttctgc 480
 aaaaaacctt cgagatattg atgaagtctc atctctactt cgtacctcca taatgagtaa 540
 acaatatggt aatgaagtat ttctggccaa gcttattgct caggcatgcg tatctatttt 600
 tcttgattcc ggccatttca atgttgataa catcagagtt tgtaaaattc tgggctctgg 660
 tatcagttcc tcttcagtat tgcattggcat gggttttaag aaggaaaccg aaggatgatg 720
 aacatctgtc aaagatgcaa aaatagcagt gtactcttgt ccttttgatg gcatgataac 780
 agaaactaag ggaacagtgt tgataaagac tgctgaagaa ttgatgaatt ttagtaaggg 840
 agaagaaaac ctcattggatg cacaagtcaa agctattgct gatactgggtg caaatgtcgt 900

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gttagtgagg ctaaactcaa aatgggatct ccgaagactt tgtaaaactg ttggtgctac      1020
agctcttcct agattgacac ctcctgtcct tgaagaaatg ggacactgtg acagtgttta      1080
cctctcagaa gttggagata ctcagggtgtt ggtttttaag catgaaaagg aagatggcgc      1140
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agtagacgat ggtgttaata ctttcaaagt tcttacaagg gataaacgtc ttgtaccggg      1260
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tggacttgaa cagtatgcta ttaagaagtt tgctgaggca tttgaagcta ttccccgcgc      1380
actggcagaa aactctggag ttaaggccaa tgaagtaatc tctaaacttt atgcagtaca      1440
tcaagaagga aataaaaacg ttggattaga tattgaggct gaagtccctg ctgtaaagga      1500
catgctggaa gctggtattc tagatactta cctgggaaaa tattgggcta tcaaactcgc      1560
tactaatgct gcagtcactg tacttagagt ggatcagatc atcatggcaa aaccagctgg      1620
tgggcccaag cctccaagtg ggaagaaaga ctgggatgat gacaaaaatg attgaaattg      1680
gcttaatttt tactgtaggt gaaggctgta tttgtagtag tactcaagaa tcacctgatg      1740
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aataaacata ttgttactgt c                                     1821

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<210> 118

<211> 548

<212> PRT

<213> Homo Sapiens

<400> 118

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Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala Gln Met Leu Lys
 1          5          10          15
Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn
 20          25          30
Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly
 35          40          45
Pro Lys Gly Met Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe
 50          55          60
Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His
 65          70          75          80
Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu
 85          90          95
Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu
100          105          110
Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val
115          120          125
Ile Glu Gly Tyr Glu Ile Ala Cys Arg Lys Ala His Glu Ile Leu Pro
130          135          140
Asn Leu Val Cys Cys Ser Ala Lys Asn Leu Arg Asp Ile Asp Glu Val
145          150          155          160
Ser Ser Leu Leu Arg Thr Ser Ile Met Ser Lys Gln Tyr Gly Asn Glu
165          170          175
Val Phe Leu Ala Lys Leu Ile Ala Gln Ala Cys Val Ser Ile Phe Pro
180          185          190
Asp Ser Gly His Phe Asn Val Asp Asn Ile Arg Val Cys Lys Ile Leu
195          200          205
Gly Ser Gly Ile Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys
210          215          220
Lys Glu Thr Glu Gly Asp Val Thr Ser Val Lys Asp Ala Lys Ile Ala
225          230          235          240
Val Tyr Ser Cys Pro Phe Asp Gly Met Ile Thr Glu Thr Lys Gly Thr
245          250          255

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Val Leu Ile Lys Thr Ala Glu Glu Leu Met Asn Phe Ser Lys Gly Glu
 260 265 270
 Glu Asn Leu Met Asp Ala Gln Val Lys Ala Ile Ala Asp Thr Gly Ala
 275 280 285
 Asn Val Val Val Thr Gly Gly Lys Val Ala Asp Met Ala Leu His Tyr
 290 295 300
 Ala Asn Lys Tyr Asn Ile Met Leu Val Arg Leu Asn Ser Lys Trp Asp
 305 310 315 320
 Leu Arg Arg Leu Cys Lys Thr Val Gly Ala Thr Ala Leu Pro Arg Leu
 325 330 335
 Thr Pro Pro Val Leu Glu Glu Met Gly His Cys Asp Ser Val Tyr Leu
 340 345 350
 Ser Glu Val Gly Asp Thr Gln Val Val Val Phe Lys His Glu Lys Glu
 355 360 365
 Asp Gly Ala Ile Ser Thr Ile Val Leu Arg Gly Ser Thr Asp Asn Leu
 370 375 380
 Met Asp Asp Ile Glu Arg Val Val Asp Asp Gly Val Asn Thr Phe Lys
 385 390 395 400
 Val Leu Thr Arg Asp Lys Arg Leu Val Pro Gly Gly Gly Ala Thr Glu
 405 410 415
 Ile Glu Leu Ala Lys Gln Ile Thr Ser Tyr Gly Glu Thr Cys Pro Gly
 420 425 430
 Leu Glu Gln Tyr Ala Ile Lys Lys Phe Ala Glu Ala Phe Glu Ala Ile
 435 440 445
 Pro Arg Ala Leu Ala Glu Asn Ser Gly Val Lys Ala Asn Glu Val Ile
 450 455 460
 Ser Lys Leu Tyr Ala Val His Gln Glu Gly Asn Lys Asn Val Gly Leu
 465 470 475 480
 Asp Ile Glu Ala Glu Val Pro Ala Val Lys Asp Met Leu Glu Ala Gly
 485 490 495
 Ile Leu Asp Thr Tyr Leu Gly Lys Tyr Trp Ala Ile Lys Leu Ala Thr
 500 505 510
 Asn Ala Ala Val Thr Val Leu Arg Val Asp Gln Ile Ile Met Ala Lys
 515 520 525
 Pro Ala Gly Gly Pro Lys Pro Pro Ser Gly Lys Lys Asp Trp Asp Asp
 530 535 540
 Asp Gln Asn Asp
 545

<210> 119
 <211> 1321
 <212> DNA
 <213> Homo Sapiens

<400> 119
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 tccaggagaa ggtgttcaag ggcttggacc tccttgagaa ggctgccgaa atgttatcgc 180
 agctcgactt gttcagccga aatgaagatt tggaagagat tgcttccacc gacctgaagt 240
 accttttggg gccagcgttt caaggagccc tcaccatgaa acaagtcaac cccagcaagc 300
 gtctagatca tttgcagcgg gctcgagaac actttataaa ctacttaact cagtgccatt 360
 gctatcatgt ggcagagttt gagctgcccc aaaccatgaa caactctgct gaaaatcaca 420
 ctgccaatc ctccatggct taccctagtc tcgttgctat ggcatctcaa agacaggcta 480
 aaatacagag atacaagcag aagaaggagt tggagcatag gttgtctgca atgaaatctg 540
 ctgtggaaag tggatcaagca gatgatgagc gtgttcgtga atattatctt cttcaccttc 600

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tgagagaaaag agactcttca agagaggcat caacttctaa ctcattctgc caggagaggc 720
ctccagtga acccttcatt ctactcggga acatgggtca agccaaagta tttggagctg 780
gttatccaag tctgccaact atgacggtga gtgactggta tgagcaacat cggaaatatg 840
gagcattacc ggatcagggg atagccaagg cagcaccaga ggaattcaga aaagcagctc 900
agcaacagga agaacaagaa gaaaaggagg aagaggatga tgaacaaaca ctccacagag 960
ccggggagtg ggatgactgg aaggacacc atcctagggg ctatgggaac cgacagaaca 1020
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gctaaatctt gctttgcatt cagtaaagt tcaagtgtat aagtgtgtat ttgtacccta 1200
gatgatatga accagcagtc ttgttttggc atcatcctca tcatgttgta ttccagcttc 1260
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c 1321

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<210> 120

<211> 339

<212> PRT

<213> Homo Sapiens

<400> 120

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Met Ala Ala Glu Asp Glu Leu Gln Leu Pro Arg Leu Pro Glu Leu Phe
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Glu Thr Gly Arg Gln Leu Leu Asp Glu Val Glu Val Ala Thr Glu Pro
20     25     30
Ala Gly Ser Arg Ile Val Gln Glu Lys Val Phe Lys Gly Leu Asp Leu
35     40     45
Leu Glu Lys Ala Ala Glu Met Leu Ser Gln Leu Asp Leu Phe Ser Arg
50     55     60
Asn Glu Asp Leu Glu Glu Ile Ala Ser Thr Asp Leu Lys Tyr Leu Leu
65     70     75     80
Val Pro Ala Phe Gln Gly Ala Leu Thr Met Lys Gln Val Asn Pro Ser
85     90     95
Lys Arg Leu Asp His Leu Gln Arg Ala Arg Glu His Phe Ile Asn Tyr
100    105    110
Leu Thr Gln Cys His Cys Tyr His Val Ala Glu Phe Glu Leu Pro Lys
115    120    125
Thr Met Asn Asn Ser Ala Glu Asn His Thr Ala Asn Ser Ser Met Ala
130    135    140
Tyr Pro Ser Leu Val Ala Met Ala Ser Gln Arg Gln Ala Lys Ile Gln
145    150    155    160
Arg Tyr Lys Gln Lys Lys Glu Leu Glu His Arg Leu Ser Ala Met Lys
165    170    175
Ser Ala Val Glu Ser Gly Gln Ala Asp Asp Glu Arg Val Arg Glu Tyr
180    185    190
Tyr Leu Leu His Leu Gln Arg Trp Ile Asp Ile Ser Leu Glu Glu Ile
195    200    205
Glu Ser Ile Asp Gln Glu Ile Lys Ile Leu Arg Glu Arg Asp Ser Ser
210    215    220
Arg Glu Ala Ser Thr Ser Asn Ser Ser Arg Gln Glu Arg Pro Pro Val
225    230    235    240
Lys Pro Phe Ile Leu Thr Arg Asn Met Ala Gln Ala Lys Val Phe Gly
245    250    255
Ala Gly Tyr Pro Ser Leu Pro Thr Met Thr Val Ser Asp Trp Tyr Glu
260    265    270
Gln His Arg Lys Tyr Gly Ala Leu Pro Asp Gln Gly Ile Ala Lys Ala

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gttatccaag tctgccaact atgacggtga gtgactggta tgagcaacat cggaaatatg 840
gagcattacc ggatcaggga atagccaagg cagcaccaga ggaattcaga aaagcagctc 900
agcaacagga agaacaagaa gaaaaggagg aagaggatga tgaacaaca ctccacagag 960
cccgaggatg ggatgactgg aaggacaccc atcctagggg ctatgggaac cgacagaaca 1020
tgggctgata tttccacaac accacaggac tgcagggtgc acaactccct gccaaaggaa 1080
accatgcagt cctcccctcc ctgggtctcct gcttcagctc tgtacaacga gggcaaagat 1140
gctaaatctt gctttgcatt cagtaaagtg tcaagtgatt aagtgtgtat ttgtacccta 1200
gatgatatga accagcagtc ttgttttggc atcatcctca tcatgttgta ttccagcttc 1260
ttaagtggaa ggaaaagagt gctgagaaat ggctctgtat aatctatggc tatccgaatt 1320
c 1321

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<210> 120

<211> 339

<212> PRT

<213> Homo Sapiens

<400> 120

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Met Ala Ala Glu Asp Glu Leu Gln Leu Pro Arg Leu Pro Glu Leu Phe
 1          5          10          15
Glu Thr Gly Arg Gln Leu Leu Asp Glu Val Glu Val Ala Thr Glu Pro
 20          25          30
Ala Gly Ser Arg Ile Val Gln Glu Lys Val Phe Lys Gly Leu Asp Leu
 35          40          45
Leu Glu Lys Ala Ala Glu Met Leu Ser Gln Leu Asp Leu Phe Ser Arg
 50          55          60
Asn Glu Asp Leu Glu Glu Ile Ala Ser Thr Asp Leu Lys Tyr Leu Leu
 65          70          75          80
Val Pro Ala Phe Gln Gly Ala Leu Thr Met Lys Gln Val Asn Pro Ser
 85          90          95
Lys Arg Leu Asp His Leu Gln Arg Ala Arg Glu His Phe Ile Asn Tyr
100          105          110
Leu Thr Gln Cys His Cys Tyr His Val Ala Glu Phe Glu Leu Pro Lys
115          120          125
Thr Met Asn Asn Ser Ala Glu Asn His Thr Ala Asn Ser Ser Met Ala
130          135          140
Tyr Pro Ser Leu Val Ala Met Ala Ser Gln Arg Gln Ala Lys Ile Gln
145          150          155          160
Arg Tyr Lys Gln Lys Lys Glu Leu Glu His Arg Leu Ser Ala Met Lys
165          170          175
Ser Ala Val Glu Ser Gly Gln Ala Asp Asp Glu Arg Val Arg Glu Tyr
180          185          190
Tyr Leu Leu His Leu Gln Arg Trp Ile Asp Ile Ser Leu Glu Glu Ile
195          200          205
Glu Ser Ile Asp Gln Glu Ile Lys Ile Leu Arg Glu Arg Asp Ser Ser
210          215          220
Arg Glu Ala Ser Thr Ser Asn Ser Ser Arg Gln Glu Arg Pro Pro Val
225          230          235          240
Lys Pro Phe Ile Leu Thr Arg Asn Met Ala Gln Ala Lys Val Phe Gly
245          250          255
Ala Gly Tyr Pro Ser Leu Pro Thr Met Thr Val Ser Asp Trp Tyr Glu
260          265          270
Gln His Arg Lys Tyr Gly Ala Leu Pro Asp Gln Gly Ile Ala Lys Ala

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<210> 121
<211> 2965
<212> DNA
<213> Homo Sapiens
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-89-

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<210> 122
 <211> 862
 <212> PRT
 <213> Homo Sapiens

<400> 122

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Met Ala Gln Pro Gly Pro Ala Ser Gln Pro Asp Val Ser Leu Gln Gln
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Arg Val Ala Glu Leu Glu Lys Ile Asn Ala Glu Phe Leu Arg Ala Gln
      20          25          30
Gln Gln Leu Glu Gln Glu Phe Asn Gln Lys Arg Ala Lys Phe Lys Glu
      35          40          45
Leu Tyr Leu Ala Lys Glu Glu Asp Leu Lys Arg Gln Asn Ala Val Leu
      50          55          60
Gln Ala Ala Gln Asp Asp Leu Gly His Leu Arg Thr Gln Leu Trp Glu
      65          70          75          80
Ala Gln Ala Glu Met Glu Asn Ile Lys Ala Ile Ala Thr Val Ser Glu
      85          90          95
Asn Thr Lys Gln Glu Ala Ile Asp Glu Val Lys Arg Gln Trp Arg Glu
      100         105         110
Glu Val Ala Ser Leu Gln Ala Val Met Lys Glu Thr Val Arg Asp Tyr
      115         120         125
Glu His Gln Phe His Leu Arg Leu Glu Gln Glu Arg Thr Gln Trp Ala
      130         135         140
Gln Tyr Arg Glu Tyr Ala Glu Arg Glu Ile Ala Asp Leu Arg Arg Arg
      145         150         155         160
Leu Ser Glu Gly Gln Glu Glu Glu Asn Leu Glu Asn Glu Met Lys Lys
      165         170         175
Ala Gln Glu Asp Ala Glu Lys Leu Arg Ser Val Val Met Pro Met Glu
      180         185         190
Lys Glu Ile Ala Ala Leu Lys Asp Lys Leu Thr Glu Ala Glu Asp Lys
      195         200         205
Ile Lys Glu Leu Glu Ala Ser Lys Val Lys Glu Leu Asn His Tyr Leu
      210         215         220
Glu Ala Glu Lys Ser Cys Arg Thr Asp Leu Glu Met Tyr Val Ala Val
      225         230         235         240
Leu Asn Thr Gln Lys Ser Val Leu Gln Glu Asp Ala Glu Lys Leu Arg
      245         250         255
Lys Glu Leu His Glu Val Cys His Leu Leu Glu Gln Glu Arg Gln Gln
      260         265         270
His Asn Gln Leu Lys His Thr Trp Gln Lys Ala Asn Asp Gln Phe Leu
      275         280         285
Glu Ser Gln Arg Leu Leu Met Arg Asp Met Gln Arg Met Glu Ile Val

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290 295 300
 Leu Thr Ser Glu Gln Leu Arg Gln Val Glu Glu Leu Lys Lys Lys Asp
 305 310 315 320
 Gln Glu Asp Asp Glu Gln Gln Arg Leu Asn Lys Arg Lys Asp His Lys
 325 330 335
 Lys Ala Asp Val Glu Glu Glu Ile Lys Ile Pro Val Val Cys Ala Leu
 340 345 350
 Thr Gln Glu Glu Ser Ser Ala Gln Leu Ser Asn Glu Glu Glu His Leu
 355 360 365
 Asp Ser Thr Arg Gly Ser Val His Ser Leu Asp Ala Gly Leu Leu Leu
 370 375 380
 Pro Ser Gly Asp Pro Phe Ser Lys Ser Asp Asn Asp Met Phe Lys Asp
 385 390 395 400
 Gly Leu Arg Arg Ala Gln Ser Thr Asp Ser Leu Gly Thr Ser Gly Ser
 405 410 415
 Leu Gln Ser Lys Ala Leu Gly Tyr Asn Tyr Lys Ala Lys Ser Ala Gly
 420 425 430
 Asn Leu Asp Glu Ser Asp Phe Gly Pro Leu Val Gly Ala Asp Ser Val
 435 440 445
 Ser Glu Asn Phe Asp Thr Ala Ser Leu Gly Ser Leu Gln Met Pro Ser
 450 455 460
 Gly Phe Met Leu Thr Lys Asp Gln Glu Arg Ala Ile Lys Ala Met Thr
 465 470 475 480
 Pro Glu Gln Glu Glu Thr Ala Ser Leu Leu Ser Ser Val Thr Gln Gly
 485 490 495
 Met Glu Ser Ala Tyr Val Ser Pro Ser Gly Tyr Arg Leu Val Ser Glu
 500 505 510
 Thr Glu Trp Asn Leu Leu Gln Lys Glu Val His Asn Ala Gly Asn Lys
 515 520 525
 Leu Gly Arg Arg Cys Asp Met Cys Ser Asn Tyr Glu Lys Gln Leu Gln
 530 535 540
 Gly Ile Gln Ile Gln Glu Ala Glu Thr Arg Asp Gln Val Lys Lys Leu
 545 550 555 560
 Gln Leu Met Leu Arg Gln Ala Asn Asp Gln Leu Glu Lys Thr Met Lys
 565 570 575
 Asp Lys Gln Glu Leu Glu Asp Phe Ile Lys Gln Ser Ser Glu Asp Ser
 580 585 590
 Ser His Gln Ile Ser Ala Leu Val Leu Arg Ala Gln Ala Ser Glu Ile
 595 600 605
 Leu Leu Glu Glu Leu Gln Gln Gly Leu Ser Gln Ala Lys Arg Asp Val
 610 615 620
 Gln Glu Gln Met Ala Val Leu Met Gln Ser Arg Glu Gln Val Ser Glu
 625 630 635 640
 Glu Leu Val Arg Leu Gln Lys Asp Asn Asp Ser Leu Gln Gly Lys His
 645 650 655
 Ser Leu His Val Ser Leu Gln Gln Ala Glu Asp Phe Ile Leu Pro Asp
 660 665 670
 Thr Thr Glu Ala Leu Arg Glu Leu Val Leu Lys Tyr Arg Glu Asp Ile
 675 680 685
 Ile Asn Val Arg Thr Ala Ala Asp His Val Glu Glu Lys Leu Lys Ala
 690 695 700
 Glu Ile Leu Phe Leu Lys Glu Gln Ile Gln Ala Glu Gln Cys Leu Lys
 705 710 715 720
 Glu Asn Leu Glu Glu Thr Leu Gln Leu Glu Ile Glu Asn Cys Lys Glu
 725 730 735

Glu Ile Ala Ser Ile Ser Ser Leu Lys Ala Glu Leu Glu Arg Ile Lys
 740 745 750
 Val Glu Lys Gly Gln Leu Glu Ser Thr Leu Arg Glu Lys Ser Gln Gln
 755 760 765
 Leu Glu Ser Leu Gln Glu Ile Lys Ile Ser Leu Glu Glu Gln Leu Lys
 770 775 780
 Lys Glu Thr Ala Ala Lys Ala Thr Val Glu Gln Leu Met Phe Glu Glu
 785 790 795 800
 Lys Asn Lys Ala Gln Arg Leu Gln Thr Glu Leu Asp Val Ser Glu Gln
 805 810 815
 Val Gln Arg Asp Phe Val Lys Leu Ser Gln Thr Leu Gln Val Gln Leu
 820 825 830
 Glu Arg Ile Arg Gln Ala Asp Ser Leu Glu Arg Ile Arg Ala Ile Leu
 835 840 845
 Asn Asp Thr Lys Leu Thr Asp Ile Asn Gln Leu Pro Glu Thr
 850 855 860

<210> 123
 <211> 544
 <212> DNA
 <213> Homo Sapiens

<400> 123
 gggagtggcg tggcgcaggg atggcacaaa agaaatatct tcaagcaaaa ttgaccaggt 60
 ttttaaggga agacaggatt caacttttga aacctccata tacagatgaa aataaaaaag 120
 ttggtttggc attaaaggac cttgctaagc agtactctga cagactagaa tgctgtgaaa 180
 atgaagtaga aaaggttaata gaagaaatac gttgcaaggc aattgagcgt ggaacaggaa 240
 atgacaatta tagaacaacg ggaattgcta caatcgagggt gtttttacca ccaagactaa 300
 aaaaagatag gaaaaacttg ttggagaccc gattgcacat cactggcaga gaactgaggt 360
 ccaaaatagc tgaaaccttt ggacttcaag aanattatat caaaattgtc ataaataaga 420
 agcaactacn actagggaaa acccttgaag ancaaggcgt ggctcacaat gtgaaagcga 480
 tgggtgcttga actaaaacaa tctgaagagg acgcgaggaa aaacttccag ttagaggaag 540
 agga 544

<210> 124
 <211> 178
 <212> PRT
 <213> Homo Sapiens

<400> 124
 Glu Trp Arg Gly Ala Gly Met Ala Gln Lys Lys Tyr Leu Gln Ala Lys
 1 5 10 15
 Leu Thr Gln Phe Leu Arg Glu Asp Arg Ile Gln Leu Trp Lys Pro Pro
 20 25 30
 Tyr Thr Asp Glu Asn Lys Lys Val Gly Leu Ala Leu Lys Asp Leu Ala
 35 40 45
 Lys Gln Tyr Ser Asp Arg Leu Glu Cys Cys Glu Asn Glu Val Glu Lys
 50 55 60
 Val Ile Glu Glu Ile Arg Cys Lys Ala Ile Glu Arg Gly Thr Gly Asn
 65 70 75 80
 Asp Asn Tyr Arg Thr Thr Gly Ile Ala Thr Ile Glu Val Phe Leu Pro
 85 90 95
 Pro Arg Leu Lys Lys Asp Arg Lys Asn Leu Leu Glu Thr Arg Leu His
 100 105 110
 Ile Thr Gly Arg Glu Leu Arg Ser Lys Ile Ala Glu Thr Phe Gly Leu

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      115      120      125
Gln Glu Tyr Ile Lys Ile Val Ile Asn Lys Lys Gln Leu Leu Gly Lys
      130      135      140
Thr Leu Glu Gln Gly Val Ala His Asn Val Lys Ala Met Val Leu Glu
145      150      155      160
Leu Lys Gln Ser Glu Glu Asp Ala Arg Lys Asn Phe Gln Leu Glu Glu
      165      170      175
Glu Glu

```

<210> 125
 <211> 1302
 <212> DNA
 <213> Homo Sapiens

```

<400> 125
atggagggtgg tggacccgca gcagctgggc atgttcacgg agggcgagct gatgtcggtg      60
ggtatggaca cggtcatcca ccgcacgcac tccaccgagg tcatctacca gccgcgccgc      120
aagcggggcca agctcatcgg caagtacctg atgggggacc tgctggggga aggtctcttac      180
ggcaagggtga aggaggtgct ggactcggag acgctgtgca ggagggccgt caagatcctc      240
aagaagaaga agttgcgaag gatccccaac ggggaggcca acgtgaagaa ggaaattcaa      300
ctactgagga ggttacggca caaaaatgtc atccagctgg tggatgtgtt atacaacgaa      360
gagaagcaga aaatgtatat ggtgatggag tactgcgtgt gtggcatgca ggaaatgctg      420
gacagcgtgc cggagaagcg tttcccagtg tgccaggccc acgggtactt ctgtcagctg      480
attgacggcc tggagtagct gcatagccag ggcatgtgtg acaaggacat caagccgggg      540
aacctgctgc tcaccaccgg tggcaccttc aaaatctccg acctgggcgt ggccgaggca      600
ctgcaccogt tcgcggcgga cgacacctgc cggaccagcc agggctcccc ggctttccag      660
ccgcccagaga ttgccaacgg cctggacacc ttctccggct tcaaggtgga catctggtcg      720
gctgggggtca ccctctacaa catcaccacg ggtctgtacc ccttcgaagg ggacaacatc      780
tacaagttgt ttgagaacat cgggaagggg agctacgcca tcccgggcga ctgtggcccc      840
ccgctctctg acctgctgaa agggatgctt gactacgaac cggccaagag gttctccatc      900
cggcagatcc ggcagcacag ctgggttccg aagaacatc ctccggctga agcaccagtg      960
cccatcccac cgagcccaga caccaaggac cggtgggcga gcatgactgt ggtgccgtac      1020
ttggaggacc tgacggcgcc ggacgaggac gaggacctct tcgacatcga ggatgacatc      1080
atctacactc aggacttcac ggtgcccgga caggctccag aagaggaggc cagtcacaat      1140
ggacagcgcc ggggcctccc caaggccgtg tgatatgaac gcacagaggc ggcgcagctg      1200
agcaccaaat ccaggggcga gggccgggcc cccaacctg cccgcaaggc ctgctccgcc      1260
agcagcaaga tccgccggct gtcggcctgc aagcagcagt ga      1302

```

<210> 126
 <211> 433
 <212> PRT
 <213> Homo Sapiens

```

<400> 126
Met Glu Val Val Asp Pro Gln Gln Leu Gly Met Phe Thr Glu Gly Glu
 1      5      10      15
Leu Met Ser Val Gly Met Asp Thr Phe Ile His Arg Ile Asp Ser Thr
      20      25      30
Glu Val Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys
      35      40      45
Tyr Leu Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys
      50      55      60
Glu Val Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu
65      70      75      80

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Lys Lys Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys
 85 90 95
 Lys Glu Ile Gln Leu Leu Arg Arg Leu Arg His Lys Asn Val Ile Gln
 100 105 110
 Leu Val Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val
 115 120 125
 Met Glu Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro
 130 135 140
 Glu Lys Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Cys Gln Leu
 145 150 155 160
 Ile Asp Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp
 165 170 175
 Ile Lys Pro Gly Asn Leu Leu Leu Thr Thr Gly Gly Thr Leu Lys Ile
 180 185 190
 Ser Asp Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Ala Asp Asp
 195 200 205
 Thr Cys Arg Thr Ser Gln Gly Ser Pro Ala Phe Gln Pro Pro Glu Ile
 210 215 220
 Ala Asn Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser
 225 230 235 240
 Ala Gly Val Thr Leu Tyr Asn Ile Thr Thr Gly Leu Tyr Pro Phe Glu
 245 250 255
 Gly Asp Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Lys Gly Ser Tyr
 260 265 270
 Ala Ile Pro Gly Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Lys Gly
 275 280 285
 Met Leu Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg
 290 295 300
 Gln His Ser Trp Phe Arg Lys Lys His Pro Pro Ala Glu Ala Pro Val
 305 310 315 320
 Pro Ile Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr
 325 330 335
 Val Val Pro Tyr Leu Glu Asp Leu His Gly Ala Asp Glu Asp Glu Asp
 340 345 350
 Leu Phe Asp Ile Glu Asp Asp Ile Ile Tyr Thr Gln Asp Phe Thr Val
 355 360 365
 Pro Gly Gln Val Pro Glu Glu Glu Ala Ser His Asn Gly Gln Arg Arg
 370 375 380
 Gly Leu Pro Lys Ala Val Cys Met Asn Gly Thr Glu Ala Ala Gln Leu
 385 390 395 400
 Ser Thr Lys Ser Arg Ala Glu Gly Arg Ala Pro Asn Pro Ala Arg Lys
 405 410 415
 Ala Cys Ser Ala Ser Ser Lys Ile Arg Arg Leu Ser Ala Cys Lys Gln
 420 425 430
 Gln

<210> 127

<211> 1488

<212> DNA

<213> Homo Sapiens

<400> 127

gaggggcccgg gcggtgccgg caagatggct gcgcccagaga agatgacgtt tcccagagaaa
 ccaagccaca aaaagtacag ggccgcctg aagaaggaga aacgaaagaa acgtcggcag

60

120

```

gaacttgctc gactgagaga ctcaggactc tcacagaagg aggaagagga ggacactttt 180
attgaagaac aacaactaga agaagagaag ctattggaaa gagagaggca aagattacat 240
gaggagtggg tgctaagaga gcagaaggca caagaagaat tcagaataaa gaaggaaaag 300
gaagaggcgg ctaaaaaacg gcaagaagaa caagagagaa agttaagga acaatgggaa 360
gaacagcaga ggaaagagag agaagaggag gagcagaaac gacaggagaa gaaagaaaaa 420
gaggaagctt tgcagaagat gctggatcag gctgaaaatg agttggaaaa tgggtaccaca 480
tggcaaaacc cagaaccacc cgtggatttc agagtaatgg agaaggatcg agctaattgt 540
cccttctaca gtaaaacagg agcttgcaga tttggagata gatgttcacg taaacataat 600
ttcccaacat ccagtcctac ccttcttatt aagagcatgt ttacgacgtt tggaatggag 660
cagtgcagga gggatgacta tgaccctgac gcaagcctgg agtacagcga ggaagaaacc 720
taccaacagt tcttagactt ctatgaggat gtgttgcccg agttcaagaa cgtggggaaa 780
gtgattcagt tcaaggtcag ctgcaatttg gaacctcacc tgagggggcaa tgtatatgtt 840
cagtaccagt cggaagaaga atgccaagca gccctttctc tgtttaacgg acgatgggat 900
gcaggacgac agctgcagtg tgaattctgc cccgtgaccc ggtggaaaat ggcgatttgt 960
ggtttatttg aaatacaaca atgtccaaga ggaaagcact gcaactttct tcatgtgttc 1020
agaaatccca acaatgaatt ctgggaagct aatagagaca tctacttgtc tccagatcgg 1080
actggctcct cctttgggaa gaactccgaa aggagggaga ggatggggca ccacgacgac 1140
tactacagca ggtgcggggg aaggagaaac cctagtccag accactccta caaaagaaat 1200
ggggaatccg agaggaaaaag tagtcgtcac agggggaaga aatctcaca acgcacatca 1260
aagagtcggg agaggcaciaa ttcacgaagc agaggaagaa atagggaccg cagcagggac 1320
cgcagccggg gccggggcag ccggagccgg agccggagcc ggagccgcag gagccgccgc 1380
agccggagcc aaagtctctc taggtcccga agtcgtggca ggaggaggtc gggtaataga 1440
gacagaactg ttcagagtcc caaatccaaa taaactagtt ttgttctt 1488

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<210> 128

<211> 482

<212> PRT

<213> Homo Sapiens

<400> 128

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Met Ala Ala Pro Glu Lys Met Thr Phe Pro Glu Lys Pro Ser His Lys
 1          5          10          15
Lys Tyr Arg Ala Ala Leu Lys Lys Glu Lys Arg Lys Lys Arg Arg Gln
          20          25          30
Glu Leu Ala Arg Leu Arg Asp Ser Gly Leu Ser Gln Lys Glu Glu Glu
          35          40          45
Glu Asp Thr Phe Ile Glu Glu Gln Gln Leu Glu Glu Glu Lys Leu Leu
          50          55          60
Glu Arg Glu Arg Gln Arg Leu His Glu Glu Trp Leu Leu Arg Glu Gln
          65          70          75          80
Lys Ala Gln Glu Glu Phe Arg Ile Lys Lys Glu Lys Glu Glu Ala Ala
          85          90          95
Lys Lys Arg Gln Glu Glu Gln Glu Arg Lys Leu Lys Glu Gln Trp Glu
          100          105          110
Glu Gln Gln Arg Lys Glu Arg Glu Glu Glu Gln Lys Arg Gln Glu
          115          120          125
Lys Lys Glu Lys Glu Glu Ala Leu Gln Lys Met Leu Asp Gln Ala Glu
          130          135          140
Asn Glu Leu Glu Asn Gly Thr Thr Trp Gln Asn Pro Glu Pro Pro Val
          145          150          155          160
Asp Phe Arg Val Met Glu Lys Asp Arg Ala Asn Cys Pro Phe Tyr Ser
          165          170          175
Lys Thr Gly Ala Cys Arg Phe Gly Asp Arg Cys Ser Arg Lys His Asn
          180          185          190
Phe Pro Thr Ser Ser Pro Thr Leu Leu Ile Lys Ser Met Phe Thr Thr

```

195 200 205
 Phe Gly Met Glu Gln Cys Arg Arg Asp Asp Tyr Asp Pro Asp Ala Ser
 210 215 220
 Leu Glu Tyr Ser Glu Glu Glu Thr Tyr Gln Gln Phe Leu Asp Phe Tyr
 225 230 235 240
 Glu Asp Val Leu Pro Glu Phe Lys Asn Val Gly Lys Val Ile Gln Phe
 245 250 255
 Lys Val Ser Cys Asn Leu Glu Pro His Leu Arg Gly Asn Val Tyr Val
 260 265 270
 Gln Tyr Gln Ser Glu Glu Glu Cys Gln Ala Ala Leu Ser Leu Phe Asn
 275 280 285
 Gly Arg Trp Tyr Ala Gly Arg Gln Leu Gln Cys Glu Phe Cys Pro Val
 290 295 300
 Thr Arg Trp Lys Met Ala Ile Cys Gly Leu Phe Glu Ile Gln Gln Cys
 305 310 315 320
 Pro Arg Gly Lys His Cys Asn Phe Leu His Val Phe Arg Asn Pro Asn
 325 330 335
 Asn Glu Phe Trp Glu Ala Asn Arg Asp Ile Tyr Leu Ser Pro Asp Arg
 340 345 350
 Thr Gly Ser Ser Phe Gly Lys Asn Ser Glu Arg Arg Glu Arg Met Gly
 355 360 365
 His His Asp Asp Tyr Tyr Ser Arg Leu Arg Gly Arg Arg Asn Pro Ser
 370 375 380
 Pro Asp His Ser Tyr Lys Arg Asn Gly Glu Ser Glu Arg Lys Ser Ser
 385 390 395 400
 Arg His Arg Gly Lys Lys Ser His Lys Arg Thr Ser Lys Ser Arg Glu
 405 410 415
 Arg His Asn Ser Arg Ser Arg Gly Arg Asn Arg Asp Arg Ser Arg Asp
 420 425 430
 Arg Ser Arg Gly Arg Gly Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg
 435 440 445
 Arg Ser Arg Arg Ser Arg Ser Gln Ser Ser Ser Arg Ser Arg Ser Arg
 450 455 460
 Gly Arg Arg Arg Ser Gly Asn Arg Asp Arg Thr Val Gln Ser Pro Lys
 465 470 475 480
 Ser Lys

<210> 129

<211> 1663

<212> DNA

<213> Homo Sapiens

<400> 129

aggccttgag ccaactccgg gtgctctgct gtgagtggct gagggccgag atccacacca 60
 aggagcagat cctggagcta ctggtgctgg agcagttcct gaccatcctg cccaggagc 120
 tccaggcctg ggtgcaggag cattgcccgg agagcgctga agaggctgtc actctcctcg 180
 aagatctgga gcgggaactg gatgagccag gacaccaggt ctcaactcct ccaaaccgaac 240
 agaaaccggt gtgggagaag atatcctcct caggaactgc aaaggaatcc ccgagcagca 300
 tgcagccaca gcccttgagg accagtcaca aatacagatc ttgggggccc ctgtacatcc 360
 aagagtctgg tgaggagcag gagttcgctc aagatccaag aaaggtccga gattgcagat 420
 tgagtaccca gcacgaggaa tcagcagatg agcagaaagg ttctgaagca gagggggtca 480
 aaggggatat aatttctgtg attatcgcca ataaacctga ggccagctta gagaggcagt 540
 gcgtaaacct tgaaaatgaa aaaggaacaa aacccctct tcaaggaggca ggctccaaga 600
 aaggtagaga atcagttcct actaaaccta cccaggaga gagacgttat atatgtgctg 660

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<210> 130
<211> 412
<212> PRT
<213> Homo Sapiens
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-97-

245 250 255
 Ser Asn Leu Thr Leu His Tyr Arg Thr His Leu Val Asp Arg Pro Tyr
 260 265 270
 Asp Cys Lys Cys Gly Lys Ala Phe Gly Gln Ser Ser Asp Leu Leu Lys
 275 280 285
 His Gln Arg Met His Thr Glu Glu Ala Pro Tyr Gln Cys Lys Asp Cys
 290 295 300
 Gly Lys Ala Phe Ser Gly Lys Gly Ser Leu Ile Arg His Tyr Arg Ile
 305 310 315 320
 His Thr Gly Glu Lys Pro Tyr Gln Cys Asn Glu Cys Gly Lys Ser Phe
 325 330 335
 Ser Gln His Ala Gly Leu Ser Ser His Gln Arg Leu His Thr Gly Glu
 340 345 350
 Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Asn His Ser Ser
 355 360 365
 Asn Phe Asn Lys His His Arg Ile His Thr Gly Glu Lys Pro Tyr Trp
 370 375 380
 Cys His His Cys Gly Lys Thr Phe Cys Ser Lys Ser Asn Leu Ser Lys
 385 390 395 400
 His Gln Arg Val His Thr Gly Glu Gly Glu Ala Pro
 405 410

<210> 131
 <211> 724
 <212> DNA
 <213> Homo Sapiens

<400> 131
 ggagaatgaa aagcagaaag tggcagagct gtattctatc cataactctg gagacaaatc 60
 tgatattcag gacctcctgg agagtgtcag gctggacaaa gaaaaagcag agactttggc 120
 tagtagcttg caggaagatc tggctcatac ccgaaatgat gccaatcgat tacaggatgc 180
 cattgctaag gtagaggatg aataccgagc cttccaagaa gaagctaaga aacaaattga 240
 agatttgaat atgacgttag aaaaattaag atcagacctg gatgaaaaag aaacagaaag 300
 gagtgcacatg aaagaaacca tctttgaact tgaagatgaa gtagaacaac atcgtgctgt 360
 gaaacttcat gacaacctca ttatttctga tctagagaat acagttaaaa aactccagga 420
 ccaaaagcac gacatggaaa gagaaataaa gacactccac agaagacttc gggaagaatc 480
 tgcggaatgg cggcagtttc aggctgatct ccagactgca gtagtcattg caaatgacat 540
 taaatctgaa gcccaagagg agattggtga tctaaagcgc cgggtacatg aggctcaaga 600
 aaaaaatgag aaactcaca aagaattgga ggaaataagt ccgccaagcc agaagangac 660
 gangccggta ttccantaca tgnatgcccg tgagagagaa tttggcaggc cttaaggcag 720
 ggaa 724

<210> 132
 <211> 218
 <212> PRT
 <213> Homo Sapiens

<400> 132
 Glu Asn Glu Lys Gln Lys Val Ala Glu Leu Tyr Ser Ile His Asn Ser
 1 5 10 15
 Gly Asp Lys Ser Asp Ile Gln Asp Leu Leu Glu Ser Val Arg Leu Asp
 20 25 30
 Lys Glu Lys Ala Glu Thr Leu Ala Ser Ser Leu Gln Glu Asp Leu Ala
 35 40 45
 His Thr Arg Asn Asp Ala Asn Arg Leu Gln Asp Ala Ile Ala Lys Val

50 55 60
 Glu Asp Glu Tyr Arg Ala Phe Gln Glu Glu Ala Lys Lys Gln Ile Glu
 65 70 75 80
 Asp Leu Asn Met Thr Leu Glu Lys Leu Arg Ser Asp Leu Asp Glu Lys
 85 90 95
 Glu Thr Glu Arg Ser Asp Met Lys Glu Thr Ile Phe Glu Leu Glu Asp
 100 105 110
 Glu Val Glu Gln His Arg Ala Val Lys Leu His Asp Asn Leu Ile Ile
 115 120 125
 Ser Asp Leu Glu Asn Thr Val Lys Lys Leu Gln Asp Gln Lys His Asp
 130 135 140
 Met Glu Arg Glu Ile Lys Thr Leu His Arg Arg Leu Arg Glu Glu Ser
 145 150 155 160
 Ala Glu Trp Arg Gln Phe Gln Ala Asp Leu Gln Thr Ala Val Val Ile
 165 170 175
 Ala Asn Asp Ile Lys Ser Glu Ala Gln Glu Glu Ile Gly Asp Leu Lys
 180 185 190
 Arg Arg Val His Glu Ala Gln Glu Lys Asn Glu Lys Leu Thr Lys Glu
 195 200 205
 Leu Glu Glu Ile Ser Pro Pro Ser Gln Lys
 210 215

<210> 133
 <211> 719
 <212> DNA
 <213> Homo Sapiens

<400> 133
 gagaactaca gagctgggtg cggggccaac ggccagaaag tggcgaggag gcagtgcgc 60
 tgggtggaggg ttgcagaaa caaccagga gaccaaggcg gtgactgtcc atgttcacgg 120
 ccaggaagtc ctgtcagagg agacggtgca tttaggagcg gagcctgagt cacctaata 180
 gctgcaggat cctgtgcaaa gctcgacccc cgagcagtct cctgaggaaa ccacacagag 240
 cccagatctg ggggcaccgg cagagcagcg tccacaccag gaagaggagc tccagaccct 300
 gcaggagagc gaggtcccag tgcccagga cccagacctt cctgcagaga ggagctctgg 360
 agactcagag atggttgctc ttcttactgc tctgtcacag ggactggtaa cgttcaagga 420
 tgtggccgta tgcttttccc aggaccagtg gactgatctg gacccaacac agaaagagtt 480
 ctatggagaa tatgtcttgg aagaagactg tggaattgtt gtctctctgt catttccaat 540
 cccagacct gatgagatct ccaggttag agaggaagag cccttgggtc ccagatatcc 600
 aagagcctna ggagactcaa gagccagaaa tcctgagttt tacctacaca ggagatagga 660
 gtnaagatga aggaaaatgt ctggagccag gaagaatctg agtttggagg atataccca 719

<210> 134
 <211> 217
 <212> PRT
 <213> Homo Sapiens

<400> 134
 Arg Thr Thr Glu Leu Gly Ala Gly Pro Thr Ala Arg Lys Trp Arg Gly
 1 5 10 15
 Gly Ser Asp Ala Gly Gly Gly Phe Ala Glu Thr Thr Gln Glu Thr Lys
 20 25 30
 Ala Val Thr Val His Val His Gly Gln Glu Val Leu Ser Glu Glu Thr
 35 40 45
 Val His Leu Gly Ala Glu Pro Glu Ser Pro Asn Glu Leu Gln Asp Pro
 50 55 60

Val Gln Ser Ser Thr Pro Glu Gln Ser Pro Glu Glu Thr Thr Gln Ser
65 70 75 80
Pro Asp Leu Gly Ala Pro Ala Glu Gln Arg Pro His Gln Glu Glu Glu
85 90 95
Leu Gln Thr Leu Gln Glu Ser Glu Val Pro Val Pro Glu Asp Pro Asp
100 105 110
Leu Pro Ala Glu Arg Ser Ser Gly Asp Ser Glu Met Val Ala Leu Leu
115 120 125
Thr Ala Leu Ser Gln Gly Leu Val Thr Phe Lys Asp Val Ala Val Cys
130 135 140
Phe Ser Gln Asp Gln Trp Ser Asp Leu Asp Pro Thr Gln Lys Glu Phe
145 150 155 160
Tyr Gly Glu Tyr Val Leu Glu Glu Asp Cys Gly Ile Val Val Ser Leu
165 170 175
Ser Phe Pro Ile Pro Arg Pro Asp Glu Ile Ser Gln Val Arg Glu Glu
180 185 190
Glu Pro Leu Gly Pro Arg Tyr Pro Arg Ala Gly Asp Ser Arg Ala Arg
195 200 205
Asn Pro Glu Phe Tyr Leu His Arg Arg
210 215

<210> 135
<211> 1027
<212> DNA
<213> Homo Sapiens

<400> 135
gcgagggcgca gggcgaggcg gtgctcatgg aggaggacct gatccagcag agcctggacg 60
actacgacgc cggcagggtac agcccgcggc tgctcacggc gcacgagctg cactgggacg 120
cgcacgtgct ggaaccggat gaggacctgc agcgctgca gctctcgcg cagcagctcc 180
aggtcacggg agacgcgagc gagagcgccg aggacatctt cttccggcgg gccaggagg 240
gcatgggcca ggacgaggcg cagttcagcg tggagatgcc actcaccggc aaggcctacc 300
tgtgggcca caagtaccgg ccacgcaagc cgcgcttctt caaccgcgtg cacacgggct 360
tcgagtggaa caagtacaac cagacgcact acgactttga caaccaccg cccaagatcg 420
tgcagggata caagttcaac atcttctacc cgcacctcat cgacaagcgc tccacgcccg 480
agtacttctt ggaggcctgc gccgacaaca aggatttgc catcctgcgc ttcacgcggg 540
gccgcctacg aggacatcgc tttcaagatc gtcaaccgcg agtggaata ctngcaccgc 600
cacggcttcc gctgccagtt tgccaacggc attttccanc tngctttca cttcaagcgc 660
tnccgctatc ggcgggtgac gccctggggc acggcaggcc aggaggggcg agggccacac 720
gggtggccaca gccaggtcg gactggccca gccggcaggc ttgtttttca gcatccgacg 780
ggaacatctc caacagaagc aaaacggaaa gtgcctcccg gacccccaga gggccaccca 840
acctcaccag tcaccagccc cagaccaccc acagcccctc ccagacaccc cgcctcatct 900
ggaaatagtt ccgtttgttt ctctaaaaag acttgtaggt gggaaaaaaa atcttttggt 960
ctcatggaat tggcctattg gcaagatcgc atgttttttt aataaacgtt gtatttttaga 1020
ataaaaa 1027

<210> 136
<211> 299
<212> PRT
<213> Homo Sapiens

<400> 136
Glu Gly Glu Gly Glu Ala Val Leu Met Glu Glu Asp Leu Ile Gln Gln
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Ser Leu Asp Asp Tyr Asp Ala Gly Arg Tyr Ser Pro Arg Leu Leu Thr

	20		25		30										
Ala	His	Glu	Leu	Pro	Leu	Asp	Ala	His	Val	Leu	Glu	Pro	Asp	Glu	Asp
	35						40						45		
Leu	Gln	Arg	Leu	Gln	Leu	Ser	Arg	Gln	Gln	Leu	Gln	Val	Thr	Gly	Asp
	50					55						60			
Ala	Ser	Glu	Ser	Ala	Glu	Asp	Ile	Phe	Phe	Arg	Arg	Ala	Lys	Glu	Gly
65					70					75				80	
Met	Gly	Gln	Asp	Glu	Ala	Gln	Phe	Ser	Val	Glu	Met	Pro	Leu	Thr	Gly
			85						90					95	
Lys	Ala	Tyr	Leu	Trp	Ala	Asp	Lys	Tyr	Arg	Pro	Arg	Lys	Pro	Arg	Phe
		100						105					110		
Phe	Asn	Arg	Val	His	Thr	Gly	Phe	Glu	Trp	Asn	Lys	Tyr	Asn	Gln	Thr
	115						120						125		
His	Tyr	Asp	Phe	Asp	Asn	Pro	Pro	Pro	Lys	Ile	Val	Gln	Gly	Tyr	Lys
	130					135					140				
Phe	Asn	Ile	Phe	Tyr	Pro	Asp	Leu	Ile	Asp	Lys	Arg	Ser	Thr	Pro	Glu
145					150					155				160	
Tyr	Phe	Leu	Glu	Ala	Cys	Ala	Asp	Asn	Lys	Asp	Phe	Ala	Ile	Leu	Arg
			165						170					175	
Phe	Thr	Arg	Gly	Arg	Leu	Arg	Gly	His	Arg	Phe	Gln	Asp	Arg	Gln	Pro
		180					185						190		
Arg	Val	Gly	Ile	Leu	Ala	Pro	Pro	Arg	Leu	Pro	Leu	Pro	Val	Cys	Gln
	195					200						205			
Arg	His	Phe	Pro	Leu	Ser	Leu	Gln	Ala	Leu	Pro	Leu	Ser	Ala	Val	Thr
	210					215						220			
Ala	Leu	Gly	Asn	Gly	Arg	Pro	Gly	Gly	Pro	Arg	Ala	Thr	Arg	Val	Pro
225				230						235				240	
Gln	Pro	Arg	Ser	Glu	Trp	Pro	Ser	Arg	Gln	Ala	Cys	Phe	Ser	Ala	Ser
			245						250					255	
Asp	Gly	Asn	Ile	Ser	Asn	Arg	Ser	Lys	Thr	Glu	Ser	Ala	Ser	Arg	Thr
		260						265					270		
Pro	Arg	Gly	Pro	Pro	Asn	Leu	Thr	Ser	His	Gln	Pro	Gln	Thr	Thr	His
	275					280							285		
Ser	Pro	Ser	Gln	Thr	Pro	Arg	Leu	Ile	Trp	Lys					
	290					295									

<210> 137

<211> 766

<212> DNA

<213> Homo Sapiens

<400> 137

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tggaacacca	atttggtgca	caaggggacc	tcaccacgga	atgtgctact	gcaaacaacc	180
ccacagccat	cacgcctgat	gagtacttca	atgaagagtt	tgatctgaaa	gacagggaca	240
ttggaaggcc	gaaagagctg	acgattagaa	cacagaagtt	taaagcaatg	ttgtggatgt	300
gtgaagagtt	tccccctctct	ctggtggagc	aggtcattcc	catcattgac	ctaattggctc	360
gaacagagtgc	tcattttgca	agactgagag	atttcatcaa	attggaattc	ccacctggat	420
ttcctgtcaa	aatagcttcc	cacatcacaa	actttgaggt	tgatcaatct	gtgtttgaaa	480
ttcccgaaatc	ttactatgtt	caagacaatg	gcagaaatgt	gcatttgcaa	gatgaagatt	540
acgagataat	gcagtttgcc	atccagcaaa	gtctgctgga	gtccagcagg	agccaggaac	600
tttcaggacc	agcttcgaat	ggagggatca	gccagacaaa	cacctatgac	gccagtatg	660
agagggccat	ncaggagagc	cttctaccag	cacagaaagc	ctgtgcccc	agcgcccctg	720
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<210> 138
 <211> 243
 <212> PRT
 <213> Homo Sapiens

<400> 138
 Lys Val Tyr Thr Val Asn Asn Val Asn Val Ile Thr Lys Ile Arg Thr
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 Glu His Leu Thr Glu Glu Lys Lys Arg Tyr Lys Asp Arg Asn Pro
 20 25 30
 Leu Glu Ser Leu Leu Gly Thr Val Glu His Gln Phe Gly Ala Gln Gly
 35 40 45
 Asp Leu Thr Thr Glu Cys Ala Thr Ala Asn Asn Pro Thr Ala Ile Thr
 50 55 60
 Pro Asp Glu Tyr Phe Asn Glu Glu Phe Asp Leu Lys Asp Arg Asp Ile
 65 70 75 80
 Gly Arg Pro Lys Glu Leu Thr Ile Arg Thr Gln Lys Phe Lys Ala Met
 85 90 95
 Leu Trp Met Cys Glu Glu Phe Pro Leu Ser Leu Val Glu Gln Val Ile
 100 105 110
 Pro Ile Ile Asp Leu Met Ala Arg Thr Ser Ala His Phe Ala Arg Leu
 115 120 125
 Arg Asp Phe Ile Lys Leu Glu Phe Pro Pro Gly Phe Pro Val Lys Ile
 130 135 140
 Ala Ser His Ile Thr Asn Phe Glu Val Asp Gln Ser Val Phe Glu Ile
 145 150 155 160
 Pro Glu Ser Tyr Tyr Val Gln Asp Asn Gly Arg Asn Val His Leu Gln
 165 170 175
 Asp Glu Asp Tyr Glu Ile Met Gln Phe Ala Ile Gln Gln Ser Leu Leu
 180 185 190
 Glu Ser Ser Arg Ser Gln Glu Leu Ser Gly Pro Ala Ser Asn Gly Gly
 195 200 205
 Ile Ser Gln Thr Asn Thr Tyr Asp Ala Gln Tyr Glu Arg Ala Gln Glu
 210 215 220
 Ser Leu Leu Pro Ala Gln Lys Ala Cys Ala Pro Ser Ala Pro Glu Arg
 225 230 235 240
 Asp Pro Phe

<210> 139
 <211> 3060
 <212> DNA
 <213> Homo Sapiens

<400> 139
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 gcgcagttcc cggaactcaga gccccgcgc atggagctgc gctcagtgga cgacatcgag 540
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cgcttccgca tgatctacct gcagacgttg ctggccaagg aaaagaagag ctatgaccgg 660
 cagcgatggg gcttccggcg cgcggcgag gccccgacg gcgcctccga gccccgagcg 720
 tccggtcgc gcccgcagcc agcgcccgcc gacggagcgg acccgccgccc cgcgaggag 780
 cccgaggccc ggcccgcagc cgaggggttct ccgggtaagg ccaggcccgg gaccgcccgc 840
 agggccgggg cagccgcgtc gggggaacgg gacgaccggg gacccccgc cagcgtggcg 900
 gcgctcaggt ccaacttcga gcggatccgc aagggccatg gccagcccgg ggcggacgcc 960
 gagaagccct tctactgaa cgtcgagttt caccacgagc gcggcctggg gaaggtcaac 1020
 gacaaaggag tgctcgaccg catcagctcc ctgggcagcc aggccatgca gatggagcgc 1080
 aaaaagtccc agcacggcg gggctcgagc gtgggggatg catccaggcc cccttaccgg 1140
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 cccctggagt accagcccta ccagagcatc tacgtcgggg gcatgatgga aggggagggc 1320
 aagggcccgc tctgcgcag ccagagcacc tctgagcagg agaagcgctt tacctggccc 1380
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 aactcgcaac agtccctcga cagcagcagt cccccacgc cgcagtgcc taagcggcac 1620
 cggcactgcc cgggtgtcgt gtccgaggcc accatcgtgg gcgtccgcaa gaccgggag 1680
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 tacctgagcc acctggaggc actgctgctg cccatgaagc ctttgaaagc cgctgccacc 2040
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 ctctacgaga tccacaagga gttctatgat gggctcttcc cccgcgtgca gcagtggagc 2160
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 agcttcagtg tggagctggg ggagggggcc cgcaagctgc gccacgtctt cctgttcacc 2640
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 tgcaaatggg acattccgct cacggatctc agcttccaga tgggtgatga actggaggca 2760
 gtgcccaca tccccctggg gcccgatgag gagctggagc ctttgaagat caagatctcc 2820
 cagatcaaga gtgacatcca gagagagaag agggcgaaac agggcagcaa ggctacggag 2880
 aggctgaaga agaagctgtc ggagcaggag tcaactgctg tgcttatgtc tcccagcatg 2940
 gccttcaggg tgcacagccg caacggcaag agttacacgt tctgatctc ctctgactat 3000
 gagcgtgcag agtggaggga gaacatccgg gacgagcaga agaagtgttt cagaagcttc 3060

<210> 140

<211> 872

<212> PRT

<213> Homo Sapiens

<400> 140

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
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 20 25 30
 Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
 35 40 45
 Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala

50 55 60
 Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
 65 70 75 80
 Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
 85 90 95
 Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
 100 105 110
 Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
 115 120 125
 Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
 130 135 140
 Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
 145 150 155 160
 Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
 165 170 175
 Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
 180 185 190
 Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
 195 200 205
 Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
 210 215 220
 Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
 225 230 235 240
 Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
 245 250 255
 Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
 260 265 270
 Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met
 275 280 285
 Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
 290 295 300
 Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
 305 310 315 320
 Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
 325 330 335
 Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
 340 345 350
 Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
 355 360 365
 Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
 370 375 380
 Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
 385 390 395 400
 Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
 405 410 415
 Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
 420 425 430
 Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg
 435 440 445
 His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro
 450 455 460
 His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly
 465 470 475 480
 Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu
 485 490 495

Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Thr
 500 505 510
 Tyr Leu Ser His Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys
 515 520 525
 Ala Ala Ala Thr Thr Ser Gln Pro Val Leu Thr Ser Gln Gln Ile Glu
 530 535 540
 Thr Ile Phe Phe Lys Val Pro Glu Leu Tyr Glu Ile His Lys Glu Phe
 545 550 555 560
 Tyr Asp Gly Leu Phe Pro Arg Val Gln Gln Trp Ser His Gln Gln Arg
 565 570 575
 Val Gly Asp Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Arg
 580 585 590
 Ala Phe Val Asp Asn Tyr Gly Val Ala Met Glu Met Ala Glu Lys Cys
 595 600 605
 Cys Gln Ala Asn Ala Gln Phe Ala Glu Ile Ser Glu Asn Leu Arg Ala
 610 615 620
 Arg Ser Asn Lys Asp Ala Lys Asp Pro Thr Thr Lys Asn Ser Leu Glu
 625 630 635 640
 Thr Leu Leu Tyr Lys Pro Val Asp Arg Val Thr Arg Ser Thr Leu Val
 645 650 655
 Leu His Asp Leu Lys His Thr Pro Ala Ser His Pro Asp His Pro
 660 665 670
 Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile
 675 680 685
 Asn Glu Glu Ile Thr Pro Arg Arg Gln Ser Met Thr Val Lys Lys Gly
 690 695 700
 Glu His Arg Gln Leu Leu Lys Asp Ser Phe Met Val Glu Leu Val Glu
 705 710 715 720
 Gly Ala Arg Lys Leu Arg His Val Phe Leu Phe Thr Glu Leu Leu Leu
 725 730 735
 Cys Thr Lys Leu Lys Lys Gln Ser Gly Gly Lys Thr Gln Gln Tyr Asp
 740 745 750
 Cys Lys Trp Tyr Ile Pro Leu Thr Asp Leu Ser Phe Gln Met Val Asp
 755 760 765
 Glu Leu Glu Ala Val Pro Asn Ile Pro Leu Val Pro Asp Glu Glu Leu
 770 775 780
 Asp Ala Leu Lys Ile Lys Ile Ser Gln Ile Lys Ser Asp Ile Gln Arg
 785 790 795 800
 Glu Lys Arg Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys
 805 810 815
 Lys Leu Ser Glu Gln Glu Ser Leu Leu Leu Leu Met Ser Pro Ser Met
 820 825 830
 Ala Phe Arg Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile
 835 840 845
 Ser Ser Asp Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln
 850 855 860
 Gln Lys Lys Cys Phe Arg Ser Phe
 865 870

<210> 141

<211> 691

<212> DNA

<213> Homo Sapiens

<400> 141

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gttggaagtct gatcttttcc cgacgtctac ttccctgagt cccttctacc ttcggccacc      180
ctccttctctg cgggcaccca gctggtttga cactggactc tcagagatgc gcctggagaa      240
ggacagggttc tctgtcaacc tggatgtgaa gcacttctcc ccagaggaaac tcaaagttaa      300
ggtgttggga gatgtgattg aggtgcatgg aaaacatgaa gagcgccagg atgaacatgg      360
tttcatctcc agggagttcc acaggaaata ccgcatocca gctgatgtag accctctcac      420
cattacttca tccctgtcat ctgatggggc cctcactgtg aatggaccaaa ggaaacaggc      480
ctctggccct gagcgacca ttccatcac ccgtgaagag aagcctgtg tcaccgcagc      540
ccccaagaaa tagatgcctt ttcttgaatt gcatttttta aaacaagaaa gtttccccac      600
cagtgaatga aagtcttctg actagtgtg aagcttatta atgctaaggg caggcccaaa      660
ttatcaagct aataaaatat cattcagcaa c                                     691

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<210> 142
 <211> 175
 <212> PRT
 <213> Homo Sapiens

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<400> 142
Met Asp Ile Ala Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro
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Phe His Ser Pro Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu
              20              25              30
Leu Glu Ser Asp Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr
              35              40              45
Leu Arg Pro Pro Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly
              50              55              60
Leu Ser Glu Met Arg Leu Glu Lys Asp Arg Phe Ser Val Asn Leu Asp
65              70              75              80
Val Lys His Phe Ser Pro Glu Glu Leu Lys Val Lys Val Leu Gly Asp
              85              90              95
Val Ile Glu Val His Gly Lys His Glu Glu Arg Gln Asp Glu His Gly
              100             105             110
Phe Ile Ser Arg Glu Phe His Arg Lys Tyr Arg Ile Pro Ala Asp Val
              115             120             125
Asp Pro Leu Thr Ile Thr Ser Ser Leu Ser Ser Asp Gly Val Leu Thr
              130             135             140
Val Asn Gly Pro Arg Lys Gln Val Ser Gly Pro Glu Arg Thr Ile Pro
145             150             155             160
Ile Thr Arg Glu Glu Lys Pro Ala Val Thr Ala Ala Pro Lys Lys
              165             170             175

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<210> 143
 <211> 1300
 <212> DNA
 <213> Homo Sapiens

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<400> 143
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tcctggatta cttttcagaa agaagtaatc ctttttatga cagaacatgt aataatgaag      120
tggtcaaaat gcagaggcta acattagaac acttgaatca gatggttggg atcgagtaca      180
tccttttgcg tgctcaagag cccattcttt tcatcattcg gaagcaacag cggcagtcct      240
ctgcccaggt tatccacta gctgattact atatcattgc tggagtgtac tatcaggcac      300
cagacttggg atcagttata aactctagag tgcttactgc agtgcatggg attcagtcag      360
cttttgatga agctatgtca tactgtcgat atcatccttc caaagggtat tgggtggcact      420

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tcaaagatca tgaagagcaa gataaagtca gacctaaagc caaaaggaaa gaagaaccaa 480
gctctatttt tcagagacaa cgtgtggatg ctttactttt agacctcaga caaaaatttc 540
cacccaaatt tgtgcagcta aagcctggag aaaagcctgt tcaagtggat caaacaaga 600
aagaggcaga acctatacca gaaactgtaa aacctgagga gaaggagacc cccnnagaat 660
gtacaaccag accgggagtg ctaaaggccc ccctgaaaaa cggatgagac ttcagtggat 720
actggacaaa agagaagcct ggaagactcc tcatgctagt tatcatacct cagtactgtg 780
gctcttgagc tttgaagtac tttattgtaa ccttcttatt tgtatggaat gcgcttattt 840
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gccatggcgg gtggatcact tgaggtcaga agttcaagac cagcctgacc aatatggtga 960
aaccctgtct ctactaaaaa tacaaaaatt agccgggcgt ggtggcgggc gcccgtagtc 1020
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tgagctgatt atcatgctgt tgcactccag cttgggcgac agagcgagac tttgtctcaa 1140
aaaagaagaa aagatattac tcccatcatg atttcttggt aatatttgtt atatgtcttc 1200
tgtaaccttt cctctcccgg acttgagcaa cctacacact cacatgttta ctggtagata 1260
tgtttaaaag caaataaaag gtatttgtat atattgaaaa 1300

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<210> 144

<211> 233

<212> PRT

<213> Homo Sapiens

<400> 144

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Ser Gly Ser Val Leu Asp Tyr Phe Ser Glu Arg Ser Asn Pro Phe Tyr
20          25          30
Asp Arg Thr Cys Asn Asn Glu Val Val Lys Met Gln Arg Leu Thr Leu
35          40          45
Glu His Leu Asn Gln Met Val Gly Ile Glu Tyr Ile Leu Leu His Ala
50          55          60
Gln Glu Pro Ile Leu Phe Ile Ile Arg Lys Gln Gln Arg Gln Ser Pro
65          70          75          80
Ala Gln Val Ile Pro Leu Ala Asp Tyr Tyr Ile Ile Ala Gly Val Ile
85          90          95
Tyr Gln Ala Pro Asp Leu Gly Ser Val Ile Asn Ser Arg Val Leu Thr
100          105          110
Ala Val His Gly Ile Gln Ser Ala Phe Asp Glu Ala Met Ser Tyr Cys
115          120          125
Arg Tyr His Pro Ser Lys Gly Tyr Trp Trp His Phe Lys Asp His Glu
130          135          140
Glu Gln Asp Lys Val Arg Pro Lys Ala Lys Arg Lys Glu Glu Pro Ser
145          150          155          160
Ser Ile Phe Gln Arg Gln Arg Val Asp Ala Leu Leu Leu Asp Leu Arg
165          170          175
Gln Lys Phe Pro Pro Lys Phe Val Gln Leu Lys Pro Gly Glu Lys Pro
180          185          190
Val Gln Val Asp Gln Thr Lys Lys Glu Ala Glu Pro Ile Pro Glu Thr
195          200          205
Val Lys Pro Glu Glu Lys Glu Thr Pro Glu Cys Thr Thr Arg Pro Gly
210          215          220
Val Leu Lys Ala Pro Leu Lys Asn Gly
225          230

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<210> 145

<211> 1528

<212> DNA

<213> Homo Sapiens

<400> 145

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gcggccaaact ccaatggggc tttccagccc gtggtccttc tccatattcg agatgttcct      180
cctgctgac aagagaagct tttatccag aagttacgtc agtgttgctg cctctttgac      240
tttgtttctg atccactaag tgacctaaag tggaaggaag taaaacgagc tgctttaagt      300
gaaatggtag aatatatcac ccataatcgg aatgtgatca cagagcctat ttaccagaa      360
gtagtccata tgtttgacgt taacatgttt cgaacattac caccttcctc caatcctacg      420
ggagcggaat ttgaccgga ggaagatgaa ccaacgttag aagcagcctg gcctcatcta      480
cagcttgttt atgaattttt cttaagattt ttagagtctc cagatttcca acctaatata      540
gcgaagaaat atattgatca gaagtgtgta ttgcagcttt tagagctctt tgacagtga      600
gatcctcggg agagagattt tcttaaaacc acccttcaca gaatctatgg gaaattccta      660
ggcttgagag cttacatcag aaaacagata aataatata tttatagggt tatttatgaa      720
acagagcatc ataatggcat agcagagtta ctggaaatat tgggaagtat aattaatgga      780
tttgccctac cactaaaaga agagcacaag attttcttat tgaagggtgt actaccttg      840
caciaagtga aatctctgag tgtctaccat cccagctgg catactgtgt agtgcagtt      900
ttagaaaaagg acagcaccct cacggaacca gtggtgatgg cacttctcaa atactggcca      960
aagactcaca gtccaaaaga agtaatgttc ttaaacgaat tagaagagat tttagatgtc     1020
attgaacatc cagaatttgt gaagatcatg gaacccctct tccggcagtt ggccaaatgt     1080
gtctccagcc cacacttcca ggtggcagag cgagctctct attactggaa taatgaatac     1140
atcatgagtt taatcagtga caacgcagcg aagattctgc ccatcatgtt tccttccttg     1200
taccgcaact caaagaccca ttggaacaag acaatacatg gcttgatata caacgccctg     1260
aagctcttca tggagatgaa ccaaaagcta ttgatgact gtacacaaca gttcaaagca     1320
gagaaactaa aagagaagct aaaaatgaaa gaacgggaag aagcatgggt taaaatagaa     1380
aatctagcca aagccaatcc ccaggtaact aaaaagagaa taacatgaaa aggccagggg     1440
ttacttgaat gtttttataa gataggaata tatgtcttca ccatgggggg ggtctcgatt     1500
tcactaacgt tgtatatgaa aatgtctg                                     1528

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<210> 146

<211> 449

<212> PRT

<213> Homo Sapiens

<400> 146

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Met Leu Thr Cys Asn Lys Ala Gly Ser Arg Met Val Val Asp Ala Ala
 1              5              10              15
Asn Ser Asn Gly Pro Phe Gln Pro Val Val Leu Leu His Ile Arg Asp
      20              25              30
Val Pro Pro Ala Asp Gln Glu Lys Leu Phe Ile Gln Lys Leu Arg Gln
      35              40              45
Cys Cys Val Leu Phe Asp Phe Val Ser Asp Pro Leu Ser Asp Leu Lys
      50              55              60
Trp Lys Glu Val Lys Arg Ala Ala Leu Ser Glu Met Val Glu Tyr Ile
65              70              75              80
Thr His Asn Arg Asn Val Ile Thr Glu Pro Ile Tyr Pro Glu Val Val
      85              90              95
His Met Phe Ala Val Asn Met Phe Arg Thr Leu Pro Pro Ser Ser Asn
      100             105             110
Pro Thr Gly Ala Glu Phe Asp Pro Glu Glu Asp Glu Pro Thr Leu Glu
      115             120             125
Ala Ala Trp Pro His Leu Gln Leu Val Tyr Glu Phe Leu Arg Phe
      130             135             140

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Leu Glu Ser Pro Asp Phe Gln Pro Asn Ile Ala Lys Lys Tyr Ile Asp
 145 150 155 160
 Gln Lys Phe Val Leu Gln Leu Leu Glu Leu Phe Asp Ser Glu Asp Pro
 165 170 175
 Arg Glu Arg Asp Phe Leu Lys Thr Thr Leu His Arg Ile Tyr Gly Lys
 180 185 190
 Phe Leu Gly Leu Arg Ala Tyr Ile Arg Lys Gln Ile Asn Asn Ile Phe
 195 200 205
 Tyr Arg Phe Ile Tyr Glu Thr Glu His His Asn Gly Ile Ala Glu Leu
 210 215 220
 Leu Glu Ile Leu Gly Ser Ile Ile Asn Gly Phe Ala Leu Pro Leu Lys
 225 230 235 240
 Glu Glu His Lys Ile Phe Leu Leu Lys Val Leu Leu Pro Leu His Lys
 245 250 255
 Val Lys Ser Leu Ser Val Tyr His Pro Gln Leu Ala Tyr Cys Val Val
 260 265 270
 Gln Phe Leu Glu Lys Asp Ser Thr Leu Thr Glu Pro Val Val Met Ala
 275 280 285
 Leu Leu Lys Tyr Trp Pro Lys Thr His Ser Pro Lys Glu Val Met Phe
 290 295 300
 Leu Asn Glu Leu Glu Glu Ile Leu Asp Val Ile Glu Pro Ser Glu Phe
 305 310 315 320
 Val Lys Ile Met Glu Pro Leu Phe Arg Gln Leu Ala Lys Cys Val Ser
 325 330 335
 Ser Pro His Phe Gln Val Ala Glu Arg Ala Leu Tyr Tyr Trp Asn Asn
 340 345 350
 Glu Tyr Ile Met Ser Leu Ile Ser Asp Asn Ala Ala Lys Ile Leu Pro
 355 360 365
 Ile Met Phe Pro Ser Leu Tyr Arg Asn Ser Lys Thr His Trp Asn Lys
 370 375 380
 Thr Ile His Gly Leu Ile Tyr Asn Ala Leu Lys Leu Phe Met Glu Met
 385 390 395 400
 Asn Gln Lys Leu Phe Asp Asp Cys Thr Gln Gln Phe Lys Ala Glu Lys
 405 410 415
 Leu Lys Glu Lys Leu Lys Met Lys Glu Arg Glu Glu Ala Trp Val Lys
 420 425 430
 Ile Glu Asn Leu Ala Lys Ala Asn Pro Gln Val Leu Lys Lys Arg Ile
 435 440 445
 Thr

<210> 147
 <211> 1580
 <212> DNA
 <213> Homo Sapiens

<400> 147
 atccccctccg gttttccctca gtctccacgt acgtccctca aagcgcgtcc taaaaccctgg 60
 ataaccggag cgctcccat ggaccacacg gagggcttgc ccgcggagga gccgcctgcg 120
 catgctccat cgcctgggaa atttggtgag cggcctccac ctaaaccgact tactagggaa 180
 gctatgcaaa attatttaaa agagcgaggg gatcaaacag tacttattct tcatgcaaaa 240
 gttgcacaga agtcatatgg aaatgaaaaa aggtttttt gccacacctc ttgtgtatat 300
 cttatgggca gcggatggaa gaaaaaaaaa gaacaaatgg aacgcgatgg ttgttctgaa 360
 caagagtctc aaccgtgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag 420
 ctaaacttgg aaggaaagaa ctattgcaca gccaaaacat tgtatatatc tgactcagac 480

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aagcgaaagc acttcatttt ttctgtaaag atgttctatg gcaacagtga tgacattggt      540
gtgttctctca gcaagcggat aaaagtcata tccaaacctt ccaaaaagaa gcagtcattg      600
aaaaatgctg acttatgcat tgcctcagga acaaagggtg ctctgtttaa tcgactacga      660
tcccagacag ttagtaccag atacttgcat gtagaaggag gtaattttca tgccagttca      720
cagcagtggtg gagccttttt tattcatctc ttggatgatg atgaatcaga aggagaagaa      780
ttcacagtcc gagatgtcta catccattat ggacaaacat gcaaacttgt gtgctcagtt      840
actggcatgg cactcccaag attgataatt atgaaagttg ataagcatac cgcattattg      900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat ttaccttaa ggatacagaa      960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca     1020
aaagaaccaa ataaagagat gataaatgat ggcgcttcct ggacaatcat tagcacagat     1080
aaggcagagt atacatttta tgaggggaatg ggccctgtcc ttgccccagt cactcctgtg     1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca     1200
ggacagaatt tcaactccaaa ttacgagtg tggtttgggg atgtagaagc tgaactatg     1260
tacaggtgtg gagagagtat gctctgtgtc gtcccagaca tttctgcatt ccgagaaggt     1320
tggagatggg tccggcaacc agtccaggtt ccagtaactt tgggtccgaa tgatggaatc     1380
atattattcca ccagccttac ctttacctac acaccagaac cagggccaag gccacattgc     1440
agtgtagcag gagcaatcct tccagccaat tcaagccagg tgccccctaa cgaatcaaac     1500
acaaacagcg aggggaagtta cacaaacgcc agcacaat caaccagtgt cacatcatct     1560
acagccacag tggatcctca

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<210> 148

<211> 500

<212> PRT

<213> Homo Sapiens

<400> 148

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Met Asp His Thr Glu Gly Leu Pro Ala Glu Glu Pro Pro Ala His Ala
 1           5           10           15
Pro Ser Pro Gly Lys Phe Gly Glu Arg Pro Pro Lys Arg Leu Thr
 20           25           30
Arg Glu Ala Met Arg Asn Tyr Leu Lys Glu Arg Gly Asp Gln Thr Val
 35           40           45
Leu Ile Leu His Ala Lys Val Ala Gln Lys Ser Tyr Gly Asn Glu Lys
 50           55           60
Arg Phe Phe Cys Pro Pro Pro Cys Val Tyr Leu Met Gly Ser Gly Trp
 65           70           75           80
Lys Lys Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln Glu
 85           90           95
Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu Met
100           105           110
Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr Leu
115           120           125
Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Ile Phe Ser Val Lys
130           135           140
Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys Arg
145           150           155           160
Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys Asn
165           170           175
Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn Arg
180           185           190
Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly Gly
195           200           205
Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His Leu
210           215           220
Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp Val

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<210> 149
<211> 1248
<212> DNA
<213> Homo Sapiens
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<400> 149						
caagatatcg	aattccaaat	ttgagggcct	cccggtctctg	gcgcgcggagg	gagagctcag	60
gccgccatgc	gcgacaggac	ccacgagctg	agacaggggg	atgacagctc	ggacgaagag	120
gacaaggagc	gggtcgcgct	ggtggtgcac	ccgggcacgg	cacggctggg	gagcccgac	180
gaggagtctt	tccacaaggt	ccggacaact	cgtcagacta	ttgtcaaat	ggggaataaa	240
gtccaggagt	tggtagaaca	gcaggtcac	atctctggcca	cgcccttcc	caggagagc	300
atgaagcagg	aggtgcagaa	cctgcgcgat	gagatcaaac	agctggggag	ggagatccgc	360
ctgcagctga	aggccataga	gccccagaag	gaggaagctg	atgagaacta	taactccgtc	420
aacacaagaa	tgagaaaaac	ccagcatggg	gtcctgtccc	agcaattcgt	ggagctcatc	480
aacaagtgc	attcaatgca	gtccgaatac	cgggagaaga	acgtggagcg	gattcggagg	540
cagctgaaga	tcaccaatgc	tggcatggtg	tctgatgagg	agttggatca	gactctggac	600
agtggggcaa	gcgaggtggt	tgtgtccaat	atccttaagg	acacgcaggt	gactgcacag	660
gccttaaat	agatctcggc	ccggcacagt	gagatcaagc	agcttgaacg	cagtattcgt	720
gagctgcacg	acatatctcac	ttttctggct	accgaagtgg	agatgcaggg	ggagatgata	780

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aatcggattg agaagaacat cctgagctca gcggactacg tggaacgtgg gcaggagcac      840
gtcaagacgg ccctggagaa ccagaagaag gtgaggaaga agaaagtctt gattgccatc      900
tgtgtgtcca tcaccgtcgt cctcctagca gtcattcatt gcgtcacagt gggtggataa      960
tgtcgcacat tgttggcact aggagcacca ggaacccagg gcctggcctt ctctcccagc     1020
agcctggggg gcaggcagag cctccagtcg gaccccttcc tcacacactg gcccctatgc     1080
agaagggcag acagttcttc tgggggttggc agctgctcat tcatgatggc ctctccttc     1140
aggcctcaat gcctggggga ggccctgact gtccctgattg gccgggacac acggttttgt     1200
aaaaaattaa aaaacaaaaa aagagcatag aaaaaaaaaa aaccgagt      1248

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<210> 150

<211> 297

<212> PRT

<213> Homo Sapiens

<400> 150

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Met Arg Asp Arg Thr His Glu Leu Arg Gln Gly Asp Asp Ser Ser Asp
 1           5           10           15
Glu Glu Asp Lys Glu Arg Val Ala Leu Val Val His Pro Gly Thr Ala
 20           25           30
Arg Leu Gly Ser Pro Asp Glu Glu Phe Phe His Lys Val Arg Thr Ile
 35           40           45
Arg Gln Thr Ile Val Lys Leu Gly Asn Lys Val Gln Glu Leu Glu Lys
 50           55           60
Gln Gln Val Thr Ile Leu Ala Thr Pro Leu Pro Glu Glu Ser Met Lys
 65           70           75           80
Gln Glu Leu Gln Asn Leu Arg Asp Glu Ile Lys Gln Leu Gly Arg Glu
 85           90           95
Ile Arg Leu Gln Leu Lys Ala Ile Glu Pro Gln Lys Glu Glu Ala Asp
100          105          110
Glu Asn Tyr Asn Ser Val Asn Thr Arg Met Arg Lys Thr Gln His Gly
115          120          125
Val Leu Ser Gln Gln Phe Val Glu Leu Ile Asn Lys Cys Asn Ser Met
130          135          140
Gln Ser Glu Tyr Arg Glu Lys Asn Val Glu Arg Ile Arg Arg Gln Leu
145          150          155          160
Lys Ile Thr Asn Ala Gly Met Val Ser Asp Glu Glu Leu Asp Gln Met
165          170          175
Leu Asp Ser Gly Gln Ser Glu Val Phe Val Ser Asn Ile Leu Lys Asp
180          185          190
Thr Gln Val Thr Arg Gln Ala Leu Asn Glu Ile Ser Ala Arg His Ser
195          200          205
Glu Ile Gln Gln Leu Glu Arg Ser Ile Arg Glu Leu His Asp Ile Phe
210          215          220
Thr Phe Leu Ala Thr Glu Val Glu Met Gln Gly Glu Met Ile Asn Arg
225          230          235          240
Ile Glu Lys Asn Ile Leu Ser Ser Ala Asp Tyr Val Glu Arg Gly Gln
245          250          255
Glu His Val Lys Thr Ala Leu Glu Asn Gln Lys Lys Val Arg Lys Lys
260          265          270
Lys Val Leu Ile Ala Ile Cys Val Ser Ile Thr Val Val Leu Leu Ala
275          280          285
Val Ile Ile Gly Val Thr Val Val Gly
290          295

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<210> 151

<211> 1953
 <212> DNA
 <213> Homo Sapiens

<400> 151
 acgcctgccca ggagcaagcc gaagagccag ccggccggcg cactccgact ccgagcagtc 60
 tctgtccttc gacccgagcc ccgcgccctt tccgggaccc ctgccccgcg ggcagcgctg 120
 ccaacctgcc ggccatggag accccgtccc agcggcgcg caccgcagc ggggcgcagg 180
 ccagctccac tccgctgtcg cccaccgca tcaccggct gcaggagaag gaggacctgc 240
 aggagctcaa tgatcgcttg gcggtctaca tcgaccgtgt gcgctcgctg gaaacggaga 300
 acgcaggggt cgcgcttcgc atcaccgagt ctgaagaggt ggtcagccgc gagggtgtccg 360
 gcatcaaggc cgcctacgag gccgagctcg gggatgccc caagaccctt gactcagtag 420
 ccaaggagcg cgcgcgctg cagctggagc tgagcaaagt gcgtgaggag ttaaggagc 480
 tgaaagcgcg caataccaag aaggaggggt acctgatagc tgctcaggct cggtgaagg 540
 acctggagcg tctgctgaac tccaaggagg ccgcaactgag cactgtcttc agtgagaagc 600
 gcacgctgga gggcgagctg catgatctgc ggggccaggt ggccaagctt gaggcagccc 660
 taggtgagcg caagaagcaa cttcaggatg agatgctgcg gcgggtggat gctgagaaca 720
 ggctgcagac catgaaggag gaactggact tccagaagaa catctacagt gaggagctgc 780
 gtgagaccaa gcgcgctcat gagaccgac tgggtggagt tgacaatggg aagcagcgtg 840
 agtttgagag ccggtggcg gatgcgctgc aggaactgag ggcccagcat gaggaccagg 900
 tggagcagta taagaaggag ctggagaaga cttattctgc caagctggac aatgccaggc 960
 agtctgctga gaggaacagc aacctgggtg gggctgccc cgaggagctg cagcagtcgc 1020
 gcatccgcat cgacagcctc tctgcccagc tcagccagct ccagaagcag ctggcagcca 1080
 aggaggcgaa gcttcgagac ctggaggact cactggccc tgagcgggac accagccggc 1140
 ggctgctggc ggaaaaggag cgggagatgg ccgagatgcg ggcaaggatg cagcagcagc 1200
 tggacgagta ccaggagctt ctggacatca agctggccct ggacatggag atccacgcct 1260
 accgcaagct cttggagggc gaggaggaga ggctacgcct gtccccagc cctacctgc 1320
 agcgcagccg tggccgtgct tcctctcact catcccagac acagggtggg ggcagcgtca 1380
 ccaaaaagcg caaactggag tccactgaga gccgcagcag cttctcacag cagcacgca 1440
 ctagcgggcg cgtggccgtg gaggaggtgg atgaggagg caagtttgtc cggctgcgca 1500
 acaagtccaa tgaggaccag tccatgggca attggcagat caagcgccag aatggagatg 1560
 atcccttgct gacttaccgg ttcccaccaa agttcaccct gaaggctggg cagggtgtga 1620
 cgatctgggc tgcaggagct ggggccaccc acagccccc taccgacctg gtgtggaagg 1680
 cacagaacac ctggggctgc gggaacagcc tgcgtacggc tctcatcaac tccactgggg 1740
 aagaagtggc catgcgcaag ctgggtgcgt cagtgaactgt ggttgaggac gacgaggatg 1800
 aggatggaga tgacctgtc catcaccacc acgtgagtgg tagccgccc tgaggccgag 1860
 cctgcactgg ggccaccagc caggcctggg ggcagcctc cccagcctc cccgtgccaa 1920
 aaatcttttc attaaagaat gttttggaac ttt 1953

<210> 152
 <211> 572
 <212> PRT
 <213> Homo Sapiens

<400> 152
 Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala
 1 5 10 15
 Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
 20 25 30
 Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
 35 40 45
 Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
 50 55 60
 Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
 65 70 75 80

Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala
 85 90 95
 Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu
 100 105 110
 Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile
 115 120 125
 Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys
 130 135 140
 Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly
 145 150 155 160
 Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu
 165 170 175
 Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp
 180 185 190
 Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys
 195 200 205
 Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr
 210 215 220
 Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg
 225 230 235 240
 Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val
 245 250 255
 Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp
 260 265 270
 Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala
 275 280 285
 His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala
 290 295 300
 Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu
 305 310 315 320
 Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg
 325 330 335
 Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met
 340 345 350
 Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala
 355 360 365
 Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu
 370 375 380
 Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly
 385 390 395 400
 Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr
 405 410 415
 Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln
 420 425 430
 His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu
 435 440 445
 Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met
 450 455 460
 Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr
 465 470 475 480
 Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr
 485 490 495
 Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu
 500 505 510
 Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr

515 520 525
 Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val
 530 535 540
 Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp
 545 550 555 560
 Leu Leu His His His His Val Ser Gly Ser Arg Arg
 565 570

<210> 153
 <211> 1610
 <212> DNA
 <213> Homo Sapiens

<400> 153
 ctgcaggaat tcggcacgag cggtcacgcc gagccagcgc ctgggcctgg aaccgggccc 60
 tagcccccca gtttcgcca ccacctccct accatggacc cccgcaaagt gaacgagctt 120
 cgggcctttg tgaaaatgtg taagcaggat ccgagcgctt tgtacaccga ggaaatgcgc 180
 ttcctgaggg agtgggtgga gagcataggt ggtaaagtac cacctgctac tcagaaaagct 240
 atatcagaag aaaataccaa ggaagaaaaa cctgatagta agaagggtgga ggaagactta 300
 aaggcagacg aaccatcaag tgaggaaaagt gatctagaaa ttgataaaga aggtgtgatt 360
 gaaccagaca ctgatgctcc tcaagaaatg ggagatgaaa atgcggagat aacggaggag 420
 atgatggatc aggc aaatga taaaaaagt gctgctattg aagccctaaa tgatggtgaa 480
 ctccagaaag ccattgactt attcacagat gccatcaagc tgaatcctcg cttggccatt 540
 ttgtatgcca agagggccag tgtcttcgct aaattacaga agccaaatgc tgccatccga 600
 gactgtgaca gagccattga aataaatcct gattcagctc agccttaca gtggcggggg 660
 aaagcacaca gacttctagg ccactgggaa gaagcagccc atgatcttgc ccttgccctgt 720
 aaattggatt atgatgaaga tgctagtga atgctgaaag aagttcaacc tagggcacag 780
 aaaattgcag aacatcggag aaagtatgag cgaaaacgtg aagagcgaga gatcaaagaa 840
 agaatagaac gagttaagaa ggctcgagaa gagcatgaga gagcccagag ggaggaagaa 900
 gccagacgac agtcaggagc tcagtatggc tcttttccag gtggccttcc tgggggaatg 960
 cctggttaatt ttcccggagg aatgcctgga atgggagggg gcatgcctgg aatggctgga 1020
 atgcctggac tcaatgaaat tcttagtgat ccagagggtt ttgcagccat gcaggatcca 1080
 gaagttatgg tggttttcca ggatgtggct cagaacccag caaatatgtc aaaataccag 1140
 agcaacccaa aggttatgaa tctcatcagt aaattgtcag ccaaatttgg aggtcaagcg 1200
 taatgtcctt ctgataaata aagcccttgc tgaaggaaaa gcaacctaga tcacctatg 1260
 gatgtcgcaa taatacaaac cagtgtacct ctgaccttct catcaagaga gctggggtgc 1320
 tttgaagata atccctaccc ctctccccca aatgcagctg aagcatttta cagtgggttg 1380
 ccattagggg attcattcag ataatgtttt cctactagga attacaaact ttaaacactt 1440
 tttaaatctt caaaatattt aaaacaaatt taaagggcct gttaattctt atatttttct 1500
 ttactaatca ttttggattt ttttctttga attattggca gggaatatac ttatgtatgg 1560
 aagattactg ctctgagtga aataaaagtt attagtgcga ggcaaacata 1610

<210> 154
 <211> 369
 <212> PRT
 <213> Homo Sapiens

<400> 154
 Met Asp Pro Arg Lys Val Asn Glu Leu Arg Ala Phe Val Lys Met Cys
 1 5 10 15
 Lys Gln Asp Pro Ser Val Leu Tyr Thr Glu Glu Met Arg Phe Leu Arg
 20 25 30
 Glu Trp Val Glu Ser Ile Gly Gly Lys Val Pro Pro Ala Thr Gln Lys
 35 40 45
 Ala Ile Ser Glu Glu Asn Thr Lys Glu Glu Lys Pro Asp Ser Lys Lys

50 55 60
 Val Glu Glu Asp Leu Lys Ala Asp Glu Pro Ser Ser Glu Glu Ser Asp
 65 70 75 80
 Leu Glu Ile Asp Lys Glu Gly Val Ile Glu Pro Asp Thr Asp Ala Pro
 85 90 95
 Gln Glu Met Gly Asp Glu Asn Ala Glu Ile Thr Glu Glu Met Met Asp
 100 105 110
 Gln Ala Asn Asp Lys Lys Val Ala Ala Ile Glu Ala Leu Asn Asp Gly
 115 120 125
 Glu Leu Gln Lys Ala Ile Asp Leu Phe Thr Asp Ala Ile Lys Leu Asn
 130 135 140
 Pro Arg Leu Ala Ile Leu Tyr Ala Lys Arg Ala Ser Val Phe Val Lys
 145 150 155 160
 Leu Gln Lys Pro Asn Ala Ala Ile Arg Asp Cys Asp Arg Ala Ile Glu
 165 170 175
 Ile Asn Pro Asp Ser Ala Gln Pro Tyr Lys Trp Arg Gly Lys Ala His
 180 185 190
 Arg Leu Leu Gly His Trp Glu Glu Ala Ala His Asp Leu Ala Leu Ala
 195 200 205
 Cys Lys Leu Asp Tyr Asp Glu Asp Ala Ser Ala Met Leu Lys Glu Val
 210 215 220
 Gln Pro Arg Ala Gln Lys Ile Ala Glu His Arg Arg Lys Tyr Glu Arg
 225 230 235 240
 Lys Arg Glu Glu Arg Glu Ile Lys Glu Arg Ile Glu Arg Val Lys Lys
 245 250 255
 Ala Arg Glu Glu His Glu Arg Ala Gln Arg Glu Glu Glu Ala Arg Arg
 260 265 270
 Gln Ser Gly Ala Gln Tyr Gly Ser Phe Pro Gly Gly Phe Pro Gly Gly
 275 280 285
 Met Pro Gly Asn Phe Pro Gly Gly Met Pro Gly Met Gly Gly Gly Met
 290 295 300
 Pro Gly Met Ala Gly Met Pro Gly Leu Asn Glu Ile Leu Ser Asp Pro
 305 310 315 320
 Glu Val Leu Ala Ala Met Gln Asp Pro Glu Val Met Val Ala Phe Gln
 325 330 335
 Asp Val Ala Gln Asn Pro Ala Asn Met Ser Lys Tyr Gln Ser Asn Pro
 340 345 350
 Lys Val Met Asn Leu Ile Ser Lys Leu Ser Ala Lys Phe Gly Gly Gln
 355 360 365
 Ala

<210> 155
 <211> 1323
 <212> DNA
 <213> Homo Sapiens

<400> 155
 cacaaaggca ccaaaccaca aaacgtcaca cgtaaacatc atacgtggca accacaagcc 60
 aatcagttgg atatttcatt cattggtata catatggact gtaagggtgc tttcaggttg 120
 cagaaaagat ggaaaaaagg acatgtgcac tctgccccaa agatgtcgaa tataatgtcc 180
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<210> 156

<211> 191

<212> PRT

<213> Homo Sapiens

<400> 156

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Met Glu Lys Arg Thr Cys Ala Leu Cys Pro Lys Asp Val Glu Tyr Asn
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Val Leu Tyr Phe Ala Gln Ser Glu Asn Ile Ala Ala His Glu Asn Cys
20          25          30
Leu Leu Tyr Ser Ser Gly Leu Val Glu Cys Glu Asp Gln Asp Pro Leu
35          40          45
Asn Pro Asp Arg Ser Phe Asp Val Glu Ser Val Lys Lys Glu Ile Gln
50          55          60
Arg Gly Arg Lys Leu Lys Cys Lys Phe Cys His Lys Arg Gly Ala Thr
65          70          75          80
Val Gly Cys Asp Leu Lys Asn Cys Asn Lys Asn Tyr His Phe Phe Cys
85          90          95
Ala Lys Lys Asp Asp Ala Val Pro Gln Ser Asp Gly Val Arg Gly Ile
100         105         110
Tyr Lys Leu Leu Cys Gln Gln His Ala Gln Phe Pro Ile Ile Ala Gln
115         120         125
Ser Ala Lys Phe Ser Gly Val Lys Arg Lys Arg Gly Arg Lys Lys Pro
130         135         140
Leu Ser Gly Asn His Val Gln Pro Pro Glu Thr Met Lys Cys Asn Thr
145         150         155         160
Phe Ile Arg Gln Val Lys Glu Glu His Gly Arg His Thr Asp Ala Thr
165         170         175
Val Lys Val Pro Phe Leu Lys Lys Cys Lys Gly Ser Arg Thr Ser
180         185         190

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<210> 157

<211> 4065

<212> DNA

<213> Homo Sapiens

<400> 157

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gccagcaaa	agagtgatat	tgagcaattg	cgtgctaaac	ttttggacct	ctcggattct	3300
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<210> 158

<211> 1354

<212> PRT

<213> Homo Sapiens

<400> 158

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      20             25             30
Gly Leu Asp Ala Leu Val Tyr Asp Leu Asp Phe Pro Ala Leu Arg Lys
      35             40             45
Asn Lys Asn Ile Asp Asn Phe Leu Ser Arg Tyr Lys Asp Thr Ile Asn
      50             55             60
Lys Ile Arg Asp Leu Arg Met Lys Ala Glu Asp Tyr Glu Val Val Lys
      65             70             75             80
Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His Lys
      85             90             95
Ser Thr Arg Lys Val Tyr Ala Met Lys Leu Leu Ser Lys Phe Glu Met
      100            105            110
Ile Lys Arg Ser Asp Ser Ala Phe Phe Trp Glu Glu Arg Asp Ile Met
      115            120            125
Ala Phe Ala Asn Ser Pro Trp Val Val Gln Leu Phe Tyr Ala Phe Gln
      130            135            140
Asp Asp Arg Tyr Leu Tyr Met Val Met Glu Tyr Met Pro Gly Gly Asp
      145            150            155            160
Leu Val Asn Leu Met Ser Asn Tyr Asp Val Pro Glu Lys Trp Ala Arg
      165            170            175
Phe Tyr Thr Ala Glu Val Val Leu Ala Leu Asp Ala Ile His Ser Met
      180            185            190
Gly Phe Ile His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys
      195            200            205
Ser Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asn
      210            215            220
Lys Glu Gly Met Val Arg Cys Asp Thr Ala Val Gly Thr Pro Asp Tyr
      225            230            235            240
Ile Ser Pro Glu Val Leu Lys Ser Gln Gly Gly Asp Gly Tyr Tyr Gly
      245            250            255
Arg Glu Cys Asp Trp Trp Ser Val Gly Val Phe Leu Tyr Glu Met Leu
      260            265            270
Val Gly Asp Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser
      275            280            285

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Lys Ile Met Asn His Lys Asn Ser Leu Thr Phe Pro Asp Asp Asn Asp
 290 295 300
 Ile Ser Lys Glu Ala Lys Asn Leu Ile Cys Ala Phe Leu Thr Asp Arg
 305 310 315 320
 Glu Val Arg Leu Gly Arg Asn Gly Val Glu Glu Ile Lys Arg His Leu
 325 330 335
 Phe Phe Lys Asn Asp Gln Trp Ala Trp Glu Thr Leu Arg Asp Thr Val
 340 345 350
 Ala Pro Val Val Pro Asp Leu Ser Ser Asp Ile Asp Thr Ser Asn Phe
 355 360 365
 Asp Asp Leu Glu Glu Asp Lys Gly Glu Glu Glu Thr Phe Pro Ile Pro
 370 375 380
 Lys Ala Phe Val Gly Asn Gln Leu Pro Phe Val Gly Phe Thr Tyr Tyr
 385 390 395 400
 Ser Asn Arg Arg Tyr Leu Ser Ser Ala Asn Pro Asn Asp Asn Arg Thr
 405 410 415
 Ser Ser Asn Ala Asp Lys Ser Leu Gln Glu Ser Leu Gln Lys Thr Ile
 420 425 430
 Tyr Lys Leu Glu Glu Gln Leu His Asn Glu Met Gln Leu Lys Asp Glu
 435 440 445
 Met Glu Gln Lys Cys Arg Thr Ser Asn Ile Lys Leu Asp Lys Ile Met
 450 455 460
 Lys Glu Leu Asp Glu Glu Gly Asn Gln Arg Arg Asn Leu Glu Ser Thr
 465 470 475 480
 Val Ser Gln Ile Glu Lys Glu Lys Met Leu Leu Gln His Arg Ile Asn
 485 490 495
 Glu Tyr Gln Arg Lys Ala Glu Gln Glu Asn Glu Lys Arg Arg Asn Val
 500 505 510
 Glu Asn Glu Val Ser Thr Leu Lys Asp Gln Leu Glu Asp Leu Lys Lys
 515 520 525
 Val Ser Gln Asn Ser Gln Leu Ala Asn Glu Lys Leu Ser Gln Leu Gln
 530 535 540
 Lys Gln Leu Glu Glu Ala Asn Asp Leu Leu Arg Thr Glu Ser Asp Thr
 545 550 555 560
 Ala Val Arg Leu Arg Lys Ser His Thr Glu Met Ser Lys Ser Ile Ser
 565 570 575
 Gln Leu Glu Ser Leu Asn Arg Glu Leu Gln Glu Arg Asn Arg Ile Leu
 580 585 590
 Glu Asn Ser Lys Ser Gln Thr Asp Lys Asp Tyr Tyr Gln Leu Gln Ala
 595 600 605
 Ile Leu Glu Ala Glu Arg Arg Asp Arg Gly His Asp Ser Glu Met Ile
 610 615 620
 Gly Asp Leu Gln Ala Arg Ile Thr Ser Leu Gln Glu Glu Val Lys His
 625 630 635 640
 Leu Lys His Asn Leu Glu Lys Val Glu Gly Glu Arg Lys Glu Ala Gln
 645 650 655
 Asp Met Leu Asn His Ser Glu Lys Glu Lys Asn Asn Leu Glu Ile Asp
 660 665 670
 Leu Asn Tyr Lys Leu Lys Ser Leu Gln Gln Arg Leu Glu Gln Glu Val
 675 680 685
 Asn Glu His Lys Val Thr Lys Ala Arg Leu Thr Asp Lys His Gln Ser
 690 695 700
 Ile Glu Glu Ala Lys Ser Val Ala Met Cys Glu Met Glu Lys Lys Leu
 705 710 715 720
 Lys Glu Glu Arg Glu Ala Arg Glu Lys Ala Glu Asn Arg Val Val Gln

725 730 735
 Ile Glu Lys Gln Cys Ser Met Leu Asp Val Asp Leu Lys Gln Ser Gln
 740 745 750
 Gln Lys Leu Glu His Leu Thr Gly Asn Lys Glu Arg Met Glu Asp Glu
 755 760 765
 Val Lys Asn Leu Thr Leu Gln Leu Glu Gln Glu Ser Asn Lys Arg Leu
 770 775 780
 Leu Leu Gln Asn Glu Leu Lys Thr Gln Ala Phe Glu Ala Asp Asn Leu
 785 790 795 800
 Lys Gly Leu Glu Lys Gln Met Lys Gln Glu Ile Asn Thr Leu Leu Glu
 805 810 815
 Ala Lys Arg Leu Leu Glu Phe Glu Leu Ala Gln Leu Thr Lys Gln Tyr
 820 825 830
 Arg Gly Asn Glu Gly Gln Met Arg Glu Leu Gln Asp Gln Leu Glu Ala
 835 840 845
 Glu Gln Tyr Phe Ser Thr Leu Tyr Lys Thr Gln Val Lys Glu Leu Lys
 850 855 860
 Glu Glu Ile Glu Glu Lys Asn Arg Glu Asn Leu Lys Lys Ile Gln Glu
 865 870 875 880
 Leu Gln Asn Glu Lys Glu Thr Leu Ala Thr Gln Leu Asp Leu Ala Glu
 885 890 895
 Thr Lys Ala Glu Ser Glu Gln Leu Ala Arg Gly Leu Leu Glu Glu Gln
 900 905 910
 Tyr Phe Glu Leu Thr Gln Glu Ser Lys Lys Ala Ala Ser Arg Asn Arg
 915 920 925
 Gln Glu Ile Thr Asp Lys Asp His Thr Val Ser Arg Leu Glu Glu Ala
 930 935 940
 Asn Ser Met Leu Thr Lys Asp Ile Glu Ile Leu Arg Arg Glu Asn Glu
 945 950 955 960
 Glu Leu Thr Glu Lys Met Lys Lys Ala Glu Glu Glu Tyr Lys Leu Glu
 965 970 975
 Lys Glu Glu Glu Ile Ser Asn Leu Lys Ala Ala Phe Glu Lys Asn Ile
 980 985 990
 Asn Thr Glu Arg Thr Leu Lys Thr Gln Ala Val Asn Lys Leu Ala Glu
 995 1000 1005
 Ile Met Asn Arg Lys Asp Phe Lys Ile Asp Arg Lys Lys Ala Asn Thr
 1010 1015 1020
 Gln Asp Leu Arg Lys Lys Glu Lys Glu Asn Arg Lys Leu Gln Leu Glu
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 1045 1050 1055
 Lys Glu Leu Asn Asp Met Gln Ala Gln Leu Val Glu Glu Cys Ala His
 1060 1065 1070
 Arg Asn Glu Leu Gln Met Gln Leu Ala Ser Lys Glu Ser Asp Ile Glu
 1075 1080 1085
 Gln Leu Arg Ala Lys Leu Leu Asp Leu Ser Asp Ser Thr Ser Val Ala
 1090 1095 1100
 Ser Phe Pro Ser Ala Asp Glu Thr Asp Gly Asn Leu Pro Glu Ser Arg
 1105 1110 1115 112
 Ile Glu Gly Trp Leu Ser Val Pro Asn Arg Gly Asn Ile Lys Arg Tyr
 1125 1130 1135
 Gly Trp Lys Lys Gln Tyr Val Val Val Ser Ser Lys Lys Ile Leu Phe
 1140 1145 1150
 Tyr Asn Asp Glu Gln Asp Lys Glu Gln Ser Asn Pro Ser Met Val Leu
 1155 1160 1165

Asp Ile Asp Lys Leu Phe His Val Arg Pro Val Thr Gln Gly Asp Val
 1170 1175 1180
 Tyr Arg Ala Glu Thr Glu Glu Ile Pro Lys Ile Phe Gln Ile Leu Tyr
 1185 1190 1195 1200
 Ala Asn Glu Gly Glu Cys Arg Lys Asp Val Glu Met Glu Pro Val Gln
 1205 1210 1215
 Gln Ala Glu Lys Thr Asn Phe Gln Asn His Lys Gly His Glu Phe Ile
 1220 1225 1230
 Pro Thr Leu Tyr His Phe Pro Ala Asn Cys Asp Ala Cys Ala Lys Pro
 1235 1240 1245
 Leu Trp His Val Phe Lys Pro Pro Pro Ala Leu Glu Cys Arg Arg Cys
 1250 1255 1260
 His Val Lys Cys His Arg Asp His Leu Asp Lys Lys Glu Asp Leu Ile
 1265 1270 1275 1280
 Cys Pro Cys Lys Val Ser Tyr Asp Val Thr Ser Ala Arg Asp Met Leu
 1285 1290 1295
 Leu Leu Ala Cys Ser Gln Asp Glu Gln Lys Lys Trp Val Thr His Leu
 1300 1305 1310
 Val Lys Lys Ile Pro Lys Asn Pro Pro Ser Gly Phe Val Arg Ala Ser
 1315 1320 1325
 Pro Arg Thr Leu Ser Thr Arg Ser Thr Ala Asn Gln Ser Phe Arg Lys
 1330 1335 1340
 Val Val Lys Asn Thr Ser Gly Lys Thr Ser
 1345 1350

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 <211> 683
 <212> DNA
 <213> Homo Sapiens

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 aggcaccggc atccccctggt gctggaaacc cacctgggac cccaaaggga aagagagagc 180
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 tagacagttg ctcggcagca gacggcagtt tggctgctga gatgcctaaa ctggaagcag 360
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 gcaaaacgga caaaaacctc tctaaactga aaagtgcctg gccattgcc cctgccccag 480
 cccccactcc ccgcagcta atcgctatac ccactgcaac ctttacaacg accaccactg 540
 ggacaatacc cggactgcc tccctcacia caactgttgt tcaggctaca ccaaagagtc 600
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<210> 160
 <211> 227
 <212> PRT
 <213> Homo Sapiens

<400> 160
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 1 5 10 15
 Glu Gly Leu Ser Asn Val Ala Leu Glu Cys Ser Glu Pro Ser Thr Ser
 20 25 30
 Val Ser Ala Tyr Asp Gln Leu Lys Ala Pro Ala Ser Pro Gly Ala Gly

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      35              40              45
Asn Pro Pro Gly Thr Pro Lys Gly Lys Arg Glu Leu Met Ser Asn Gly
  50              55              60
Pro Gly Ser Ile Ile Gly Ala Lys Ala Gly Lys Asn Ser Gly Lys Lys
  65              70              75              80
Lys Gly Leu Asn Asn Glu Leu Asn Asn Leu Pro Val Ile Ser Asn Met
      85              90              95
Thr Ala Ala Leu Asp Ser Cys Ser Ala Ala Asp Gly Ser Leu Ala Ala
      100              105              110
Glu Met Pro Lys Leu Glu Ala Glu Gly Leu Ile Asp Lys Lys Asn Leu
      115              120              125
Gly Asp Lys Glu Lys Gly Lys Lys Ala Asn Asn Cys Lys Thr Asp Lys
      130              135              140
Asn Leu Ser Lys Leu Lys Ser Ala Arg Pro Ile Ala Pro Ala Pro Ala
      145              150              155              160
Pro Thr Pro Pro Gln Leu Ile Ala Ile Pro Thr Ala Thr Phe Thr Thr
      165              170              175
Thr Thr Thr Gly Thr Ile Pro Gly Leu Pro Ser Leu Thr Thr Thr Val
      180              185              190
Val Gln Ala Thr Pro Lys Ser Pro Pro Leu Lys Pro Ile Gln Pro Lys
      195              200              205
Pro Thr Ile Met Gly Glu Pro Ile Thr Val Asn Pro Ala Leu Val Ser
      210              215              220
Leu Lys Asp
      225

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<210> 161
 <211> 662
 <212> DNA
 <213> Homo Sapiens

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<400> 161
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agtactggcc tgcttgtaaa aatggggatg agtgtgccta ccatcacccc atctcacct      180
gcaaagcctt cccaattgt aaatttgctg aaaaatgttt gtttgttcac ccaaattgta      240
aatatgatgc aaagtgtact aaaccagatt gtcccttcac tcatgtgagt agaagaattc      300
cagtactgtc tccaaaacca gttgcaccac cagcaccacc ttccagtagt cagctctgcc      360
gttacttccc tgcttgtaag aagatggaat gtcccttcta tcatccaaa cattgtaggt      420
ttaacactca atgtacaaga ccggactgca cattctacca tcccaccatt aatgtccac      480
cacgacatgc cttgaaatgg attcgacctc aaaccagcga atagcaccca gtctgcctg      540
gcagaagatc atgcagtttg gaagttttca tgtctgatga aagatctcta cagaacttgt      600
caaatctttg aaacttgga tatattgctt tcataatatg aaggtttatt ggctatctaa      660
aa

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<210> 162
 <211> 173
 <212> PRT
 <213> Homo Sapiens

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<400> 162
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Ser Phe Ser Asn Ala Glu Met Ser Glu Leu Ser Val Ala Gln Lys Pro
      20              25              30

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Glu Lys Leu Leu Glu Arg Cys Lys Tyr Trp Pro Ala Cys Lys Asn Gly
 35 40 45
 Asp Glu Cys Ala Tyr His His Pro Ile Ser Pro Cys Lys Ala Phe Pro
 50 55 60
 Asn Cys Lys Phe Ala Glu Lys Cys Leu Phe Val His Pro Asn Cys Lys
 65 70 75 80
 Tyr Asp Ala Lys Cys Thr Lys Pro Asp Cys Pro Phe Thr His Val Ser
 85 90 95
 Arg Arg Ile Pro Val Leu Ser Pro Lys Pro Val Ala Pro Pro Ala Pro
 100 105 110
 Pro Ser Ser Ser Gln Leu Cys Arg Tyr Phe Pro Ala Cys Lys Lys Met
 115 120 125
 Glu Cys Pro Phe Tyr His Pro Lys His Cys Arg Phe Asn Thr Gln Cys
 130 135 140
 Thr Arg Pro Asp Cys Thr Phe Tyr His Pro Thr Ile Asn Val Pro Pro
 145 150 155 160
 Arg His Ala Leu Lys Trp Ile Arg Pro Gln Thr Ser Glu
 165 170

<210> 163
 <211> 2912
 <212> DNA
 <213> Homo Sapiens

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<211> 732

<212> PRT

<213> Homo Sapiens

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35     40     45
Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile Arg Tyr Glu Thr Leu
50     55     60
Thr Asp Pro Ser Lys Leu Asp Ser Gly Lys Glu Leu His Ile Asn Leu
65     70     75     80
Ile Pro Asn Lys Gln Asp Arg Thr Leu Thr Ile Val Asp Thr Gly Ile
85     90     95
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Ala Glu Lys Val Thr Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr
145    150    155    160
Ala Trp Glu Ser Ser Ala Gly Gly Ser Phe Thr Val Arg Thr Asp Thr
165    170    175
Gly Glu Pro Met Gly Arg Gly Thr Lys Val Ile Leu His Leu Lys Glu
180    185    190
Asp Gln Thr Glu Tyr Leu Glu Glu Arg Arg Ile Lys Glu Ile Val Lys
195    200    205
Lys His Ser Gln Phe Ile Gly Tyr Pro Ile Thr Leu Phe Val Glu Lys
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Glu Arg Asp Lys Glu Val Ser Asp Asp Glu Ala Glu Glu Lys Glu Asp

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 <212> DNA
 <213> Homo Sapiens

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 <212> PRT
 <213> Homo Sapiens

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 35 40 45
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 65 70 75 80
 Lys Ser Pro Asp Glu Ala Tyr Ala Ile Ala Lys Lys Leu Gly Ser Lys
 85 90 95
 Asp Val Val Ile Lys Ala Gln Val Leu Ala Gly Gly Arg Gly Lys Gly
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 180 185 190
 Val Asn Ile Glu Asp Val Ala Ala Glu Ser Pro Glu Ala Ile Ile Lys
 195 200 205
 Glu Pro Ile Asp Ile Glu Glu Gly Ile Lys Lys Glu Gln Ala Leu Gln
 210 215 220
 Leu Ala Gln Lys Asn Gly Ile Ser Pro Asn Ile Gly Ile Ser Ser Arg
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<211> 5307

<212> DNA

<213> Homo Sapiens

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5307

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 <212> PRT
 <213> Homo Sapiens

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 50 55 60
 Gly Arg Lys Pro Pro Leu Leu Lys Lys Lys Leu Arg Ser Ser Val Ala
 65 70 75 80
 Ala Pro Glu Lys Ser Ser Ser Asn Asp Ser Val Asp Glu Glu Thr Ala
 85 90 95
 Glu Ser Asp Thr Ser Pro Val Leu Glu Lys Glu His Gln Pro Asp Val
 100 105 110
 Asp Ser Ser Asn Ile Cys Thr Val Gln Thr His Val Glu Asn Gln Ser
 115 120 125
 Ala Asn Cys Leu Lys Ser Cys Asn Glu Gln Ile Glu Glu Ser Glu Lys
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 145 150 155 160
 Glu Ser Cys Ala Gln Asp Leu Pro Val Leu Val Gly Glu Glu Gly Glu
 165 170 175
 Val Lys Lys Leu Glu Asn Thr Gly Ile Glu Ala Asn Val Leu Cys Leu
 180 185 190
 Glu Ser Glu Ile Ser Glu Asn Ile Leu Glu Lys Gly Gly Asp Pro Leu
 195 200 205
 Glu Lys Gln Asp Gln Ile Ser Gly Leu Ser Gln Ser Glu Val Lys Thr
 210 215 220
 Asp Val Cys Thr Val His Leu Pro Asn Asp Phe Pro Thr Cys Leu Thr
 225 230 235 240
 Ser Glu Ser Lys Val Tyr Gln Pro Val Ser Cys Pro Leu Ser Asp Leu
 245 250 255
 Ser Glu Asn Val Glu Ser Val Val Asn Glu Glu Lys Ile Thr Glu Ser
 260 265 270
 Ser Leu Val Glu Ile Thr Glu His Lys Asp Phe Thr Leu Lys Thr Glu
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 Gln Thr Val Asp Arg Gln Ser Val Lys Ser Pro Glu Val Gln Leu Leu
 305 310 315 320
 Gly His Val Glu Thr Glu Asp Val Glu Ile Ile Ala Thr Cys Asp Thr
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 Phe Gly Asn Glu Asp Phe Asn Asn Ile Gln Asp Ser Glu Asn Asn Leu
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385              390              395              400
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      405              410              415
Glu Val Glu Pro Ser Val Asn Ala Asp Leu Lys Gln Met Asn Glu Asn
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Ser Val Thr His Cys Ser Glu Asn Asn Met Pro Ser Ser Asp Leu Ala
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<211> 597
<212> DNA
<213> Homo Sapiens
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-132-

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gcaacaagg gacagggcct caaagtgtgc ggtagggagc caggaccccg ccagtggcgt	420
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aagggctggc taagggaggc cggggcggag gaagccaagc tctgcaggcc ctgacaaagt	540
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<210> 170

<211> 3344

<212> DNA

<213> Homo Sapiens

<400> 170

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ctctaacagc aagtgaatc cggcagcgat ttatagattt cttcaagagg aacgagcata	180
cgtatgttca ctgctctgcc accatcccat tggatgacct cactttgctc tttgccaatg	240
caggcatgaa ccagtttaaa cccattttcc tgaacacaat tgacctatct caccctatgg	300
caaagctgag cagagctgcc aatacccaga agtgcacccg ggctgggggc aaacaaaatg	360
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tgatcgctac gctcgcatct atagataacg gctctccaga cctgagcttt ccgctgcagc 3300
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<210> 171
 <211> 1004
 <212> PRT
 <213> Homo Sapiens

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<400> 171
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Val Thr Phe Lys Met Asp Ser Thr Leu Thr Ala Ser Glu Ile Arg Gln
      35             40             45
Arg Phe Ile Asp Phe Phe Lys Arg Asn Glu His Thr Tyr Val His Ser
      50             55             60
Ser Ala Thr Ile Pro Leu Asp Asp Pro Thr Leu Leu Phe Ala Asn Ala
      65             70             75             80
Gly Met Asn Gln Phe Lys Pro Ile Phe Leu Asn Thr Ile Asp Pro Ser
      85             90             95
His Pro Met Ala Lys Leu Ser Arg Ala Ala Asn Thr Gln Lys Cys Ile
      100            105            110
Arg Ala Gly Gly Lys Gln Asn Asp Leu Asp Asp Val Gly Lys Asp Val
      115            120            125
Tyr His His Thr Phe Phe Glu Met Leu Gly Ser Trp Ser Phe Gly Asp
      130            135            140
Tyr Phe Lys Glu Leu Ala Cys Lys Met Ala Leu Glu Leu Leu Thr Gln
      145            150            155            160
Glu Phe Gly Ile Pro Ile Glu Arg Leu Tyr Val Thr Tyr Phe Gly Gly
      165            170            175
Asp Glu Ala Ala Gly Leu Glu Ala Asp Leu Glu Cys Lys Gln Ile Trp
      180            185            190
Gln Asn Leu Gly Leu Asp Asp Thr Lys Ile Leu Pro Gly Asn Met Lys
      195            200            205
Asp Asn Phe Trp Glu Met Gly Asp Thr Gly Pro Cys Gly Pro Cys Ser
      210            215            220
Glu Ile His Tyr Asp Arg Ile Gly Gly Arg Asp Ala Ala His Leu Val
      225            230            235            240
Asn Gln Asp Asp Pro Asn Val Leu Glu Ile Trp Asn Leu Val Phe Ile
      245            250            255
Gln Tyr Asn Arg Glu Ala Asp Gly Ile Leu Lys Pro Leu Pro Lys Lys
      260            265            270

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Ser Ile Asp Thr Gly Met Gly Leu Glu Arg Leu Val Ser Val Leu Gln
 275 280 285
 Asn Lys Met Ser Asn Tyr Asp Thr Asp Leu Phe Val Pro Tyr Phe Glu
 290 295 300
 Ala Ile Gln Lys Gly Thr Gly Ala Arg Pro Tyr Thr Gly Lys Val Gly
 305 310 315 320
 Ala Glu Asp Ala Asp Gly Ile Asp Met Ala Tyr Arg Val Leu Ala Asp
 325 330 335
 His Ala Arg Thr Ile Thr Val Ala Leu Ala Asp Gly Gly Arg Pro Asp
 340 345 350
 Asn Thr Gly Arg Gly Tyr Val Leu Arg Arg Ile Leu Arg Arg Ala Val
 355 360 365
 Arg Tyr Ala His Glu Lys Leu Asn Ala Ser Arg Gly Phe Phe Ala Thr
 370 375 380
 Leu Val Asp Val Val Val Gln Ser Leu Gly Asp Ala Phe Pro Glu Leu
 385 390 395 400
 Lys Lys Asp Pro Asp Met Val Lys Asp Ile Ile Asn Glu Glu Glu Val
 405 410 415
 Gln Phe Leu Lys Thr Leu Ser Arg Gly Arg Arg Ile Leu Asp Arg Lys
 420 425 430
 Ile Gln Ser Leu Gly Asp Ser Lys Thr Ile Pro Gly Asp Thr Ala Trp
 435 440 445
 Leu Leu Tyr Asp Thr Tyr Gly Phe Pro Val Asp Leu Thr Gly Leu Ile
 450 455 460
 Ala Glu Glu Lys Gly Leu Val Val Asp Met Asp Gly Phe Glu Glu Glu
 465 470 475 480
 Arg Lys Leu Ala Gln Leu Lys Ser Gln Gly Lys Gly Ala Gly Gly Glu
 485 490 495
 Asp Leu Ile Met Leu Asp Ile Tyr Ala Ile Glu Glu Leu Arg Ala Arg
 500 505 510
 Gly Leu Glu Val Thr Asp Asp Ser Pro Lys Tyr Asn Tyr His Leu Asp
 515 520 525
 Ser Ser Gly Ser Tyr Val Phe Glu Asn Thr Val Ala Thr Val Met Ala
 530 535 540
 Leu Arg Arg Glu Lys Met Phe Val Glu Glu Val Ser Thr Gly Gln Glu
 545 550 555 560
 Cys Gly Val Val Leu Asp Lys Thr Cys Phe Tyr Ala Glu Gln Gly Gly
 565 570 575
 Gln Ile Tyr Asp Glu Gly Tyr Leu Val Lys Val Asp Asp Ser Ser Glu
 580 585 590
 Asp Lys Thr Glu Phe Thr Val Lys Asn Ala Gln Val Arg Gly Gly Tyr
 595 600 605
 Val Leu His Ile Gly Thr Ile Tyr Gly Asp Leu Lys Val Gly Asp Gln
 610 615 620
 Val Trp Leu Phe Ile Asp Glu Pro Arg Arg Arg Pro Ile Met Ser Asn
 625 630 635 640
 His Thr Ala Thr His Ile Leu Asn Phe Ala Leu Arg Ser Val Leu Gly
 645 650 655
 Glu Ala Asp Gln Lys Gly Ser Leu Val Ala Pro Asp Arg Leu Arg Phe
 660 665 670
 Asp Phe Thr Ala Lys Gly Ala Met Ser Thr Gln Gln Ile Lys Lys Ala
 675 680 685
 Glu Glu Ile Ala Asn Glu Met Ile Glu Ala Ala Lys Ala Val Tyr Thr
 690 695 700
 Gln Asp Cys Pro Leu Ala Ala Ala Lys Ala Ile Gln Gly Leu Arg Ala

705 710 715 720
 Val Phe Asp Glu Thr Tyr Pro Asp Pro Val Arg Val Val Ser Ile Gly
 725 730 735
 Val Pro Val Ser Glu Leu Leu Asp Asp Pro Ser Gly Pro Ala Gly Ser
 740 745 750
 Leu Thr Ser Val Glu Phe Cys Gly Gly Thr His Leu Arg Asn Ser Ser
 755 760 765
 His Ala Gly Ala Phe Val Ile Val Thr Glu Glu Ala Ile Ala Lys Gly
 770 775 780
 Ile Arg Arg Ile Val Ala Val Thr Gly Ala Glu Ala Gln Lys Ala Leu
 785 790 795 800
 Arg Lys Ala Glu Ser Leu Lys Lys Cys Leu Ser Val Met Glu Ala Lys
 805 810 815
 Val Lys Ala Gln Thr Ala Pro Asn Lys Asp Val Gln Arg Glu Ile Ala
 820 825 830
 Asp Leu Gly Glu Ala Leu Ala Thr Ala Val Ile Pro Gln Trp Gln Lys
 835 840 845
 Asp Glu Leu Arg Glu Thr Leu Lys Ser Leu Lys Lys Val Met Asp Asp
 850 855 860
 Leu Asp Arg Ala Ser Lys Ala Asp Val Gln Lys Arg Val Leu Glu Lys
 865 870 875 880
 Thr Lys Gln Phe Ile Asp Ser Asn Pro Asn Gln Pro Leu Val Ile Leu
 885 890 895
 Glu Met Glu Ser Gly Ala Ser Ala Lys Ala Leu Asn Glu Ala Leu Lys
 900 905 910
 Leu Phe Lys Met His Ser Pro Gln Thr Ser Ala Met Leu Phe Thr Val
 915 920 925
 Asp Asn Glu Ala Gly Lys Ile Thr Cys Leu Cys Gln Val Pro Gln Asn
 930 935 940
 Ala Ala Asn Arg Gly Leu Lys Ala Ser Glu Trp Val Gln Gln Val Ser
 945 950 955 960
 Gly Leu Met Asp Gly Lys Gly Gly Gly Lys Asp Val Ser Ala Gln Ala
 965 970 975
 Thr Gly Lys Asn Val Gly Cys Leu Gln Glu Ala Leu Gln Leu Ala Thr
 980 985 990
 Ser Phe Ala Gln Leu Arg Leu Gly Asp Val Lys Asn
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<210> 172

<211> 659

<212> DNA

<213> Homo Sapiens

<400> 172

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gaaccaaccg	agtcggatcc	tgaccctaaa	acctagtatt	ttccacttgt	tcatcaatat	180
ggaaaaactca	gattccaatg	acaaaggaag	tggtgatcag	tctgcagcac	agcgcagaag	240
tcagatggac	cgattggatc	gagaagaagc	tttctatcaa	tttgtaaata	acctgagtga	300
agaagattat	aggcttatga	gagataacaa	tttgctaggc	accccagggtg	aaagtactga	360
ggaagagttg	ctgagacgac	tacagcaaat	taaagaaggc	ccaccaccgc	aaaactcaga	420
tgaaaataga	ggaggagact	cttcagatga	tgtgtctaata	ggtgactcta	taatagactg	480
gcttaactct	gtcagacaaa	ctggaaatac	aacaagaagt	gggcaaagag	gaaaccaatc	540
ttggagagca	gtgagtcgga	ctaataccaa	cagtggtgga	tttcagattc	agtttagaga	600
taaatgttaa	cccgtataaa	tgggagccaa	aattcagaga	atgaaaatga	gccatctgc	659

<210> 173
 <211> 192
 <212> PRT
 <213> Homo Sapiens

<400> 173
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 Glu Gln Pro Arg Arg Arg Arg Pro Asn Gln Pro Ser Arg Ile Leu Thr
 35 40 45
 Leu Lys Pro Ser Ile Phe His Leu Phe Ile Asn Met Glu Asn Ser Asp
 50 55 60
 Ser Asn Asp Lys Gly Ser Gly Asp Gln Ser Ala Ala Gln Arg Arg Ser
 65 70 75 80
 Gln Met Asp Arg Leu Asp Arg Glu Glu Ala Phe Tyr Gln Phe Val Asn
 85 90 95
 Asn Leu Ser Glu Glu Asp Tyr Arg Leu Met Arg Asp Asn Asn Leu Leu
 100 105 110
 Gly Thr Pro Gly Glu Ser Thr Glu Glu Glu Leu Leu Arg Arg Leu Gln
 115 120 125
 Gln Ile Lys Glu Gly Pro Pro Pro Gln Asn Ser Asp Glu Asn Arg Gly
 130 135 140
 Gly Asp Ser Ser Asp Asp Val Ser Asn Gly Asp Ser Ile Ile Asp Trp
 145 150 155 160
 Leu Asn Ser Val Arg Gln Thr Gly Asn Thr Thr Arg Ser Gly Gln Arg
 165 170 175
 Gly Asn Gln Ser Trp Arg Ala Val Ser Arg Thr Asn Pro Asn Ser Gly
 180 185 190

<210> 174
 <211> 610
 <212> DNA
 <213> Homo Sapiens

<400> 174
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 caaccccaaaa tctgccacag agcagtcagg aactggtatc cgatcagaga gtgagacaga 180
 gtccgaggcc tcagaaatta ctattcctcc cagcaccocg gcagttccac aggctccgt 240
 ccaggggggag gactacggca aagggtgtcat cttctacctc agggacaaag tggctcgtggg 300
 gattgtgcta tggaacatct ttaaccgaat gccaatagca aggaagatca ttaaggacgg 360
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 agcatttttt tattcagcag actttctctg tgtatgagtg tgaatgatca agtcctttgt 540
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 cttctaataaa 610

<210> 175
 <211> 138
 <212> PRT
 <213> Homo Sapiens

<400> 175

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 Tyr Glu Ala Ile Gly Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val
 20 25 30
 Phe Ala Lys Ala Thr Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln
 35 40 45
 Ser Gly Thr Gly Ile Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser
 50 55 60
 Glu Ile Thr Ile Pro Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val
 65 70 75 80
 Gln Gly Glu Asp Tyr Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys
 85 90 95
 Val Val Val Gly Ile Val Leu Trp Asn Ile Phe Asn Arg Met Pro Ile
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 Ala Arg Lys Ile Ile Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu
 115 120 125
 Val Ala Lys Leu Phe Asn Ile His Glu Asp
 130 135

<210> 176
 <211> 805
 <212> DNA
 <213> Homo Sapiens

<400> 176
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 gaaagtcca aaaaangggg ccagt 805

<210> 177
 <211> 626
 <212> DNA
 <213> Homo Sapiens

<400> 177
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 caggtttgca ggcaggccgt catgagtgcg ggtggaaggc tccgagggcg tgggcagggg 180
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 aanagccatc tttaccccaa ggaggg 626

<210> 178
 <211> 793
 <212> DNA
 <213> Homo Sapiens

<400> 178
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 tgggtgatggc agaggggcaag gagatcgact ttcgggtgccc gcaagaccag ggctggaacg 480
 ccgagatcac gctgcagatg gtgcagtaca agaatcgtca ggccatcctg gcggtcaaat 540
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 agcccgagct ccaagcccca accccagcct tcagcctcaa gccngcaacc ccaagcccca 660
 attcacaac cccaagccct caagcccca cccaaagccc tcangcccca ngcaagntcc 720
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 acccaanaac nct 793

<210> 179
 <211> 786
 <212> DNA
 <213> Homo Sapiens

<400> 179
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 ctccaagatt aggaattact acggattagg tttttgaaaa taaagtctcc tttttggaaa 180
 atggtctaca ttcagaaatg tcttagaaca agcattttaa aaaaactaat aaataatcat 240
 aatcaaaat acattaaaat aaaattacag tacatcatcg ctctagaaa attcaccata 300
 caagacgatc ctttcaaagg ttcataaata aaagtcttct tgactcgaaa tcgtttcctg 360
 catcgtgatg aaaagtatgc agaaaactaa gaagaatcgc aagttttcag tagggatgag 420
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 acaatagaaa tgtgctcgct ccacttcctc aagtcctcaa aacctgtct tgcccgggag 540
 ctgccccttt cangcagagt tgggaggtgc tgcgganaaa ccggtgcccg tgcggctgcc 600
 aatgcggctg tgggtgtggg tgcngtattt ggtgccgat gcnggtgccg ggtnaagggtg 660
 tgggggtgcca antnaaggat gaaaatgtgg atnttngnat nttgattccg gatacggggt 720
 gggaacctng cngggggccn naaggcttgg ggttggggct naanggctgg ggttttttaa 780
 ttgggg 786

<210> 180
 <211> 791
 <212> DNA
 <213> Homo Sapiens

<400> 180
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 cctcatggc ctcttctccg acttctatct gtgtgtgtgg gcaggtgcca gctgggggtg 180
 gatttctgca gtgtgacctg tgctcaggact ggttccatgg gcagtggtg tcagtgcccc 240

atctcctcac	ctctccaaag	cccagtcctca	cttcatctcc	actgctagcc	tggtgggaat	300
gggacacaaa	attcctgtgt	ccactgtgta	tgcgctcacg	acggccacgc	ctagagacaa	360
tcctagcctt	gctggttgcc	ctgcagaggc	tgcccgtagc	gctgcctgag	ggtgaggccc	420
ttcagtgtct	cacagagagg	gccattggct	ggcaagaccg	tgccagaaag	gctctggcct	480
ctgaagatgt	gactgctctg	ttgcgacagc	tggtgagct	tcgccaa'cag	ctacaggcca	540
aaccanacc	agaggaggcc	tcagtctaca	cttcagccac	tgctgtgac	cctatcagag	600
aaggcagtgg	caacaatatt	tcnaangtcc	aagggtctgct	ggagaatgga	gacantgttg	660
accagtccctg	agaacatggc	tccaggaaag	ggctctgacc	tggagctacn	gtcctcactg	720
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cctggaggga	g					791

<210> 181

<211> 747

<212> DNA

<213> Homo Sapiens

<400> 181

agtatccaaa	catactcatt	gtttttat	ttt taacaaaaga	aatgaaatta	aagatagacc	60
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tgtcttcttt	tataataaga	cccaagggga	gaaaagaaaa	ggatgtacaa	tgaaggtaga	180
agttttgaag	cacccaaaata	ttttatgaca	gggacaaaaa	aacaaaaaac	aaacaaaaat	240
tgaagtacag	aaagagggtg	gtgggggcaa	aaataaaggt	acgcacttgg	gcttctctca	300
gatttggttg	tccctattca	gactagaatg	aaactgggtt	aggaaatcac	tcctgtatgc	360
tagcagggaat	gttgctggca	agacacttct	gagcatcggt	gtgtggactt	tacgaacca	420
ccttttaaca	gtaactctag	gagagaggat	atcaaaaatt	ggcagtga	aattatagat	480
aggcaaaaag	ctccttctga	ggtccaggcc	aggagatagt	angatttaag	aaacaaacaa	540
acaataacaa	ccacaaatgg	acctttgggt	ccactgtcac	aactgttgct	catcagagta	600
ggagaattgt	ancaaaggca	ttaaagaagg	g'caagcaag	ctgaagagcc	tgaatccttg	660
gggttgtaag	ccnatttttg	gn'ttctttc	azgaaaagg	ctgttggn'cg	gtggaanggg	720
tcanggaaca	ntatttcacg	ggtcngc				747

<210> 182

<211> 909

<212> DNA

<213> Homo Sapiens

<400> 182

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acctaggaat	ccaacttaca	aaggatgtga	aggacctctt	caaggagaac	tacaaaccac	120
tgctcaatga	aataaaaagag	gatacaaaaca	aatggaagaa	cattccatgc	tcattgggtag	180
gaagaatcaa	tatcgtgaaa	atggccatac	tgcccaaggt	aatgtataga	ttcaatgcca	240
tccccatcaa	gctaccaatg	actttcttca	cagaatttga	aaaaactact	caaaagtcca	300
tatggaacca	aaaaagagcc	cacattgcca	agtcaatcct	aagccaaaag	aacaaagctg	360
gaggcatcac	gctacctgac	ttcaaaactat	actacaaggc	tacagtaacc	aaaacagcgt	420
ggtactggta	ccaaaacaga	gatataaatc	aatgcaacag	aacagagccc	tcagaaataa	480
tgccacatat	ctacaactat	ctgatctttg	acaaacctga	gaaaaacaag	caatggggaa	540
aggattccct	atttaataaa	tggtgctggg	aaaactggct	agccatatgt	agaaagtcta	600
aactggatct	cttctttata	ccttatataa	aaattaattg	aagatggntt	aaaggactta	660
aaactgtagac	ctaaaaccat	aaaaacccta	gaagaaaaac	ctaggcatta	ccattcangg	720
acataggcct	gggcaaggac	ttcctgtcta	aaacaccaan	agcaatggga	ncaaaagcca	780
aaattgcaaa	tggggattct	aattaactaa	agggtctttg	cacagcnaag	aagctccatc	840
agagngaaca	ggaacntcaa	antgggagaa	at'tttgaacc	taccatcnga	naaggcta	900
nccagaatc						909

<210> 183

<211> 708

<212> DNA

<213> Homo Sapiens

<400> 183

attatcatta	tactttaagt	tttaggttac	atgtgcacaa	tgtgcagggt	agttacatat	60
gtatacatgt	gccatgctgg	tgtgctgcac	ccattaactc	gttatcttagc	attaggtata	120
tctcctaagt	ctatccctcc	cgctccccc	cacccacaa	cagtccccag	agtgtgatgt	180
tcccccttcc	gtgtccatgt	gttctcactg	ttcaattccc	acctatgagt	gagaatatgc	240
gggttttgg	ttttttgtcc	ttgccatagt	ttactgagaa	tgatgatttc	caatttcac	300
cctgtcccta	caaaggacat	gaactcatca	ttttttatgg	ctgcatagta	ttccatgggt	360
tatatgtgcc	acattttctt	aatccagtct	atcattgttg	gccatttggg	ttggttccaa	420
gtctttgcta	ttgtgaatac	tgccgcaata	aacatacgtg	tgcatgtgtc	tttatagcag	480
catgatattat	antcctttgg	gtatatactc	agtaatggga	tggctgggtc	aaatgggnatt	540
ccaantccan	atcccttang	aattgccaca	cggactccac	aanggttgaa	ctantttaca	600
gtcccancaa	cagngtnaaa	gggtccnaan	tcnccaaaat	cctctccaag	caccngttgt	660
tcccggaatt	tttaanggat	tncaattcc	aaccggngt	caaaaggg		708

<210> 184

<211> 855

<212> DNA

<213> Homo Sapiens

<400> 184

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tggaggttgc	acctcctaag	gcttatgaag	ttcgcattaa	gatggtggct	gtaggaaatct	180
gtcgcacaga	tgaccacgtg	gttagtggca	acctggtgac	cccccttcc	gtgattttag	240
gccatgaggc	agccggcatc	gtggagagtg	ttggagaagg	ggtgactaca	gtcaaaccag	300
gtgataaagt	catcccgctc	tttactcctc	agtgtggaaa	atgcagagtt	tgtaaaaacc	360
cggagagcaa	ctactgcttg	aaaaatgac	taggcaatcc	tggggggacc	ctgcaggatg	420
gcaccaggag	gttcacctgc	agggggaagc	ccatcacca	cttccttggc	accagcacct	480
tctcccagta	cacggtgggt	gatgagaatg	cagtggccaa	aattgatgca	gcctcgcccc	540
tggagaaaagt	ctgcctcatt	ggctgtggat	tctcgactgg	gttatgggtc	tgcatgtaac	600
gttgccaagg	tcaccccagg	ctctacctgt	gctgtgtgtg	gcctgggaag	ggcggccta	660
tctgctgtta	tgggtgtgta	aagcaactgg	aggcanccag	aatcaattgc	ggtggacatc	720
aacaaggaca	aattttgcaa	agggcaaaa	agttgggtgc	cactgaatgc	catcaaccct	780
caagnctnca	ngnaaaccca	tccaggnaag	tgctaaaang	gaatttaccg	attggagggt	840
ttggattttt	ccgtt					855

<210> 185

<211> 865

<212> DNA

<213> Homo Sapiens

<400> 185

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ggctgaaagg	agttattgac	ctggctcttg	agaaggctat	tgatgaacct	agtttctctg	120
tggcttacgc	aaacatgtgt	cgatgtctag	taacgctgaa	agtacccatg	gcagacaagc	180
ctggtaacac	agtgaatttc	cggaaagctgc	tactgaaccg	ttgccagaag	gagtttgaaa	240
aagataaagc	agatgatgat	gtctttgaga	agaagcagaa	agaacttgag	gctgccagtg	300
ctccagagga	gaggacaagg	cttcacatg	aactggaaga	agccaaggac	aaagcccgcc	360
ggagatccat	tggcaacatc	aagtttattg	gagaactctt	taaactcaaa	atgctgactg	420
aagccatcat	gcatgactgt	gtggtgaagc	tgctaaagaa	ccatgatgaa	gaatccctgg	480
agtgcctgtg	tcgcctgctc	accaccattg	gcaaagactt	ggactttgaa	aaagcaaagc	540

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cacgtatgga ccagtacttt aatcaagatg gagaaaattg tnaaagaaag aaaaacctca 600
tctagggatt cggttcatgc ttcaaagatg ttatanacct aaggctgttg caattgggggt 660
atctcgaaag agcagatnaa gggcctnaan ctatcgaaca gattcacaaa ganggctaaa 720
attgaaanaa caagaatagc caaagggaag gnccaacaac tcatggacca anggagaaat 780
agaataccaa ggtgttccaa aaanttggcc aaangnnggt tggaaanacn gttcaaaggg 840
ggccangaaa aantccgggt actgg 865

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<210> 186
<211> 736
<212> DNA
<213> Homo Sapiens

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<400> 186
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agagtacttt tctcagggtg gcactttngt ttttttaaac aattcttgga gttctgtggt 120
ccacagcatt tccttctgtt tcaatgttat gtatgttttg attactattg tgatttttta 180
aattttctga agcaagctga gaggcaggca gaaagatttg atgccaaaaa aaaaaaaatc 240
tttcttacct tgttcacccc aaactttctc aaatctggac taaatgctat accttaaaac 300
aaacatgagg tgcattctga aggggaggga aatttatctc tctgcttttc tattatacaa 360
gttgtttaca gaaactgcaa attaaaaaat taaactggca tttgcagtcc ttaaaataaa 420
ttaaaagttc tcaacttttt tttttttttg ctaaactttt ttttaagtat gagtccttgt 480
ttaaaaagaa aagattaaaa cagaaaatat tttctataaa taatacatgt attttggttt 540
tagtgctccc gccctaaggt ttgaagttaa cttttancca ngtacctttt tcctccatga 600
tcaccttttt ttctctttcc cctctcccaa ntccgtgcac acgtgggggt ttccggcaan 660
aattggcctt gctgnactgt gattgggcga anaacgttga aaaaaccttc taaaaaaaaa 720
tacttaaaat tgggtt 736

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<210> 187
<211> 946
<212> DNA
<213> Homo Sapiens

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<400> 187
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ctgtagacct caaataccat cccaagatta tcgggagaaa gggggcagta attacccaaa 120
tccggttga gcatgacgtg aacatccagt ttctgataa ggacgatggg aaccagcccc 180
aggacaaaat taccatcaca gggtagcaaa agaacacaga agctgccagg gatgctatac 240
tgagaattgt ggggtgaactt gagcagatgg tttctgagga cgtcccgtg gaccaccg 300
ttcacgccc catcattggt gcccgcggca aagccattcg caaaatcatg gacgaattca 360
aggtggacat tcgcttccca cagagcggag cccagacccc caactgcgtc actgtgacgg 420
ggctcccaga gaatgtggag gaagccatcg accacatcct caatctggag gaggaatacg 480
tgagtctctg tgggccttgg agccctgagg cgccctggca cgtccaccgg cctgaggccc 540
agccaggagc ttcaggggac aaggtggcac ttgtgtttcc agaggcaagc naagtgcagg 600
ggtgagcaag cnggcgggat gctgggggtg ctggggcaaa ctgaccctgt ctctctgtct 660
tccgcctgca gctagcctga cgttgtggac agtnaangcg cctgcangtt atacatgaaa 720
ccccagcac acgaanaagc caanggnacc tttcaaaaagg ctttnttggg gccgggacca 780
acctgggacc gccagcaacc aatnaaaaaa ggcncgtgacn ttaaccaagc tcngagggaa 840
tttcccance tttgggggcc caaggtggct cccaaagaac cctccccntt ngggggcccc 900
aaacnaatna ttgttcaaaa anggaacaaa aaccctctc aagccc 946

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<210> 188
<211> 802
<212> DNA
<213> Homo Sapiens

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<400> 188

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ggagtcngtt	atcntaacac	gaatgccc	gaccttgggt	taatgttaa	cantggagca	180
ngtcctganc	gggcacggcc	angcctggag	gancggccgc	acacacahcc	angcgcnaag	240
ctccctgcg	gacctcngga	agggggaana	gcgtcaacaa	tttacggng	gtccaaccgc	300
tgggtcaaat	tgagacaaac	cantgtgtg	ttgggttcg	gtcancangc	tggananggt	360
tcngttcntt	ttgatcanta	ncntttggg	ccccaggga	nggtcntggg	anccacctga	420
nccccaaagc	tgggaaattc	ctcaaagctg	cncatgtcaa	gagccttcnc	antgctgctg	480
gcggtccaag	gtgcgtcccg	caccacaaag	cctctggaag	gngccntggc	ctcttctctg	540
gccgggggtt	tcattgtntac	ctgcancgcc	tactgtcca	ccaangtcag	ctaactgcag	600
gcnaagaca	ggaatnacag	ggtcagtctg	ccaacaacc	ccancatccc	ggcccgcctt	660
ggctcaaacc	ctgcaacctt	gcctgccttc	cggaanac	aatttccac	ccttgtntcc	720
ctgaaanccn	cctggntctg	ggccntcaaa	ggcgttgga	ncttccanag	gncnccccca	780
gggntcccc	angggccac	aa				802

<210> 189

<211> 807

<212> DNA

<213> Homo Sapiens

<400> 189

aaaatggcgg	cggcagcgg	gtcgtttgt	ttccgcggt	cctgcggcg	tggcagtggt	60
agcggccttt	gagctgtgg	gaggttccag	cagcagctac	agtgcagact	aagactccag	120
tgcatttcta	tcgtaaccgg	gcgcggggga	gcgcagatcg	gcgccagca	atcacagaag	180
ccgacaaggc	gttcaagcga	aaacatgacc	gctgagccca	tgagtgaag	caagttgaat	240
acattgggtg	agaagcttca	tgacttcctt	gcacactcat	cagaagaatc	tgaagaaaca	300
agttctcctc	cacgacttgc	aatgaatcaa	aacacagata	aaatcagtg	ttctggaagt	360
aactctgata	tgatggaaaa	cagcaaggaa	gagggaacta	gctcttcaga	aaaatccaag	420
tcttcaggat	cgtcacgac	aaagaggaaa	ccttcaattg	taacaaagta	tgtagaatca	480
gatgatgaaa	aacctttgga	tgatgaaact	gtaaatgaag	atgcgtctaa	tgaaaattca	540
gaaaatgata	ttactatgca	nagcttgcca	aaaggtacag	tgattgttca	gccagagcca	600
gtgctgaatg	aagacaaaga	tgattttaaa	ggggcctgaa	tttagaagca	gaagttaaaa	660
tgaaaactga	naatctcaaa	aaacgcccga	gaanatgggc	ttcatgggga	ttgtgangcc	720
tgcactggcn	tggtggacaa	caaggtcaat	caatttcaaa	aaggttccat	ttatagacaa	780
cccttcaatg	caaggtcnta	tttgta				807

<210> 190

<211> 608

<212> DNA

<213> Homo Sapiens

<400> 190

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agattggctt	taatttcttc	taaaagcatc	ttcttgcaa	ttctattctc	aggatcattg	120
tcgtcatcat	catcatccac	tgtgacaggc	actgatttag	ataaggcttc	atctcctgaa	180
gattggcaaa	atccagtatg	tgaagacagc	actaaatctt	cagtcacagg	cttaattttc	240
tgttcatcgc	tgcttccctc	acctatagaa	ttctgatcat	catcttctat	atcagaagaa	300
gatgaggatg	taatgtcagc	ttgcttccct	ttagtgtctg	ttcttaggga	gtttctcttt	360
ttctccttga	caatgactgc	cttcttttta	gatgaagttc	tttgcttctt	ctttttacta	420
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gaagagtac	aancatcttc	tttcatggga	agtatcaaga	tgatgaacaa	tcttgtcnct	600
tccttgaa						608

<210> 191
 <211> 786
 <212> DNA
 <213> Homo Sapiens

<400> 191
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 ttatgagaaa agtgaagttt tatgatgaaa acacaaggca gtggtggatg ccggataccg 180
 gaggagctaa catccagct ctgaatgagc tgctgtctgt gtggaacatg gggttcagcg 240
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 gcagcatcgc gaagtttcca gaagatggcg tcgtgataac acagactttc aaggaccaag 360
 gattggagggt tttaaagcag gaaacagcag ttgttgaaaa cgtccccatt ttgggacttt 420
 atcagattcc agctgagggt ggaggccgga ttgtactgta tggggactcc aattgcttgg 480
 atgacagtca ccgacagaag gactgctttt ggcttctgga tgccctcctc cagtacacat 540
 cgtatgggggt gacaccgcct agcctcagtc actctgggaa ccgccagcgc cctcccantt 600
 ggagcaagct cagtcaactcc agagaggatg gaaggaaacc atctcatcgg tactccaagg 660
 ttctggangg ccattttggga aaaccaaacc ctcgggctcn acaaccctgt ccangcctgt 720
 nctgggccaa gccaanagcc tttaaaccan aacgngccc aattaaccct ttggaaaaca 780
 tcagaa 786

<210> 192
 <211> 819
 <212> DNA
 <213> Homo Sapiens

<400> 192
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 aaattacaaa acatgggtggc aggtgatact tacaaaaata aagcgaagggt ctatgtttta 120
 cagattttgtg catgtttcct tcaaattctca gtctgtactg tcattaaaaa gatcatggaa 180
 tctatgttgt tctcatgat ggaatagtaa aaaaactgca ttccactgac aaaaaaata 240
 gctttgcttc caaatagcac aagtctttaa agtgactttt cccaacaata aatatagaaa 300
 atagccttta acaagcgtct tttagcttgg tcagggttgt atcatttgtt tggaaagtac 360
 atccttcccc tgcaagtcaga agaccccaga cagcctttcc agttctcccc agtcttttgt 420
 gcgcacagct gccggcgga agtctcactg gcggcagagc cactaagtc ctcctgacgg 480
 gatccacagg aatcttctcg atgtaccagg agcctctgcc catcacagga gggcaggccc 540
 atgtagaaca agactctaac aaacctgcag ctggaactg gattcctttt aaaccaacct 600
 gccaacacag ctccgntcac ccaccancgc cgtccgtnaa aggggctctc tgggcctcac 660
 gggtcagcca ggttgccggt cacaccgaaa ggggtccttg ggcgggtgaa cctgctgcat 720
 gaanctggcg gggngcttca accctgggct tctccggct ttcggcctgg ncctgggcct 780
 tgttgaantt gntccacaaa agaaaggcca ggagcaaca 819

<210> 193
 <211> 744
 <212> DNA
 <213> Homo Sapiens

<400> 193
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 tgtctgctgt acctactggc agtcagattg caaatattgg tcagcaagca aacataccta 120
 ctgcagtgca gcagccctct acccaggttc caccttcagt tattcagcag ggtgctctc 180
 catcttcgca agtgggtcca cctgctcaaa ctgggattat tcatcaggga gttcaacta 240
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 cagttagttc ttgcccctct gctagtagta tttctgttac aagtcagggt agttcaactg 420

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cccctgctac	ccaaaatggt	aatttgggtc	aaagtgttaa	gtcaacctcc	cttgatagca	540
actaatacaa	atttgccttt	ggcacaacag	ataccactaa	gttctaccca	agttctccgc	600
acaatcatta	gtccaggcaa	ttggaagcca	aattgaagat	gccaggcggt	gcagcggagc	660
cctccttaag	ttggcttacc	tcaagactaa	tcagttggtg	acaattgggg	ggaatgttca	720
gcaagtttca	agattgggaa	gtta				744

<210> 194
 <211> 567
 <212> DNA
 <213> Homo Sapiens

<400> 194						
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ttacaattgt	gtagagaaca	tgcacagaaa	catatgcata	taactactat	acaggtgata	120
tgcagaaacc	cctactggga	aatccatttc	attagttaga	actgagcatt	tttcaaagta	180
ttcaaccagc	tcaattgaaa	gacttcagtg	aacaaggatt	tacttcagcg	tattcagcag	240
ctagatttca	ggattacaca	aagtgcgtta	ctgtgccaaa	ttcttaaaat	ttcttttaggt	300
gtggtttttg	tcattgtagca	gtttttatgt	agatcnatat	ntaaaagtcc	acacctcttc	360
agacangcca	atgaaacnac	taaatttcaa	tctgtacaan	ctaaatagta	attacagtcc	420
tctangtgnn	caangatact	tacaccacat	anacaaatnt	acnntacgca	naacaacctt	480
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gttttggtgt	ccaatccatt	ggttttg				567

<210> 195
 <211> 771
 <212> DNA
 <213> Homo Sapiens

<400> 195						
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tagttgacaa	tgcatacagc	tgtgatccaa	ggataaaaaa	gttcaaggaa	gaagaaaaag	120
ccaagaaaga	ancanaaaaag	aaagcaaaaag	cagaagctaa	acggaaggag	caagaagcta	180
aagaaaaaca	aagacaagct	gaattagaag	ctgctcggtt	agctaaggag	aaagaagagg	240
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ctgcttttga	aaaacagata	gaagaaataa	atgagcaaat	cagaaaagag	aaagaggaag	540
ctgaggctcg	tatgcgacaa	gcatctaaga	acacagagaa	atcaactggt	ggaagggtgga	600
aaatggaagt	aaaaattggg	cacaaagatg	ntctacaatt	actaatttna	aagctgtgaa	660
tcctgttncc	tgctggaaca	aantcaagat	gggaagttat	tgccaantac	atgaacatac	720
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<210> 196
 <211> 561
 <212> DNA
 <213> Homo Sapiens

<400> 196						
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tccttgatc	gtttcatgca	gtccttcttt	gtcctgccag	gcaccgettc	tgctattttt	180
tcccatcttt	caggtgtatt	tactgggtat	gttttcaaag	cttggttccaa	aagcttctgt	240
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gcgttgctctg cttgaggtac cactccatgt tcttttttga acttatcaaa tgccttttta	360
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tctttggnan gttcttttga ctccaagagg aagaangtnt ngttcatgtn antangcaan	480
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<210> 197

<211> 691

<212> DNA

<213> Homo Sapiens

<400> 197

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<210> 198

<211> 646

<212> DNA

<213> Homo Sapiens

<400> 198

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<210> 199

<211> 811

<212> DNA

<213> Homo Sapiens

<400> 199

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gatgaaatta tttctaagac aaagcaagta attcaggggc tggaagcttt gaagaatgag	180
cacaattcca ttttacaag tttgctggag aactgaagt gtttgaagaa agatgatgaa	240
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<210> 200

<211> 763

<212> DNA

<213> Homo Sapiens

<400> 200

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agttcacaga gaggtgcagc tctgacaaga tcctagaggc tgctagacac agcgggcagc	180
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tgtttgtaga cattgtcaag accctgttta cgagacctca tagcagcttc ttctaactgt	480
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gtaacagttg gntatcaac tttgcangct ttgtaccaac cgccatactc tccaaaaaga	600
tgtcccatcc ttttgcttcc ctttgcatte ttctctttcc tcaacaatgc atccaaatgg	660
gtttaatttc aacatctaca gaaccaaact ccctttcatg tgcacaagtg agaatcnctt	720
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<210> 201

<211> 717

<212> DNA

<213> Homo Sapiens

<400> 201

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agaatganca caattccatt ttacaaagt tgcgtggagc actgaagtgt ttgaagaaag	180
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ttgcagccgc ggctgcccga gcaaggcggc tacgagattc ccgcccggc tgccggacgc	660
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<210> 202

<211> 647

<212> DNA

<213> Homo Sapiens

<400> 202

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tatattacta	agtacatatc	tggcaaagct	acatgtatac	agaaatcagg	aaccccccca	420
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gcgccaaccc	gtcatgccag	gggacagtgt	ganagtcacg	ggncgggcta	ngccaatggg	600
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<210> 203

<211> 786

<212> DNA

<213> Homo Sapiens

<400> 203

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tggaggagga	gcagcaggcc	ctccagaaga	agctgaaggg	gacagaggat	gaggtggaaa	180
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aagcaaaaagt	ttgccnaaaa	ggtctgtggg	caaaaatttg	ggngaaaaac	catcnaatga	780
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<210> 204

<211> 738

<212> DNA

<213> Homo Sapiens

<400> 204

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tcctggccac	ctcttcata	ttgcggcttg	aatcctcagc	gatgtgcttg	gcctccttca	480
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aaggaaggca	anatctgcct	caacaacaat	tggccttctt	cncggccngc	tccaattttc	720
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<210> 205

<211> 818

<212> DNA

<213> Homo Sapiens

<400> 205

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gttctcctcc	ttggcactgg	ccaaggtctc	ttctaggtca	tcgatggttt	tctccaactt	180
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nctngcncca	attttctecn	ggggcctncc	tttcangggg	tnaagaanaa	atttcaaatt	780
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<210> 206

<211> 927

<212> DNA

<213> Homo Sapiens

<400> 206

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tggaggagga	gcagcaggcc	ctccagaaga	agctgaaggg	gacagaggat	gaggtggaaa	180
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<210> 207

<211> 910

<212> DNA

<213> Homo Sapiens

<400> 207

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<210> 208
 <211> 745
 <212> DNA
 <213> Homo Sapiens

<400> 208						
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<210> 209
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 <212> DNA
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<400> 209						
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<210> 210
 <211> 867

<212> DNA

<213> Homo Sapiens

<400> 210

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<210> 211

<211> 972

<212> DNA

<213> Homo Sapiens

<400> 211

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tcttgactat	gagtaaaagg	gaaaaggctc	gactggagat	tgaaccagaa	tgggcttacg	600
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gagataaatc	ccttatgaat	ccctgggtcta	aaatactttc	ctacagctgt	gtaaaaatac	900
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<210> 212

<211> 817

<212> DNA

<213> Homo Sapiens

<400> 212

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tctcgcaaag	agcgggaagc	tgagcttgga	gccaaagcca	aggaattcac	caatgtttat	180
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tttgtgagtt	acgaaaaaca	cgaggatgcc	aataaggctg	tggagagat	gaatggaaaa	360
gaaataaagt	gtaaaatcat	atltgtaggc	cgtgcacaaa	agaaagtaga	acggcaggca	420
gagttaaaac	ggaatattga	acagttgaaa	caggagagaa	ttagtcgata	tcaggggggtg	480
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tggacgcatt	ttggggctcc	aaccactata	tgttgccctg	gccccanagg	aagggaanag	720
agaaaggntc	accttgacca	accagtttta	tgcaacgaan	tggctgggaa	tngagaacca	780
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<210> 213

<211> 756

<212> DNA

<213> Homo Sapiens

<400> 213

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ggcactttat	gatacttttt	ctgcttttgg	aaacatactg	tcctgcaagg	tgggtgtgtga	180
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ggccatcgag	aagatgaatg	gcatgctcct	caatgaccgc	aaagtatttg	tgggcagatt	300
caagtctcgc	aaagagcggg	aagctgagct	tggagccaaa	gccaaggaat	tcaccaatgt	360
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gtttggttaag	accctaagtg	tcaaggtgat	gagagatccc	aatgggaaat	ccaaaggcctt	480
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ggtgaatccc	cacattaaga	acttggatga	cactattgat	gatgaagaaa	attaaggaaa	720
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<210> 214

<211> 728

<212> DNA

<213> Homo Sapiens

<400> 214

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ttgatacaaa	atgacctatt	aaatttgcaa	tttghtaatcc	ttggtgttga	ggtccatagg	240
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tgatcttccc	agccagattt	gaatgcattg	tttggatgan	tgggaacaag	cgttctccca	540
gcatctgctt	ctgttcctgg	gggggtgctg	canccaacag	gaggcaatca	ntggntccng	600
gccctgcaca	tggaccgcaa	ggctgggggtg	cctgcaaaaan	gctgtatggc	aaggatgaag	660
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<210> 215

<211> 710

<212> DNA

<213> Homo Sapiens

<400> 215

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canaacccaa	agaacatatt	cgtataattg	aaaaattcta	ggtgcttcan	aattgacctt	180
ttgatacaaa	atgacctatt	aaatttgcaa	tttgtaancc	ttggtgttga	ggtccatagg	240
acaagctagg	aagtcttcaa	accttgagtt	gaattccana	aggggttatt	tggcttttga	300
atcggttttt	ccttgcttaa	naggtagcag	cagcaacagc	gccacacctt	tgggcagctt	360
ctttcttggc	atgatgagcc	tgtanaactg	ctacagcttc	atccaccttg	gagcgganag	420
actcggggga	ctctaacatg	tgcagcagct	canagtgtgc	tatctccagc	agcattcccc	480
tgatcttccc	agccagattt	gaatgcattg	tttgatgan	tgggaacaag	cgttctccca	540
gcctctgctt	ctgttcctgn	gggggtgctg	canccangca	tggaggcaan	tcagtggctc	600
ctgcccctgc	acaatggacc	gcaaggctgg	ggggtgcctg	canaaggctg	tttgggcaag	660
gangaagggc	ctgcggaana	ctgggangcg	tatttgttan	ggggggcaaa		710

<210> 216

<211> 824

<212> DNA

<213> Homo Sapiens

<400> 216

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tatagataac	aaggcacttt	atgatacttt	ttctgctttt	ggaaacatac	tgtcctgcaa	360
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ggctgccgac	aaggccatcg	agaagatgaa	tggcatgctc	ctcaatgacc	gcaaagtatt	480
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aatccaaaag	gctttgggct	ttgtgagtn	acgaaaaaca	cnaggatgcc	aataaggctg	720
ttggaaagaa	atgaatggga	aaagaaataa	antggtaaaa	tcataatttg	tagggccgtn	780
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<210> 217

<211> 749

<212> DNA

<213> Homo Sapiens

<400> 217

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cagaacccaa	agaacatatt	cgtataattg	aaaaattcta	ggtgcttcat	aattgacctt	180
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acaagctagg	aagtcttcaa	accttgagtt	gaattccata	aggggttatt	tggcttttga	300
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ctttcttggc	atgatgagcc	tgtagaactg	ctacagcttc	atccaccttg	gagcgagag	420
actcggggga	ctctaacatg	tgcagcagct	cagagtgtgc	tatctccagc	agcattcccc	480
tgatcttccc	agccaagatt	tgaatgcatt	gtttggatga	gtgggaacaa	gcgttctccc	540
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ctgcccctgc	acatgggacc	gcaaggctgg	ggtgcctgca	naggctgtat	gggaaggatg	660
nagggtgcc	ggncaactgg	ganggcgtat	ttgtaggggg	caaacaagcc	cggggaagca	720
nccagcagca	acancaacng	cttggcgcc				749

<210> 218
 <211> 600
 <212> DNA
 <213> Homo Sapiens

<400> 218
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 ctattaaatt tgcaatttgt aatccttggg gttgaggtcc ataggacaag ctaggaagtc 240
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 anatttgaat gcattgtttg ggatgangtg gggaanaagc gttctcncag cannengctt 540
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<210> 219
 <211> 1077
 <212> DNA
 <213> Homo Sapiens

<400> 219
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 ccgctccctg ggctatgcct acgtcaactt ccagcagccg gccgacgctg agcgggcttt 180
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 agagatgaat ggaaaagaaa taagtgttaa aatcatattt gtaggccgtg cacaaaagaa 780
 agtagaacgg caagcagagt taaaacggaa atttgaacag ttgaaacagg agagaattag 840
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 attaaggaaa gaattttctc cttttggatc aattaccagt gctaaggtaa tgctggagga 960
 tggagaagc aaagggtttg gcttcgtctg cttctcatct cctgaagaan caaccaagc 1020
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<210> 220
 <211> 1007
 <212> DNA
 <213> Homo Sapiens

<400> 220
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 tctgtcaccc ttcctacag cctgaggagt acatggccta cgttcagagg caagccgact 180
 caaagcagta tggagataaa atcatagagg agctgcaaga tctaggcccc caagtgtgga 240
 gtgagaccaa gtctgggggtg gcaccccaaa agatggcagg tgcgagcccc accaaggatg 300
 acagtaagga ctcagatttc tggaaagatgc ttaatgagcc agaggaccag gccccaggag 360
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aagagcagcc	tgtggatgat	gctgcagaag	tccctcagag	ggaaccagag	aaggaaaggg	600
gtgatccaga	acggcagaga	gagatggaag	aagaggagga	tgaggatgag	gatgaggatg	660
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aagactggag	ggaaaaacaa	gagttccaaa	ncctgggtgaa	nnaagcncat	aaaaaagaag	960
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<210> 221

<211> 833

<212> DNA

<213> Homo Sapiens

<400> 221

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aggatgacag	taaggactca	gatttctgga	agatgcttaa	tgagccagag	gaccaggccc	180
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aaaggggtga	tccagaacgg	cagagagaga	tggaagaaga	ggaggatgag	gatgaggatg	480
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gaactggnaa	acatcatcca	ggagacanga	gaaaganctg	ggacccanat	ggggctgaag	660
aanggatca	aatccgggat	cgggcaatgc	tggctctcaa	aatcaactct	caacaaantc	720
attaaaaaga	ctggagggaa	aaacaagagt	tccaaancct	ggtgaannaa	gncataaaaa	780
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<210> 222

<211> 745

<212> DNA

<213> Homo Sapiens

<400> 222

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caacagaggt	gaaggctcct	caactcagaa	gcacaaattg	taggggacag	ggtgggcagg	180
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cactaagggc	aggtgggggc	ctgcttgctc	agtgcctgct	aagtgtcctg	ccctccttgc	300
tctctctacc	cacctccact	caaaagatcc	tactgaatct	ccaggtaggc	agcagggaat	360
atcctatcat	taggggacaa	taacaggaaa	agccacagag	gagagggaaga	ggattgagtg	420
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<210> 223

<211> 747

<212> DNA

<213> Homo Sapiens

<400> 223

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atgaaagann	aaggatgaaa	cgggcaagtt	actgggggaan	aattttgana	aagggaactg	720
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<210> 224

<211> 618

<212> DNA

<213> Homo Sapiens

<400> 224

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gagggtgaag	ctcctcaact	cagaagcaca	aattgtaggg	gacaggggtg	gcagggaaag	180
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ancctccan	ctgccngttt	ggccctcaag	gggttccaan	gttcngnaaa	gtgggggagg	600
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<210> 225

<211> 765

<212> DNA

<213> Homo Sapiens

<400> 225

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tcagtgtagt	aggaccttcc	agggcagctc	agatctcctc	agacatcagg	taactcatac	180
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gagagaaaact	tgaagaatgt	gagaaaaact	tcagcaagga	tganggagct	taggggagag	660
cagaaaattc	accanggaag	agaaagcctt	attggngta	atcagtgtgg	tanggctttc	720
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<210> 226
 <211> 791
 <212> DNA
 <213> Homo Sapiens

<400> 226
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 tgcaacgtcc ctgaacacca taacttagag aatgaagttt cttagattaga agacataaatg 180
 cagcatttaa aatcaaagaa gcgggaagaa aggtggatga gagcatccaa gcggcagtcg 240
 gagaaagaaa tggaagaact gcatcataat attgatgac ttttgcaaga gaagaaaagc 300
 ttagagtgtg aagtagaaga attacataga actgtccaga aacgtcaaca gcaaaaaggac 360
 ttcattgatg gaaatgtaga gagtcttatg actgaactag aaatagaaaa atcactcaaa 420
 catcatgaag atattgtaga tgaaattgag tgcattgaga agactcttct gaaacgtcgc 480
 tcanagctca ggggaagctga ccgactcctg gcagaggctg agagtgaact ttcattgact 540
 aaagaaaaga caaaaaatgc tgttgaaaag ttactgatg ccaagagaag tttattgcaa 600
 actgagtcag atgctgaggg aattagaaag gagagctcan gaaactgctg ttaanctcgt 660
 caaanctgat cagcagctaa gatcgctcca agctgatgca aaaggatttg gancancaca 720
 angatcaagc aagaaagaa cttgaaaaga aattaacnaa aattntntna gcaaaaagact 780
 cagacttcaa a 791

<210> 227
 <211> 687
 <212> DNA
 <213> Homo Sapiens

<400> 227
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 gacactataa aaanagaggg ccttaagtac attctttttg ttaataagat ttaccagttt 120
 gtaggttcaa atatgcagtt aaaatcactg ttttttttta aacatgttac gaagattaaa 180
 aaaaaaaagg ctccagccaca tgttggttta aattcccata tgcaactatt cccatattga 240
 ctatgtacaa gtgatttata aaaacattgg cattaatggt acaggcaaag taaactacag 300
 tggagtttca naatctcagt tcaactgacg ttgattaaaa aaaccatgtg acattccaat 360
 tatgaagtca gtgaggtagt ggaggtgttt tccttgaata tatttacaca agacagtatt 420
 cctcatctgg ctgaggcatt cttttccgga ttttgtccaa gttganagtc ctctgtgagg 480
 gaagactcca agctgagaca gactgggtga tgacgtgaa tctgcaaagg tgccctgggtga 540
 ccaattcccc ctaanagcat cctacttgtc tcncaaaact gtgntaaagt gccctctgtc 600
 ctgccgcttt cctttaatna aaacttctgg cttngcttgg ggcanacagt gtcggantt 660
 gggccttgag tcnggcttcc cggggaa 687

<210> 228
 <211> 810
 <212> DNA
 <213> Homo Sapiens

<400> 228
 gtctgggcag cgccaggcga tggccctgct gctgggtgct ctgcctctt ggggcctggg 60
 gcagtgaagg ggcgggcggg cgtgggcccga gtggccgcgg gcgccatgga gggggtgctg 120
 tacaantgga ccaactatct gagcgggttg cagcctcgat gggtccttct ctgtggggga 180
 atattgtcct attatgattc tcctgaagat gcctggaaag gttgcaaagg gagcatacaa 240
 atggcagtcg gtgaaattca agttcattct gtagataata cacgcatgga cctgataatc 300
 cctggggaac agtatttcta cctgaaggcc agaagtgtgg ctgaaagaca gcggtggctg 360
 gtggccctgg gatcagccaa ggcttgctg actgacagta ggaccagaa ggagaaagag 420
 tttgctgaaa aactgaaaa cttgaaaacc aaaaatgtcan aactaagact ctactgtgac 480
 ctcttgttcc ancaagtaga ttaaaacata agaagtgacc acaactgggt tgtccaattc 540

tgaggtaaag	gagtcctcca	ctctgggtgt	ttcgtangag	ggaattgatg	tgaggaaacttt	600
gctgaaatca	anctgntata	ctttttctga	aagaccttgg	taagaattca	tgcanatngc	660
aaattgcagc	cttnaanctc	ctgaagcctn	cttctaaccg	gcaactccaac	canggaatna	720
anctnaagct	gggccaatgg	ctccaaagtt	ccaacnaaag	gttaaaanct	cccagctcaa	780
atttgggcng	caaacaaagg	gcaatccaac				810

<210> 229
 <211> 552
 <212> DNA
 <213> Homo Sapiens

<400> 229						
gtaaaattgt	ttgagttcat	tgtagattct	ggatattagc	ccttttgtca	gatgagtaga	60
ttgcaaaaat	tttctcccat	tctgtaggtt	gcctgttcac	tctgatggta	gtttcccttg	120
ctgtgcggaa	gctctttagt	ttaattagat	cccatttgtc	aatttcggct	tttgttgcca	180
ttgctttcgg	tggttttagac	atgaagtcct	tgcccatgcc	tatgtcctga	atggttttcc	240
taggttttct	tctagggttt	ttatggtttt	aggtctaaca	tttaagtctc	gaatccatct	300
tgaattaatt	tttgtataag	gtgtaaggaa	gggatccact	ttcagctttc	tacgtatggc	360
tagccagttt	ttccancacc	atattataaa	tagggaaatc	tttccccant	tctgtttttt	420
gtcangtttg	tcaaagatca	natggctgta	natatgcanc	attatttccg	agggctctgt	480
tcngttccat	tggtctacat	ttccgttttg	gttcnctac	catgctgttt	tttgttacng	540
gtanaccttg	gt					552

<210> 230
 <211> 842
 <212> DNA
 <213> Homo Sapiens

<400> 230						
ctcatcagtt	agaagaaaaa	gaaaatcaaa	ttaagagcat	gaaggctgat	attgaaagtc	60
ttgtaacaga	aaaagaagcc	ttacagaagg	aaggaggcaa	tcagcaacag	gctgcttctg	120
aaaaggagtc	ttgtataaca	cagttgaaga	aagagttatc	tgaaaacatc	aatgctgtca	180
cattgatgaa	agaagagctt	aaagaaaaaa	aagttgagat	tagcagtcct	agtaaacaac	240
taactgattt	gaatgttcag	cttcaaaaata	gcacagcctt	atccgaaaaa	gaagcagcca	300
tttcatcact	aagaaaagcag	tatgatgaag	aaaaatgtga	attgctggat	cagggtgcaag	360
atttatcttt	taaagttgac	actctgagta	aagagaaaat	ttctgctctt	gagcaggtag	420
atgactggtc	caataaatcc	tcagaatgga	agaagaaaagc	acagtcaaga	tttacacagc	480
atcaaaacac	tggttaaagaa	ttgcagatcc	agcttgagtt	aaaatcaaa	gaagcttatg	540
aaaaggatga	gcagataaat	ttattgaagg	aagagcttga	tcagcaaaat	aaaagatttg	600
attgtttaaa	gggtgaaatg	gaagacgaca	agagcaagat	gggagaaaaa	ggagtctaata	660
ttagaacacag	agttaaagtc	tcaaacagca	agaattatgg	gattagagga	ccatattanc	720
caagaaaact	atttggaaat	tagagtcctt	aaatngaaag	ttccttaaaa	aattacaatc	780
aacaaaaagg	atattggacc	acaaagnaat	tggttcaaaa	aaccttcaac	aantttcaag	840
ga						842

<210> 231
 <211> 781
 <212> DNA
 <213> Homo Sapiens

<400> 231						
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tttgataaca	atacagttat	gtattggcta	ttcacaatct	acagtagtgt	tttttctctt	120
gaaaaatata	agtacaaaag	ctaagtaaac	aatgaggtac	tgccatttgg	gattttttac	180
atgtcttagc	ttaaagaact	ggtcttttagc	aaatattcaa	cagatcaacc	tgaataaaat	240

agtcaattaa atgctctaatt ttatcagaaa aaatccacta agtttcacct caaaatgtat	300
tgcacaagtc tttttaaaaa atcacccctaa aaataaatag gaaaggtaag ccgttcttta	360
aaaagaatgg atgaaaggaa tattatgtaa gcccataaag cagggttaagt tatcaaaata	420
tcttttaaac aacataaaaac tcttcccaag agaaaactga agaaaaaact atcaccattt	480
ctccactgat aaaatctatt ttaaaggcag tctgcaactt atctgtgggc cagatttttc	540
ttgggtcttt tggetacatg aggggccctg aatgacaact tcattctcaa agagtagcaa	600
agtgtggaca agttttccaa gcagcangtc acccaatgtc actcttcctc aagatgaagg	660
atcggagcca tgacacatgt ttaactaagc acagaccgga tgggtttacc cagaagatac	720
cactggcaan ggtgaagtaa acatcaggcc gaggcaacct tccccntttc aaaaantttt	780
c	781

<210> 232

<211> 767

<212> DNA

<213> Homo Sapiens

<400> 232

ggtatatagt aaataaactt tatttatctg tttctcagag atgacactgc caacaatcac	60
agatttgcatt acaatacagt tatgtattgg ctattcacaa tttacagtag tggtttttcc	120
tctgaaaaat ataagtacaa aagctaagta aacaatgagg tactgccatt tgggattttt	180
tacatgtctt agcttaaaaga actggtcttt agcaaatatt caacagatca acctgaataa	240
aatagtcaat taaatgctct aatttatcag aaaaaatcca ctaagtttca cctcaaaatg	300
tattgcacaa gtcttttttaa aaaatcaccc taaaaataaa taggaaagggt aagccgttct	360
ttaaaaaagaa tggatgaaag gaatattatg taagcccata aagcaggtta agttatcaaa	420
atatctttta aacaacataa aactcttccc aagagaaaaac tgaagaaaaa actatcacca	480
tttctccact gataaaatct attttanagg cagtctgcaa cttatctgtg ggccagattt	540
ttcttggctt tttggetaca tgagggggccc tgaatgaaaa cttcattctc aaaggagtag	600
caagtgtggg acagttttcc aagcagcagt cacccaatgt cactcttctt caagatgaaa	660
gatcggagnc atgacacatg ttaacctaaag nacangactg gagggtttac ncangaagat	720
acactgcgaa ggtgaaagtt aaacatcaag ccgaggaacc tccccctt	767

<210> 233

<211> 879

<212> DNA

<213> Homo Sapiens

<400> 233

gggagtttaa tacacagctg gcacaaaagg aacaagagct ggaaatgacc ataaaagaaa	60
ctatcaataa ggcccaggag gtggaggctg aacttttaga aagccatcaa gaagagacaa	120
atcagttact taaaaaaatt gctgagaaag atgatgatct aaaacgaaca gccaaaagat	180
atgaagaaat ccttgatgct cgtgaagaag aaatgactgc aaaagtaagg gacctgcaga	240
ctcaacttga ggagctgcag aagaaatacc agcaaaagct agagcaggag gagaaccctg	300
gcaatgataa tgtaacaatt atggagctac agacacagct agcacagaag acgactttaa	360
tcagtgatcc gaaattgaaa gagcaagagt tcagagaaca gattcacaaat ttagaagacc	420
gtttgaagaa atatgaaaag aatgtatatg caacaactgt ggggacacct taaaagggtg	480
gcaatttgta ccatacggat gtctcactct ttggagaacc taccgaattt gagtatttgc	540
gaaaagtgtc ttttgagtat atgatgggtc gtgagactaa gaccatggca aaagttataa	600
ccaccgtact gaagttccct gatgatcaga ctacagaaaat tttgggaaaa gagaagatct	660
cggctgatgt ttacttcacc tcgcagtggg atcctcngag taaaccatca gtcgtgccta	720
agttttacatg tgtcatgggt ccgattcttc atcctttgaa gaaagagtgg acattggggg	780
naccggctgc cttgggaaaa ctgtccanac nttgcnaacn ccttgggggaa atggaagntt	840
ttccanttca agggccccct caangnttgc ccaaacagg	879

<210> 234

<211> 780

<212> DNA

<213> Homo Sapiens

<400> 234

aaactttatt	tatctgtttc	tcagagatga	cactgccaac	aatcacagat	ttgcatacaa	60
tacagttatg	tattggnnng	gcacaattta	cagtagtggt	ttttctctcg	aaaaatataa	120
gtacaaaagc	taagtaaaca	atgagggtact	gccatttggg	attttttaca	tgtcttagct	180
taaagaactg	gtcttttagca	aatattcaac	agatcaacct	gaataaaaata	gtcaattaaa	240
tgtcttaatt	tatcagaaaa	aatccactaa	gtttcacctc	aaaatgtatt	gcacaagtct	300
ttttaaaaaa	tcaccctaaa	aataaatagg	aaaggtaagc	cgttctttaa	aaagaatgga	360
tgaaaggaat	attatgtaag	cccataaagc	aggttaagtt	atcaaaatat	cttttaaaca	420
acataaaact	cttcccaaga	gaaaactgaa	gaaaaaacta	tcaccatttc	tccactgata	480
aaatctatct	ttaaaggcagt	ctgcaactta	tctgtgggcc	agatttttct	tgggtctttg	540
gctacatgag	gggcccgtgaa	tgaaaacttc	attctcaaag	agtagcaagt	gtggacaagt	600
tttccaagca	gcagtcanc	aatgtcactc	ttcttcaaga	tgaaagatcg	gagccatgac	660
acatgttaac	taagcacaga	cntgatgggt	tactncagaa	gattaccact	gcnaagggtga	720
aagttaaaca	tcaagncgag	catncntctc	tttccaaaaa	ttttccgng	tccggattca	780

<210> 235

<211> 780

<212> DNA

<213> Homo Sapiens

<400> 235

attctgaggg	tatathtaagt	cagagtcagg	ataaatcact	tcggagaata	gcagaattaa	60
gagaggagct	ccaaatggac	cagcaggcaa	agaaacatct	gcaagaggag	tttgatgcat	120
cttttagagga	gaaagatcag	tatatcagt	ttctccaaac	tcaggtttct	ctactgaaac	180
aacgattacg	aaatggcccg	atgaatgttg	atgtactgaa	accacttcct	cagctggaac	240
cacaggctga	agtccttact	aaagaagaga	atccagaaag	tgatggagag	ccagtagtgg	300
aagatggaa	ttctgtaaaa	acactggaaa	cactccagca	aagagtgaag	cgtcaagaga	360
acctacttaa	gcgttgtaag	gaaacaattc	agtcacataa	ggaacaatgt	acactattaa	420
ctagtgaaaa	agaagctctg	caagaacaac	tggatgaaag	acttcaagaa	ctagaaaaga	480
taaaggacct	tcatatggcc	gagaagacta	aacttatcac	tcagttgcgt	gatgcaaaga	540
acttaattga	acagcttgaa	caaggataag	ggaatggtta	tcgcagagac	aaaacgtcag	600
atgcatgaaa	ccctggaaat	gaaagaagaa	gaaattgtct	aactccgtag	tcgcatcaaa	660
cagatgacta	cccaaggag	aggaattacg	ggaacaagan	agaaaagtc	gaaagaactg	720
cntttgaggg	aacttgaaaa	agccttgagt	acagnccaaa	aanacagngg	aagccaccgg	780

<210> 236

<211> 711

<212> DNA

<213> Homo Sapiens

<400> 236

cttggttttt	aaatttggtt	tcatattcct	cattcaaaat	atgaatactg	tcctccttgg	60
ctgacaattt	ctgtgtgagt	atctcaattt	ctttcttctg	tccttctctc	atttgtaaaa	120
tcatattttc	cttttccacc	aagatttgct	ttgtctgttc	ctgttctttg	ttaccatctt	180
caagtttggg	ctcatagact	tgggttaaa	attttacttt	ttgtccatt	tcactatttt	240
gtttttcaag	ttgtctgcatt	aagtcctgca	cctggatttt	gtgagcatct	aactcagtac	300
aaacatcttt	tttttgtgct	tcaacttcag	caacctgttt	ggtaagaaga	attctttctg	360
tttccaaatc	caacaacttc	tgtctgaatt	gggccaactg	ttctcatat	gcttttgtct	420
gtcatgtgt	ggcactctgg	taagactgaa	aaacgtccag	cttagcagat	gcctgctgga	480
gttccccttc	agacctttta	atatctgcct	ccaaattttc	tacatgagcc	tgatgtctct	540
tcaaatgctt	gtccctttcc	ttcaagagaa	gctcaagttg	nttaanttga	tcttttaaa	600
ccttctcaan	tcctccggga	tanaaaacnt	cgtgttcttt	naatgagaac	ggtcaacntg	660

ccggctgggt gataantttt ccgttcance anccttgggg ctccaaattc c

711

<210> 237
 <211> 658
 <212> DNA
 <213> Homo Sapiens

<400> 237
 atagtaaata aactttatct atctgtttct cagagatgac actgccaaaca atcacagatt 60
 tgcatacaat acagttatgt attggctatt cacaatttac agtagtggtt tttcctctga 120
 aaaatataag tacaaaagct aagtaaaca tgaggtactg ccatttgga ttttttacat 180
 gtcttagctt aaagaactgg tcttttagcaa atattcaaca gatcaacctg aataaaatag 240
 tcaattaaat gctctaattt atcagaaaaa atccactaag tttcacctca aaatgtattg 300
 cacaagtctt tttaaaaaat caccctaaan ataaatagga aaggtaagcc gttcttttaa 360
 aagaatggat gaaaggaata ttatgtaagc ccataagagc aggttaagtt atcaaaatat 420
 cttttaaaca ncataaaaact cttcccanga gaaaactgaa gaaaaaacta tcaccatttc 480
 tccactgata aaatctattt taaaggcagt ctgcantta tctgtgggcc aagatttttc 540
 ttggnctttt ggctacatga gggggccctg gaatgaaaaa cttcattccc aanggagttt 600
 gcnaggtgtg ggacaggttt tccaaggcaa gcaagtnaag caaatngtca gctcttcc 658

<210> 238
 <211> 678
 <212> DNA
 <213> Homo Sapiens

<400> 238
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 agatttgcac acaatacagt tatgtattgg ctattcaca tttacagtag tgttttttcc 120
 tctgaaaaat ataagtacaa aagctaagta aacaatggg tactgccatt tgggattttt 180
 tacatgtctt agcttaaaaga actggtcttt agcaaatatt caacagatca acctgaataa 240
 aatagtcaat taaatgctct aatttatcag aaaaaatcca ctaagtttca cctcaaaatg 300
 tattgcacaa gtctttttta aaaatcacc taaaaataaa taggaaagg aaanccgttct 360
 ttaaaaaagaa tggatgaaag gaattattatg taagcccata aagcaggtta agttatcaaa 420
 atatctttta aacaacataa gaactcttcc caaggagaaa actgaannaa aaaactatca 480
 ncatttcnnc actgataaaa tctantttta aggnagtcn gcaacttanc tgtgggccag 540
 atttttccgt ggggcttttg ggctacantn agggggccct gaatgaaaaa nttcaattcc 600
 ncaaatgng tagcaaatg tgggncangt ttttccaaag cagncaantt cancccnana 660
 tgtcactcct tccttcaa 678

<210> 239
 <211> 1402
 <212> DNA
 <213> Homo Sapiens

<400> 239
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 atcagttact taaaaaaatt gctgagaaag atgatgatct aaaacgaaca gccaaaagat 180
 atgaagaaat ccttgatgct cgtgaagaag aaatgactgc aaaagtaagg gacctgcaga 240
 ctcaacttga ggagctgcag aagaaatacc agcaaaagct agagcaggag gagaacctg 300
 gcaatgataa tgtaacaatt atggagctac agacacagct agcacagaag acgactttaa 360
 tcagtgatcc gaaattgaaa gagcaagagt tcagagaaca gattcacaat ttagaagacc 420
 gtttgaagaa atatgaaaag aatgtatatg caacaactgt ggggacacct taaaagggtg 480
 gcaatttgta ccatacggat gtctcactct ttggagaacc taccgaattt gagtatttgc 540
 gaaaagtgtc ttttgagtat atgatgggtc gtgagactaa gaccatggca aaagttataa 600

ccaccgtact	gaagttccct	gatgatcaga	ctcagaaaat	tttgaaaga	gaagatgctc	660
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gtaacatgt	gtcatggctc	cgatcttcat	cttgaagaag	agtgacattg	ggtgactgct	780
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catgtagcca	aaagaccaag	aaaaatctgg	cccacagata	agttgcagac	tgcttttaa	900
atagatttta	tcagtggaga	aatggtgata	gttttttctt	cagttttctc	ttgggaagag	960
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gttctttaag	ctaagacatg	taaaaaatcc	caaattggcag	tacctcattg	tttacttagc	1260
ttttgtactt	atatttttca	gaggaaaaaa	cactactgta	aattgtgaat	agccaataca	1320
taactgtatt	gtatgcaaat	ctgtgattgt	tggcagtgtc	atctctgaga	aacagataaa	1380
taaagtatat	ttactatata	ac				1402

<210> 240

<211> 760

<212> DNA

<213> Homo Sapiens

<400> 240

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aaaataatgg	cttttggctt	tttggctttt	ttattatctt	aatatgtgta	tccacaatta	120
tggtatcaac	tcaatatgaa	aaactcaact	taattttgtg	catgattttc	ataccttcct	180
tcactttgct	ggggtatgtc	atgttattga	tccagctcga	ctttatgaga	aacttggaca	240
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aaataatgaa	taaagaccca	gttttcagaa	tctctccacg	gagtagagaa	actcatccca	420
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atgcactcac	tgctccaaac	ttggaggagg	aaccagtcac	aactgcaagc	tgtttacaca	540
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gaaatgtttc	cntttgtgtt	aaaaaagggtg	aaagttttgg	ggattaccta	ggacacaatg	660
ggagctggta	aaagtacttc	cattaaaatg	ataacntggg	tgacaaaagc	caaactgcan	720
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<210> 241

<211> 745

<212> DNA

<213> Homo Sapiens

<400> 241

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cncnggtatt	acatcaatac	agctataaca	ttaatgcagc	aattatataa	cacaaaagtg	120
ctataatgac	atgggaaatg	ttcatgaact	gtgaggtgaa	aagatacaga	aatgactat	180
gcctacngat	actacctttg	aaaaaggatc	cataaaaaat	acattgaata	taagttggct	240
aaagaaaata	ttaactgctg	tactttctta	cagattangg	ctanccttct	ccatataact	300
tcaatatgta	ctaaaattca	catgcattta	ttttataatc	agaatgtcat	tataattaaa	360
tggtangctg	tgccatttca	tcagtttata	anaccttctt	atagtcaatg	tcacattaaa	420
ttagaatccg	agtaataaan	gtttaaaaat	anctgataca	tttgaagttc	aggctaaaaa	480
cctcatatatt	ttatttgtaa	aatgtttctca	ntggttagctt	tattgataat	aaccgataac	540
caacctataa	ttgtangatt	tttaaattat	ttttaagcac	aaantagacc	catgttgggg	600
atgaataaca	tgtcngattt	tgtnaatttt	ggtnacnac	ttttcccaa	aatttccttg	660
tttccttcan	ccnaaatttt	taaaantgaa	aactgtatca	attatggaan	ggtttattaa	720
aangtttncc	tttggttaacc	ngaag				745

<210> 242
 <211> 818
 <212> DNA
 <213> Homo Sapiens

<400> 242
 gcaacgcccgg ggcgcccag gtctggaagg cgcagaaatg gagcaagagc cacaaaatgg 60
 agaacctgct gaaattaaga tcatcagaga agcatataag aaggcctttt tatttggttaa 120
 caaagggtctg aatacagatg aattaggtca gaaggaagaa gcaaagaact actataagca 180
 aggaatagga cacctgctca gagggatcag ctttcatca aaagagtctg aacacacagg 240
 tcttgggtgg gaatctgcta gacagatgca acagaaaatg aaagaaactc tacagaatgt 300
 acgcaccagg ctggaaatc tagagaaggg tcttgccact tctctgcaga atgatcttca 360
 ggaggtgccc aagttatata cagaatttcc acctaaaagc atgtgtgaaa aattaccaga 420
 gcctcagtct tttagttcag ctctcagca tgctgaagta aatggaaaca cctcaactcc 480
 aagtgcaggg gcagttgctg cacctgcttc tctgtcttta ccatcacaaa gttgtccagc 540
 agaagctcct cctgcttata ctctcaagc tgctgaaggc cactacactg taccctatgg 600
 aacagattct ggggagtttt catcagttgg agaggagttt tatagggaat cattctcagc 660
 caacggcctc ttnagaacct taagggtctg gattcangat gaaattgatt ttgataccaa 720
 atgggagtagc annttttttt tgtaaatcct gcaangggga ngttatgcan ctctgtancc 780
 ccgggggtacc ttcnaattgt gaagggtttt gggntaaa 818

<210> 243
 <211> 799
 <212> DNA
 <213> Homo Sapiens

<400> 243
 aatttcttga agtacttttt taatccaatt aagctgataa taatcacttc gaattttaat 60
 acaatacaat catgttccca aatttccnag gtcataaca atacagtctc aatacaaaag 120
 acgtaataat ctattttttat tcatttttaa tcaaagaaac cattccattt cctaacaaac 180
 aggtaagtta caaaagtagt ccattttact tttcatcagt ctttccctgt tttgaacaag 240
 tctttttgag aattcttagt tttagttttt gtttagctta cacactgaaa attttgagaa 300
 gcatctaaaa aaatccacaa ttagtgcaaa aagaggggac aatactttta gtcatctcctt 360
 ctataaaaaag aattaagggt actaaatgcc aatttttaag caaatatata gtttcctatt 420
 tgccttctga aagacagcag atataaaaa agttcaatat taggtttaac aagggttgaa 480
 caacacatgt actatcagct ttattttacc tgcaaaaata ttttagctac acttggaata 540
 aaaataaact tgagaatata acttcacatt tctaaggcca gatgcaagaa tacttaatct 600
 tttcctttta aatagaagac atgccataaa atttatgaaa agttaatttg taggaatggn 660
 atacatttaa aaaatacngg ttaaacnngg tgagggaatt ccacatttgg cctatttaac 720
 aaaaatttta aaccaatttt caaaaggggc tttggggtta aaagtngatt cccaagcaac 780
 ntcaancant ttaaccttc 799

<210> 244
 <211> 726
 <212> DNA
 <213> Homo Sapiens

<400> 244
 gtgagttgag cgctgctgct ccgcggtgga gtcaccgcac cgctcccggg atcatggtgt 60
 tctacttcac cagcagcagc gttaattcat ctgcctacac tatttacatg ggaaaagata 120
 aatatgaaaa tgaagatctg atcaagcatg gctggcctga agatatctgg tttcatgtgg 180
 acaaactctc ttcgggtcat gtatacttc gattacataa gggagagaat atagaagaca 240
 tcccaaagga agtgctgatg gactgtgccc acctgtgaa ggccaatagc attcaaggct 300
 gcaagatgaa caacgttaat gtggtatata cgccgtgggc taacctgaag aaaacagctg 360
 acatggatgt ggggcagata ggctttcaca ggcagaagga tgtaaaaatt gtgacagtgg 420

agaagaaagt aaatgagatc ctgaaccgat tagaaaagac caaagtcgag cggttcccag	480
acctancagc agagaaagaa tgcagagatc gtgaagagag gaatgagaaa aaagcccaaa	540
ttcaggaaat gaaaaagaga gaaanagaag aaatgaagaa gaanagggaa atggatgaac	600
ttangagcta ttcactacta atgaaagttt gaaaatatgt cttcanatca ggatggcaat	660
ggattcagat gaattcatgt taaaaggaga aaaggngaaa aaggaccttt gaaaaatttg	720
aatgtt	726

<210> 245
 <211> 592
 <212> DNA
 <213> Homo Sapiens

<400> 245	
ccagattaaa aaaatggtat tttattataa cttttaaaat tgcggaacat cagactgaat	60
atcatcagac acatacacia aaccactcat ctctaaagtc attttctata ccctctcaaa	120
atttggccag tgagttttgc ctcagggaat tttccagttc aaccccatac accaactggt	180
aataaatgga aacactagcc ttttggtttt gcccanaagt ccaaagtgtc attacaggtg	240
gaatatctgc tgcaggaagt cattcttgcg gctgtgggtg tgagtaaaat gcttagttcc	300
ttctaaaatc ataattgcaa tatggacttc tgcttcacgc tgcctcctaa ggcacaaatc	360
aggtaaccta catctcccaa atgatcaaca ggagcactcc atcctatttt accctcaatg	420
cnganaaatt acnctggggc ccanaagttg tcacataggt ggcttgggtt acttggggct	480
caggcaacaa ctgccacagg cccagcttg atgaanacca tcnatttctt taaaatatgt	540
tggnnactaa gatggaggcc tccggcncan aggaanacan nggacataaa ac	592

<210> 246
 <211> 821
 <212> DNA
 <213> Homo Sapiens

<400> 246	
aggatgaaga gctggagagc gccgaggacg acgagcgcag ctgtcggggc cgcgagtcgg	60
acgaagacac tgaggatgct agtgaaactg acctggcaaa gcatgatgaa gaagactatg	120
tagaaatgaa ggaacagatg tatcaggaca aactggcttc tctcaagagg cagttgcaac	180
aactgcaaga aggtacatta caggaatatc agaagagaat gaaaaaacta gatcagcagt	240
acaaagagag gatacggat gcagaactct tctccagct ggaaactgaa caagtggaa	300
gaaattacat taaagaaaag aaggcagcag tgaaagaatt tgaagacaag aaggttgagc	360
tgaaagagaa cctgattgct gagctagaag aaaagaagaa aatgattgaa aatgaaaagc	420
tgacaatgga actgactgga gattctatgg aggtgaaacc tatcatgacc agaaagttgc	480
ggaggcgacc aaatgatccc gtcccacatc cagacaagag gaggaacact gctccagccc	540
agctaaacta tttgttaaca ggatgaacag atcatggagg atctgagaac attaaataag	600
cttaagtcac ccaagagacc agcatctcca tctctctctg agcacttgcc tgcaacaccc	660
gccggaatct ccaagcccca gaggttcnaa agccccggat anaagaatgg caaacctgtt	720
actatgacaa aaagatggtt accacaagag ccaaggccat cctatcctgg angtcaaagg	780
gacaaaccan gaaactgaag cctgcctnat taagtttccg t	821

<210> 247
 <211> 639
 <212> DNA
 <213> Homo Sapiens

<400> 247	
gttacacaaa gcatttatct ctctgagaag gccgagagcc acgagaattc atcatctcct	60
gctaggacct ctgccccaaag cttctgggca aatagtgaat tggacgcgac agggaaagta	120
gctacgtgat ccactaatca gattcaaaac atgaaatgc actggagagt gtatcccttc	180
ctgctcttct ccatggtaga gagacttaaa gataatcaat aaaaatagct gtcccttcaa	240

actcagagga	ggtttttcaaa	aacaagtata	agcaaaaaat	aaagaaataa	aaggaaagta	300
aatcaaacc	cccaatacgc	ctgaaagtaa	aacagtctca	tgggtactga	tgtctggaan	360
aagttgaggc	agaaaagact	gacaaaagtg	gaangcatcc	cggccacaaa	agtgcccnna	420
aagaattcan	tgcaagtgtc	tccatttcca	aggctgagta	actattccca	gntaagttaa	480
catttttcna	nttaaggana	nancgaanac	anntncatnt	ctanatccca	ctccagaaat	540
anggtcaatg	agaangangc	actgtannna	aagtcaagna	gctggancnc	ccgggcggn	600
tnaccaaga	gcccggcgct	nnaagcctgg	gcccaagct			639

<210> 248

<211> 846

<212> DNA

<213> Homo Sapiens

<400> 248

aacaggatgt	caaaaattaa	actgcgcttt	ccatcacaa	agaggacgat	atgttgatgg	60
ccttttccta	cctccgagca	aaactgtgtt	gcccactgtg	cctgagtcac	cagaagagga	120
agtgaaggct	agccaacttt	cagttcagca	gaacaaattg	tctgtccagt	ccaatccttc	180
ccctcagctg	cggagcggtt	tgaaagtaga	aagttccgaa	aatgttccta	gccccacgca	240
tccaccagtt	gtaattaatg	ctgcagatga	tgatgaagat	gatgatgata	agttttctga	300
ggaaggtgat	gaaaccaaaa	cacctaccct	gcaaccaact	cctgaagtcc	acaatggatt	360
acgagtgtg	tctgtccgga	aacctgcagt	caatataaag	caaggtgaat	gtttgaattt	420
tggataaaaa	actcttgagg	aaattaagtc	aaagaaaatg	aagggaaaaat	ctaagaagca	480
aggtgaggg	tcttcaggag	tttccagtct	tttactccac	cctgagcccg	ttccaggtcc	540
tgaaaaagaa	aatgtcagga	ctgtggtgag	gacagtaact	ctctccacca	aacaaggaga	600
agaacccttg	gttagattga	gtcttactga	gagactgggg	aaacgaaaat	tttcagcagg	660
cgggtgacagt	gatcctccat	taaagcgtag	cctggcacan	aggctaagg	aagaaagttg	720
aagctccaga	aactaacant	gacaaaacac	caangaaagc	tcaagtttcc	aagtcacctt	780
aaagggcgga	atttagcatg	tcagcngga	ttcaagataa	tnagggatgc	aacaagatta	840
aaggtt						846

<210> 249

<211> 763

<212> DNA

<213> Homo Sapiens

<400> 249

gactttccta	catcagtttt	atttaaaaca	caaacaagta	tttctctttc	tgtaagggca	60
aatggttcaa	ataatgcgga	acacgaaaca	ttgactaata	caagtgtctt	aaatatgaaa	120
caaaattatt	ttttaaaaaa	gcaaaagaat	aaagaatata	tacaaaagg	acctggaatc	180
tgtaagctga	ttccaaaaat	gaaataagta	gaaaatccat	ggtgaaacct	gaacattcta	240
cctctgcttt	ggagaagggc	tatcatacaa	cattcagtca	gctgaagatg	gattggtaga	300
ggtgtgtcta	tacataaaact	tcagtcattt	ttgcttgtgc	agaatcatcc	caatcttccc	360
aagactgaat	gggcagtcct	gtggctttct	tctttttcca	tattcccaac	aaggctacgt	420
gaagttcaac	tcttgatgag	ccgcttacaa	cagcagttcc	ttaggagcca	acatgacagg	480
tgggtcagat	ttccctatga	gaaacaaaac	tggccaccta	cagcaaaaata	tcaaaatggg	540
taagtccttc	cttcctcttc	ctcctgatta	tatacaacat	atctcctttc	aagactatta	600
tttccatcat	gccttattcc	ttcacaaatc	taaaccttga	ngtgatatga	angaaaccaa	660
catcaagaaa	agaaaactca	attcagaaat	gaanaaaacg	ggcaggtata	caatacaccc	720
cagagcatct	caatatcccc	tgggacagnt	acaattcagt	ggt		763

<210> 250

<211> 899

<212> DNA

<213> Homo Sapiens

<400> 250
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 gaaaaatcag tcttgacacc tcttcgggga gatgtagcct cttgcaatac ccaagtggca 120
 gagaaaccag tgctcactgc tgtgccagga atcacacggc acctgaccaa gcggcttccc 180
 acaaagtcac cccagaaggt ggaggtagaa acctcaggga ttggagactc attattgaat 240
 gtgaaatgtg cagcacagac cttggaaaaa aggggtaaag ctaaacccaa agtgaacgtg 300
 aagccatctg tggttaaagt tgtgtcatcc cccaaattgg ccccaaaacg taaggcagtg 360
 gagatgcacg ctgctgtcat tgccgctgtg aagccactca gctccagcag tgtcctacag 420
 gaacccccag ccaaaaaggc agctgtggct gttgtccgc ttgtctctga ggacaaatca 480
 gtcatctgtc ctgaagcaga aaatcctaga gacagtcttg tgcctcctcc aaccagtc 540
 tcttcagatt cctcaccccc ggaggtgtct ggccttccct catcccaat gagcatgaaa 600
 actcgcgcac tcagctctgc ctcaacaagg aaagcccca ctctctgtgg aggatgattt 660
 tgagaaacta atatgggaga tttcaaggag gcaaaattgg naactganat tgacctggat 720
 tctgggaaaa gatgaagatg acccttcctg cttngngcct atcaannaaa ngattgntan 780
 cctgaaaggg tggtaattga nggancctt naaaaaaaaa atccnccaaa aaaactnngg 840
 ccttaanttc naccaaatgg taacaatttn acctgagaat gnttaatttc ctttaggcc 899

<210> 251

<211> 755

<212> DNA

<213> Homo Sapiens

<400> 251
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 tcaaataatg cggaaacacga aacattgana nagacaagt ctttaaataat gaaacaaaat 120
 tatttttttaa aaaagcaaaa gaataaagaa tatatacaaa agggacctgg aatctgtaag 180
 gtgattccaa aaacgaaata agtagaaaat ccatggtgaa acctgaacat tctacctctg 240
 ctttgagaaa gggctatcat acaacattca gtcagctgaa gatggattgg tagaggtgtg 300
 tctatacata aacttcagtc atttttgctt gtgcagaatc atcccaatct tcccaagact 360
 gaatgggcag tcctgtggct ttcttccttt tccatattcc caacaaggct acgtgaagtt 420
 caactcttga tgagccgctt acaacagcag ttccttagga gccaacatga caggtgggtc 480
 agatttccct atgagaaaca aaactggcca cctacagcaa aatatcaaaa tgggtaagtc 540
 ctctcttctt ctctctctctg attatataca acatatctcc tttcaaagac tattatttcc 600
 atcatgctta ntccttcaca aatctaaacc ttgaggtgat atgaaggaaa ccaacatcan 660
 gaaaagaaaa ctcaattcag aaatgaagaa aacgggcang tatacaattc anccccagag 720
 caacccaata atccctgggc aaaagttcaa ttcaa 755

<210> 252

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 252
 cctacatcag ttttatttaa aacactaaca agtatttctc tttctgtaag ggcaaatgg 60
 tcaaataatg cggaaacacga aacattgact aatacaagt ctttaaataat gaaacaaaat 120
 tatttttttaa aaaagcaaaa gaataaagaa tatatacaaa agggacctgg aatctgtaag 180
 gtgattccaa aaacgaaata agtagaaaat ccatggtgaa acctgaacat tctacctctg 240
 ctttgagaaa gggctatcat acaacattca gtcagctgaa gatggattgg tagaggtgtg 300
 tctatacata aacttcagtc atttttgctt gtgcagaatc atcccaatct tcccaagact 360
 gaatgggcag tcctgtggct ttcttccttt tccatattcc caacaaggct acgtgaagtt 420
 caactcttga tgagccgctt acaacagcag ttccttagga gccaacatga caggtgggtc 480
 agatttccct atgagaaaca aaactggcca cctacagcaa aatatcaaaa tgggtaagtc 540
 ctctcttctt ctctctctctg gattatatac aacatatctc ctttcaagac tattatttcc 600
 atcatgcnta atccttcaca aatctaaac cttgaggggtg atatgaaagg aaaccaacat 660
 canagaaaag aaaactcaat tcaagaaaat taagaaaacc tggcaaggta tacaataata 720

ccccaggag catcccaaat aatccctggg aaa

753

<210> 253
<211> 793
<212> DNA
<213> Homo Sapiens

<400> 253
gactttccta catcagtttt atttaaaaca ctaacaagta tttcnccttc ngtaagggca 60
aatggttcaa ataatgcgga acacgaaaca ttgactaata caagtgcctt aaatatgaaa 120
caaaattatt ttttaaaaaa gcaaaagaat aaagaatata tacaaaaggg acctggaatc 180
tgtaaggnga ttccaaaaac gaaataagta gaaaatccat ggtgaaacct gaanattcta 240
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gggtgtgtcta tacataaaact tcagtcattt ttgcttgtgc anaatcatcc caatcttccc 360
aagactgaat gggcagtcct gtggctttct tccttttcca nattcccaac aaggctacgt 420
gaagtccaac tcttgatgag ccgcttaca cagcagttcc ttaggagcca acatgacagg 480
tgggtcagat ttccctatga gaaacaaaac tggccacct cagcaaaata tcaaatggg 540
taagtccctt cttcctcttc cncctgatta tatacaanat atctcctttc aagactatta 600
tttccatcat gcttattcct tcacanatct aaaccttgan gtgatatgaa nggnaaccaa 660
catcangaaa agaaaactca attcagnaat gaangaaaac tgggaggtat ttaatanacc 720
cccangnnga atccaaatac cctggnaana gttcaattca antgtacngc naaagnccat 780
aantaantat tgg 793

<210> 254
<211> 625
<212> DNA
<213> Homo Sapiens

<400> 254
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tcaaataatg cggaacacga aacattgact aatacaagt ctttaaatat gaaacaaaat 120
tattttttta aaaaagcaaaa gaataaagaa tatatacaaa agggacctgg aatctgtaag 180
gtgattccaa aaacgaaata agtagaaaat ccatggtgaa acctgaacat tctacctctg 240
ctttggagaa gggctatcat acaacattca gtcagctgaa gatggattgg tanagggtgtg 300
tctatacata aacttcagtc atttttgctt gtgcagaatc atcccaatct tccaagact 360
gaatgggcag tcctgtggct ttcttctttt tccatattcc caacaaggct acgtgaagtt 420
caactcttga tgagccgctt acaacancaa gttccttang agccaacatg acaggtgggg 480
tcangatttc cctatgagaa acaanactgg ccacctacag caaaaatatn aaaatgggg 540
aagtccttcc ttcctcttcc tcctgaatta tatncaacat ntctcctttt caagacnatt 600
anttccatca gggcttaatc cttca 625

<210> 255
<211> 907
<212> DNA
<213> Homo Sapiens

<400> 255
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ctgcccagca gactactcag cctggcgggc ggaagcgcaa aggcaaggct cagtatgtgc 120
tggccaagcg cgctcggcgc tgcgacgctg gcggggcccg tcagctagag cccgggctac 180
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gtgacattaa ggcatttaca gagatgaggt taagaagatt ccagtcagtg gaaagtggag 420
caaataacgt tgtcttcacg aggacacttg ggatagagcc tgagaaattg gtgcatcata 480

ttctccagga tatgtacaaa accaagaaaa agaagactcg agttattttg cgaatgttac	540
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tggaaccctg gtttaaagct ccaaacaaag ggacatttca gatttgtgtac aaaatctcga	660
nataacagtc atgtnaatag agaagaagtt atcaagagaa tttgcangga atagtgtgca	720
acctcaattc agnaaataaa gtgggtntca acaatccaca agtacacaat ngtaatanaa	780
atcatcaaan ctgtcngttc cctganngtt tgttaaagga ttacaagggt ggtttanna	840
aattcaatcn ccaagaagggt tggtnaanaa ncccctaang ggntccttca naggcnttaa	900
ctcaaag	907

<210> 256

<211> 794

<212> DNA

<213> Homo Sapiens

<400> 256	
aataacgcaa aatgacttat ggagacaacc actgatgggg caccaggagt gtagatacca	60
gacctctggt tatcagatat gatgtcaciaa aanagagata ttggcctttg ttctggcagg	120
ctcctagcaa tagaaaaagt tttctttgaa tttcatcatt taaaaatctt acaaagtcta	180
cagcatgaca aatatttagtg aaacctgttg actcatcatc ctggatagag aagctgctac	240
ttttcagtta atgacacaaa accttttttg catcatatga catatcatca gtaaatacaac	300
ttattgagaa taaagtctct tcaactttgt actgcatctt gcccagcat tttaagtta	360
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tagtccaaaa gccatttgaa aataatgaat atcctttctt gtcaagtggtg tgtgatttat	540
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aaccttggtg ctgagtcac ataaataccc cttgagaagt tancctttcc ttaattaaga	660
caagaatttc ctttggtgtc cccttggttg cactaagtat acttgaaagt ntntccagn	720
angactggaa gttcttcaat caaccaant ttttcaagaa aatgtccngt agtttcaang	780
gcctaaaaat ggggt	794

<210> 257

<211> 885

<212> DNA

<213> Homo Sapiens

<400> 257	
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cccctgcccc gcagactact cagcctggcg gcgggaagcg caaaggcaag gctcagtatg	120
tgctggccaa gcgcgtcgg cgctgcgacg ctggcgggcc ccgtcagcta gagccggggc	180
tacaggcat cctcatcacc tgcaatatga acgagcgcaa gtgcgtggag gaggcctaca	240
gcctcctcaa cgaatacggc gacgacatgt atgggccaga aaagtttaca gacaaggatc	300
agcagccctc tggaagtgtg ggagaggatg atgatgcgga ggctgccttg aagaaagaag	360
ttggtgacat taaggcatct acagagatga ggtaagaag attccagtca gtggaaagtg	420
gagcaaataa cgttgtcttc atcaggacac ttgggataga gcctgagaaa ttggtgcatc	480
atattctcca ggatatgtac aaaaccaaga aaaagaagac tcgagttatt ttgcgaatgt	540
taccatctc aggcacatgc aaggcttttt tagaagatat gaaaaaatat gcagaaacat	600
ttttggaacc ctgggtttta agctccaaac aaaggacat ttcagattgt gtacaaatct	660
cgaataaca gtcattgtgaa tngagaaaga agttatcaga gaaattggca aggaatagtt	720
gtgcaccctc aattcagaaa attaaagggt ggntctcaac caatccacag ttcacagntg	780
gtagttagaa atcaatcaaa acctgtcngt ttgccgaan ttgnttggtta aaagaattca	840
angttggttt tanaanaaat naaatcccca aagaagggtg gtgaa	885

<210> 258

<211> 798

<212> DNA

<213> Homo Sapiens

<400> 258
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 ccactgatgg ggcaccagga gtgtagatac cagacctctg gttatcagat atgatgtcac 240
 aacattatat attggccttt gttctggcag gtccttagca atagaaaaag ttttctttga 300
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 gactcatcat cctggataga gaagctgcta cttttcagtt aatgacacaa aacctttttt 420
 gcatcatatg acatatcatc aagtaaatac acttattgag aataaagtct cttcaacttt 480
 gtactgcac ttgccccagc attttaatgt tattaagatt ctcaccaacc atgcataatt 540
 tcctttcctg agataagttc tgctactaaa taatttgctt cttaaacctt ttgactaaag 600
 gtgatttctg aacaaaagcc ttactgtttt tgataagtcc caaaaagcca ttgaaaaaat 660
 aatgaatgc ctttctgtc aagtggctgt gaatttaatg ttacaattgc caagttttgt 720
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<210> 259

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 259
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 ggcaaggctc agtatgtgct ggccaagcgc gctcggcgct gcgacgctgg cgggcccgt 180
 cagctagagc ccggtgtaca gggcatcctc atcacctgca atatgaacga gcgcaagtgc 240
 gtggaggagg cctacagcct cctcaacgaa tacggcgagc acatgtatgg gccagaaaag 300
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 gagaaattgg tgcatacat tctccaggat atgtacaaaa ccaagaaaaa gaagactcga 540
 gttattttgc gaatgttacc catctcaggc acatgcaang cttttttaga agatatgaaa 600
 aaatatgcan aaacattttt ggaancctgg tttaaagctc caaacaagg gacatttcag 660
 attgtgttca aatctcgaaa ataacagtca tgttgaaatg aagaagaagt tatcagagaa 720
 nttggcaagg aataatgntg caacctcaat tcagaaaaata aaagtggatt tcaccaattc 780
 cacagtncac aantggtagt agaaatcatc aaaagctntc tgtttgcccg a 831

<210> 260

<211> 772

<212> DNA

<213> Homo Sapiens

<400> 260
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 tcctagcaat agaaaaagtt ttctttgaat ttcatcattt acaaattctta caaatgctac 180
 agcatgacaa atattagtga aacctgttga ctcatcatcc tggatagaga agctgctact 240
 tttcagttaa tgacacaaaa ctttttttgc atcatatgac atatcatcag taaatcaact 300
 tattgagaat aaagtctctt caacttttga ctgcatcttg ccccgagcatt ttaatgttat 360
 tagattctca ccaaccatgc atattttcct ttcttgagat aagttctgct actaaataat 420
 ttgcttctta aaccttttga ctaaaagtga tttctgaaca aaagccttac tgtttttgat 480
 agtccaaaag ccatttgaaa ataatagaata tcctttcttg tcaagtggcn gtgatttatt 540
 gttacaattg ctagttttgt nagttgcatg tcacagacaa tgcacaatgg gacangagag 600

cctgggactg agtccacata ataccntga gaagtannct ttctttatta agacagaant	660
ttctttgtgtc ccttggtgca caagtntact gaagtntcnc aagaaggact ggangtcntc	720
ataancaacc ttttagaat gtccgtattc ctaaggccca aaaanggggc cc	772

<210> 261
 <211> 753
 <212> DNA
 <213> Homo Sapiens

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atggcgggccc ctgcccagca gactactcag cctggcggcg ggaagcgcaa aggcaaggct	120
cagtattgtgc tggccaagcg cgctcggcgc tgcgacgctg gcgggccccg tcagctagag	180
cccggtctac agggcatcct catcacctgc aatatgaacg agcgcaagtg cgtggaggag	240
gcctacagcc tcctcaacga atacggcgac gacatgtatg ggccagaaaa gtttacagac	300
aaggatcagc agccctctgg aagtgaggga gaggatgatg atgcgagggc tgccttgaag	360
aaagaagttg gtgacattaa ggcattctaca gagatgaggt taagaagatt ccagtcagtg	420
gaaagtggag caaataacgt tgtcttcac aggcacttg gtagagagcc tgagaaattg	480
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cgaatgttac ccattctcagg cacatgcaag gcttttttag aaagatatga anaaatatgc	600
anaaaacatt tttggaaccc tgggttttaa gctccaaaca aaggacatt tcagaattgt	660
ggtacaaatc tcgaaatanc agtcatgtta antagagaan naagtttttc agaagaattt	720
ggcaaggaat nagtnntgca accctcaatt tca	753

<210> 262
 <211> 659
 <212> DNA
 <213> Homo Sapiens

<400> 262	
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tcctagcaat agaaaaagtt ttctttgaat ttcattcattt acaaatctta caaatgctac	180
agcatgacaa atattagtga aacctgttga ctcatcatcc tggatagaga agctgctact	240
tttcagttaa tgacacaaaa ccttttttgc atcatatgac atatcatcag taaatcaact	300
tattgagaat aaagtctctt caacttttga ctgcatcttg cccagcatt ttaatgttat	360
tagattctca ccangccatg catattttcc ttctctgaga taagtctctg tactaaagaa	420
tttgcttctt aaaccttttg actaaagggt atttctgaac aaaagcctta ctgtttttga	480
nnagtccana agccatttga aaaataatga atacccttc cttgtcaagt ggcngtgatt	540
tantgttaca atttgcnagg tttgtgaagt tgcattgtca cagnanaatg cacantnggg	600
acannagagan cntgggncng aagtccacat tatancctt tgagnaangt agctttccc	659

<210> 263
 <211> 673
 <212> DNA
 <213> Homo Sapiens

<400> 263	
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tttaaggggt ctgtcatgga aggtgctctt ccaggaaacct ctgtgatgga ggtcacagcc	120
acagacgcgg acgatgatgt gaacacctac aatgccgccca tcgcttacac catcctcagc	180
caagatcctg agctccctga caaaaatatg ttcaccatta acaggaacac aggagtcac	240
agtgtgtgta ccactgggct ggacogagag agtttcccta cgtataccct ggtggttcaa	300
gctgctgacc ttcaagggtga ggggttaagc acaacagcaa cagctgtgat cacagtcact	360
gacaccaacg ataatcctcc gatcttcaat cccaccacgt acaagggtca ggtgcctgaa	420

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aacgaggcta acgtcgtaat caccacactg aaagtgactg atgctgatgc ccccaatacc 480
ccagcgttgg gaggtgtat acaccatatt gaatgatgat ggtgggacaa tttgtcgtca 540
ccacaaatcc agtgaacaac gatggcattt tgaaaaacag caaagttgaa gtcaagtgat 600
tttgcgtggt cngaataaat tgttgcctcn gttgggagaa aggtntccaa cacatacccc 660
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<210> 264

<211> 661

<212> DNA

<213> Homo Sapiens

<400> 264

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gctcctcatt ttctgaaga anaatctcag cctgaaagaa tatagagcta ggtgacatat 180
gggtggccaa ccgcttctcc tcaagttcca anagagtggg caattagtga aattccatca 240
gtcatgttaa aatatacttt caccaggtan acatccttct ttcaatgcta gaggacagtg 300
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aacgcgggag tgctgaacac atgccctcgg aagggaccct gaagacccaa gtgacctgca 420
ccataaaaacc accccgaggg tcagccatgc tgccagcact caagaagcag cagggccacc 480
tgctgaaaaa ctgggcacgg ctctgggtgc ctggccctgc ctgcctctc cagctccttg 540
gagccaggtc tacggcaggg aacatgatct tcttctccag cttctgtgga aggaacanga 600
aatttttcat gatgtcttcc agctcttcta nggccaactg ggcatgganc ttggccacgt 660
c 661

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<210> 265

<211> 659

<212> DNA

<213> Homo Sapiens

<400> 265

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gctcctcatt ttctgaana anaatctcag cctgaaagaa tatanagcta ggtgacatat 180
gggtggccaa ccgcttctcc tcaagttcca ananagtggg caattagtga aattccatca 240
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tgctggaana actgggcacg gctctgggtg cctggccctg cctgcctctt ccacgtcctt 540
gganccaggt ctacggnagg accatgatct tcttctccan cttctgtgga aggaacanga 600
antttttcat gatgtcttcc actcttctag ggccaactgg gcatggactt ggccacgtc 659

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<210> 266

<211> 620

<212> DNA

<213> Homo Sapiens

<400> 266

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gctcctcatt ttctgaana anaatctcag cctgaaagaa tatagagcta ggtgacatat 180
gggtggccaa ccgcttctcc tcaagttcca ananagtggg caattagtga aattccatca 240
gtcatgttaa aatatacttt caccaggtan acatccttct ttcaatgcta gaggacagtg 300
aaaaatgtag attaatagaga tctgtaactg tcttctctta actgtacacc cctcaggctg 360

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aacgcgggag	tgctgaacac	atgccctcgg	aagggaccct	gaagacccaa	gtgacctgca	420
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tgctggaaga	cctgggcacg	gctctgggtg	cctggccctg	cctgcctcct	ccacgtcctt	540
ggagccaggt	ctacngcang	aacatgatct	tcttctccac	ttctgtggaa	ggaacaggaa	600
ntttttcatg	atgtcatcca					620

<210> 267

<211> 745

<212> DNA

<213> Homo Sapiens

<400> 267

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gcactactac	aagtcagaaa	tctggaagcg	taaccacaga	acagctccaa	gaggttcttt	120
tgctcagctta	tgacctcaa	attccaacac	gggctgctgc	cctgcgtact	ctttccact	180
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tgctgtcaga	cgtctatcct	gagaaaatct	tgccggactt	gttggtctca	tatgacagca	360
gcaaaagacaa	gcacacacca	gagaccaaga	atgaaagtcg	gggaagtcct	tatgcaatc	420
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gtggggttgt	gcctgcnnng	tttcggggga	actcaaccca	agaaaaagct	tantgtaagg	720
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<210> 268

<211> 676

<212> DNA

<213> Homo Sapiens

<400> 268

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gctcctcatt	ttcctgaana	anaatctcag	cctgaaagaa	tatagagcta	ggtgacatat	180
gggtggccaa	ccgcttctcc	tcaagttcca	ananagtggg	caattagtga	aattccatca	240
gtcatgttaa	aataactttt	caccaggtag	acatccttct	ttcaatgcta	gaggacagtg	300
aaaaatgtag	attaatgaga	tctgttaactg	tcttctctta	actgtacacc	cctcaggctg	360
aacgcgggag	tgctgaacac	atgccctcgg	aagggaccct	gaagacccaa	gtgacctgca	420
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tgctggaana	cctgggcacg	gctctgggtg	cctggccctg	cctgcctcct	ccacgtcctt	540
gggagccagg	tctacggcag	ggaacatgat	cttcttctcc	agcttctgtg	gaagggaacag	600
gaagtttttc	atgatgtcat	ccanctcttc	taaggccaac	tgggcatgga	acttggccac	660
gtcatcgggc	tccaaa					760

<210> 269

<211> 737

<212> DNA

<213> Homo Sapiens

<400> 269

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cctgttggtg	tctttattat	tgaaagagaa	acaggatggc	tgaagctctt	ctctcacgct	120
gtgtcatcca	acgggaatgc	agttgaggat	ccaatggaga	ttttgatcac	ggtaaccgat	180
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gctcttccag	gaacctctgt	gatggaggtc	acagccacag	acgaggacga	tgatgtgaac	300
acctacaatg	ccgccatgc	ttacaccatc	ctcagccaag	atcctgagct	ccctgacaaa	360
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caacactgaa	aagtgactga	tgctgatgc	cccccaatta	nccanccgt	gggaagctgt	660
ntacaccata	tngaaatgat	gatgggtggg	cnaatttgn	cgttcaccaa	caaatnccan	720
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<210> 270

<211> 726

<212> DNA

<213> Homo Sapiens

<400> 270

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atttttcatg	atgtctccan	ctcttctagg	gccactgggc	atggancttg	ggcnctcat	660
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<210> 271

<211> 814

<212> DNA

<213> Homo Sapiens

<400> 271

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<210> 272

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 272
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<210> 273

<211> 677

<212> DNA

<213> Homo Sapiens

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<210> 274

<211> 863

<212> DNA

<213> Homo Sapiens

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aggggaatta gagattctga atgggtgctca cagggccaac aaccttggcn aaccttgggg 840
aacctgtgcc anaaggctng gac 863

<210> 275
<211> 821
<212> DNA
<213> Homo Sapiens

<400> 275
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gctcctcatt ttcctgaaga agaattctcag cctgaaagaa tatagagcta ggtgacatat 180
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gtcatcgggc tccagacaca ctacgtgctt cancaagggt gtaaaagatt cttganggac 720
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<210> 276
<211> 722
<212> DNA
<213> Homo Sapiens

<400> 276
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gcctgcagtc aaatgctcca atcattctc aaggagtcaa tgagcccagc actactacaa 600
gtcagaaatc tggaagcgtt accacagaac agctccaaga ggttcntttg tcagctttat 660
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ca 722

<210> 277
<211> 805
<212> DNA
<213> Homo Sapiens

<400> 277
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gctcctcatt ttcctgaaga agaattctcag cctgaaagaa tatagagcta ggtgacatat 180
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WO 99/04265

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gcacgtcatn	cgggctccag	acacactacg	gtgcttcaac	aagggnggta	nagattcttg	720
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aagtacaaac	cacatgtttt	gggaa				805

<210> 278

<211> 1358

<212> DNA

<213> Homo Sapiens

<400> 278

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<210> 279

<211> 702

<212> DNA

<213> Homo Sapiens

<400> 279

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atthtatatc	tgcaaaagca	attagacgct	accactgatg	aaaagaagga	aacagttact	180
caactccaaa	atatcattga	ggctaattct	cagcattacc	aaaaaaatat	taatagtttg	240
caggaaagagc	ttttacagtt	gaaagctata	caccaagaag	aggtgaaaga	gttgatgtgc	300
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gagaacttag	taaaacaatg	tgaggcaagt	gaaaagaaca	tccagaagaa	atatgaatgt	420
gagttagaaa	atttaaggaa	agccacctca	aatgcaaacc	aagacaatca	gatatgttct	480
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agaagataacc ttaaaaagaa cttgaatctc aacacagtat cttaaaaaga tgagggtaac 600
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<210> 280
 <211> 874
 <212> DNA
 <213> Homo Sapiens

<400> 280
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 agaatagttg ggcattttaa taaaatttgc taaatgaatg aaaaatccaa aataaatcat 180
 gaagccattt ataaatcaca ccaatcttgc ttgggttaaa caatagaaag taacactttt 240
 gaaagagaag gcaaacaggt gttagagggg caagaatgtg agctcgagga aaagacagct 300
 acgaactgtg tttttaacaa ctcattatct ggctactata tttcccaatc tattctaaca 360
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 ggaatcctan attttacagg ggggaaaaaa aaacacnaaa caaaacaaaa accagaatca 540
 gaattcattt tccataatga actggccatc ntgttaagca taanaaaatc actatcaaag 600
 anaattccta cagaaaccaa tttggtcaca gaatttcctt tggttanacca gaaaattaat 660
 actgaactta ctatgcataat ggcatttact attaaaaaaa aaaaagtant aaccaaggcc 720
 aaganaaaca acctgaaaca ttaaatacat ntttataagg aaaaantaaa tgaattttta 780
 tcttaatttt aaanaaaaac cnaaaatttt nncatacccc cccgctctta cttaaaaaant 840
 gncttaccaa aataactaanc ctttcccaa aacc 874

<210> 281
 <211> 730
 <212> DNA
 <213> Homo Sapiens

<400> 281
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 ggcccaggct ctgcacacac atcctgggan aactgccata ggccctagaa ggagggatga 180
 aaggcgtatg ggagggaana cagcgggtccc cggatcagca gcagcaccac catcctctga 240
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 tgggccccag gagccanaca ggaggagggc agcaggaang gctggcatgg aagggtgag 360
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 agcttcttca ggaagcctcc aactgactct catccttgat gccacaaaac ttgtccacca 480
 cgtecccatc cttcatggcc agcacagtgg gcaccgctga caccctatc tcaatggcga 540
 agtctgtgtg gtctntcaata tccaccttgg ccataccac cttcccgtgc tgcttgacca 600
 ccatcttctc taacctccgn cccangatct tcagggtcca caccactgtg cgtggaaatc 660
 cacaaccact ggtgtctcct gtttgaacac tccgtcttga aantcngtcc ntcctgnata 720
 ttaaagggtg 730

<210> 282
 <211> 699
 <212> DNA
 <213> Homo Sapiens

<400> 282
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 aatttaagtc tatccgtgag accatgaagg agaagggtt gctgggggag ttcctgagga 180

cccacaagta	tgatcctgct	tggaagtacc	gctttggtga	cctcagcgtg	acctacgagc	240
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acttcctggt	cctttttgac	accggctcct	ccaacttggt	ggtgccctct	gtctactgcc	360
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aatnagcctg	ggtaccaact	tcgtctaagc	gcanttttga	tgggatcaag	ggcctgggcc	600
taacctggct	ctgtcccgtt	ggattaaggc	caccacaagc	tatntagggc	nattnggntc	660
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<210> 283

<211> 759

<212> DNA

<213> Homo Sapiens

<400> 283

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tctatctttt	tgcaacaagt	ggatactcca	gtttcccatc	ccaacatggt	gttcgcaatg	120
tgtgagaacg	tgatgaaaga	cgatatcccc	gtttacacac	aaattcaact	gattcacctg	180
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tgggcggatt	ccacangang	tgtctctgca	tgttgggctt	cctgtccact	gctattaatg	660
catgttacat	tactggctcc	accattttgt	aatatgttgc	acaagtttta	gtccttgctc	720
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<210> 284

<211> 764

<212> DNA

<213> Homo Sapiens

<400> 284

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tgggtccgaga	tgctcaaca	aaaatgcagg	gagattatac	tttgactttg	cggaaggagg	300
gcaataataa	gttaataaag	atctatcacc	gggatggtaa	atatggcttt	tctgacacctc	360
tgacatttaa	ttccgtgggt	gagctcatta	accactatca	ccatgaatct	cttgctcagt	420
acaatcccaa	acttgatgtg	aagctgatgt	acccaagtgt	ccagatacca	acaggatcag	480
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aaggaaatac	agatgaagag	gactgcaata	gaaagctttt	aatgaaaaca	ttaaaatatt	660
tggaaagaca	ntgtcacaca	caaggaaacca	acattnccaa	agaatatatt	gagnngattt	720
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<210> 285

<211> 586

<212> DNA

<213> Homo Sapiens

<400> 285
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atccccacaa aaagaatgct attccncatc tcagagaaac aggcaggaag gacanaaggg 180
gttagttaca gtgatcaatt ttagcgtttg ctaaaacnca caaattcnag nctttttaag 240
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gtttttttta acanctnggc ttaaattatt taaatgaaan cccaagcctc ccnatttncc 480
tttggtngcc ttttncanaa aatcccattc natcacaaaa ccctaaaaag ccttcttcgt 540
nggggggaaa aaananactg ccaaangcaa aaacaaaaac ncccaa 586

<210> 286

<211> 666

<212> DNA

<213> Homo Sapiens

<400> 286
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agtttagcgag ccaatgagag accaagtcgc acggactcat ttgacagagg acactcccaa 180
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gcagtgcctt gtcattcttg agggcgctga tatcaagaat ggaactgaaa gaccttcctt 600
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atttct 666

<210> 287

<211> 782

<212> DNA

<213> Homo Sapiens

<400> 287
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<210> 288

<211> 707

<212> DNA

<213> Homo Sapiens

<400> 291

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gcatactgtg	gtggcctcat	ccacggnchna	aaccanggta	aggcaaggcc	catgatgcca	780
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<210> 292

<211> 664

<212> DNA

<213> Homo Sapiens

<400> 292

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ggggaaccca	cctgtctctg	cattgagcaa	tgcaaacctc	acaagaggcc	tgtgtgtggc	180
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gccagcccag	ttgtttgcta	tcagtccaac	cgatgatgagc	tccgacgtcg	catcatccaa	360
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aattcctgaa	gtttgtggga	acangaatga	aactgccatc	aatattacaa	cgtttccagn	540
accaagggag	aacaacaagt	ttgcctaang	ggactccggg	ngttgatgcc	tctcaatttg	600
aactggtctg	gatgaaaaat	gcctgattgg	gnaattnaag	cttcccaant	agtttcncca	660
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<210> 293

<211> 719

<212> DNA

<213> Homo Sapiens

<400> 293

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<210> 294
 <211> 762
 <212> DNA
 <213> Homo Sapiens

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 ctcaaaccga tctttcaacc ctctgagaa agaagtgtgc cctgngaggg attaaacgta 660
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<210> 295
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 <212> DNA
 <213> Homo Sapiens

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<210> 296
 <211> 652
 <212> DNA
 <213> Homo Sapiens

<400> 296
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 aacagaaact tgtttanatt gtttcttgaa gtttgactac ttaaaaacat aggtgtaaag 180
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<210> 300

<211> 625

<212> DNA

<213> Homo Sapiens

<400> 300

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<210> 301

<211> 792

<212> DNA

<213> Homo Sapiens

<400> 301

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<210> 302

<211> 738

<212> DNA

<213> Homo Sapiens

<400> 302

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<210> 303

<211> 635

<212> DNA

<213> Homo Sapiens

<400> 303

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<210> 304

<211> 847

<212> DNA

<213> Homo Sapiens

<400> 304

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<210> 305

<211> 767

<212> DNA

<213> Homo Sapiens

<400> 305

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<211> 1659

<212> DNA

<213> Homo Sapiens

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<211> 833

<212> DNA

<213> Homo Sapiens

<400> 308

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<212> DNA

<213> Homo Sapiens

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<212> DNA

<213> Homo Sapiens

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ccaaaatgac	aggttcagca	ccacccctt	ctccaacacc	taacaaagag	atgaagaaca	180
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agaccaaatc	ttgtcagaca	gatgatactt	ggaggacaga	atatgttcca	gtgcctatcc	300
ctgtgcctgt	gtatatccca	gttcctatgc	acatgtacag	tcagaatatt	cctgttccta	360
ctacagttcc	tgttcctgtg	ccagttcctg	tttttctgcc	tgctccattg	gacagcagtg	420
agaagattcc	tcagcaat	gaggagctaa	aaagcaaggt	ttcttcagat	gctcttgata	480
cagagttgct	tacaatgacg	gatatgatga	gtgaagacga	ggggaaaaca	gagacaacca	540
acatcaacag	tgtaattatt	gaaacagata	taattggttc	agaccttttg	aagaactctg	600
acccagagac	acagtccagc	atgcctgatg	taccatatga	accaagattt	ggatatcgaa	660
atagattttc	ccagagctgc	tgaggagctt	gatatggaaa	atgaattttt	attaccacct	720
gtttttggcg	aagaatatga	ggaacagccc	aagacctcga	tctaaaaaaa	aaggagacca	780
agagaaaangc	tgatatcaagg	ataccaagtc	ccatgatgat	aagtctgaca	atttcagaat	840
gcagcnttcc	tttcaaatta	tacgtatggg	cgtaaatgca	tgggnaacac	cgggtcaaaa	900
actaagnnac	ttggatgaaa	gatcntccgg	gnaattagaa	tgagttaaaa	tccttccaaa	960
tccantnaag	tttaaaagag	ggtntaatcc	cctcaaaacc	anagctggng	ccttaacaag	1020
ggggttaacc						1030

<210> 311

<211> 546

<212> DNA

<213> Homo Sapiens

<400> 311

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atatgaagtc	ttgggagtat	actgattaaa	aagcacacat	tgggagtgat	agtaagaaga	120
gctaaaataa	aaagcacaga	aggaaaaaat	aattgatattg	tacataagct	aaattataat	180
tccttttaaaa	ttgtttataa	caagatggaa	tacagaatga	cgattagatt	tataacgtgt	240
gtttatatga	atatgttggt	aacagtgaga	tttctgatat	ggtataacaa	agtatatgat	300
tggaggacct	gcaaaatgta	tactcgggtt	gtttttcttt	ttaaaaatat	tgtnaaacag	360
gcaagtggag	cttaacagca	ttatggttca	ttacnggggtt	tgggntatat	acctttttca	420
gcttctgttna	tgagcaagtt	gtgttttcaa	tccccacttt	caatgtctat	gggaaggggcg	480
cnttttgcgn	tgttttgttt	tgtcttttaa	ncntttttnaa	acnggggaca	canatggang	540
ccggcc						546

<210> 312

<211> 518

<212> DNA

<213> Homo Sapiens

<400> 312
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 gggaggaatg ggggtggggct naccctgna acccatnata aacctattct nctnaggggtg 120
 ctgggaaana attgggggtct ggaataaaanc tncaaagggg tcncngctt cactaaaacc 180
 ttggcaacta aggtcattt ttccaaaggg gtttctnang tcnnctccct ntnaaatcnt 240
 tttattatnc cagggtggct gttgctaang cttnggtggg aaancangaa ntttctgctn 300
 ctntgctgc tggtgctgct gggcantnca agggaaaacc ccccgacaa actgggataa 360
 ngtgacctgn ttgncacnt ctngggccct attnccntac ctgncctgna aatncttccc 420
 nctctgcccc ctttactnnt gccaanctt tccccccgg ttaggataaa aattccctn 480
 aacctccnac ctttggttan cgggggtccc ctnccccc 518

<210> 313
 <211> 660
 <212> DNA
 <213> Homo Sapiens

<400> 313
 gccaaagtgt gaatacggcc caggggtgtg gcctgaaagt ggctgtgtc tcagccgccc 60
 tatcggacga gtcagtggct ggagacagt gtgtgtacga ggcttccgtg cagagactgg 120
 gtgcttcaga agctgtgca ttgacagt acgaatcgga agcagtgggt gcgaccgaa 180
 ttcagattgc cctgaagtat gatgagaaga ataagcaatt tgcaatatta atcatccagc 240
 tgagtaacct ttctgctctg ttgcagcaac aagaccagaa agtgaatatc cgcgtggctg 300
 tccttccctg ctctgaaagc acaacctgcc tgttccggac ccggcctctg gacgcctcaa 360
 gacactctag tgttcaatga ggtgttctg gtatccatgt cctatccaag cccttcacca 420
 agaagacctt aagagtcat gtctgtacca ccgacaggag ccctctggga aaagtgcctg 480
 ggaggcgccc aaatnagcct ggcggagggtc tgccggctctg ggggaaaagt cgactcgctn 540
 gtacaacctt ctacgtaca aatacttgaa gaaacaagac aangggactc aagccantgg 600
 gagtcatggg ccctggcctc angggtgccc aacaacgggc cccgtgttct ggccccgttt 660

<210> 314
 <211> 516
 <212> DNA
 <213> Homo Sapiens

<400> 314
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 ctcatgttag tggcttnact gggcatctga gaccagcgtg gcctgtcacc cacatanact 120
 aggtgtgcta gcccaccag cctatcacac tgcccgtcc acgttgggca gccacataaa 180
 aacacgtcac agctcaanaa natecgtgga tgcacctctg aatccccccc aatggtttct 240
 gtgcattttt ttaatatgtt acaaaatag ttaactagga aaaattagct gtactgtgac 300
 aagtgcggga cgtcctatta ggattaccgt ccccaggca ttacttctta ttgcagtaag 360
 acctctaaaa ggtggagctg tncaaacc aaataatcta aacgatttta agaanagcag 420
 caactcaata ctgctttagt tcatttaaat tttctttccc aaaaatacac tcctaaatat 480
 acaaactata caatcttatt attttaatgc tgggtt 516

<210> 315
 <211> 677
 <212> DNA
 <213> Homo Sapiens

<400> 315
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 tccttacatc catattcaaa catgagatac catattatga gttccagtct cttcaaaactg 120
 aaatttggtc tcaaaacaaa tatactcatt tcaaagaact tccaactctt ctccactgtg 180
 cagcaaaatt tggcttaaag aacctggcta ttcatttgct tcaatgttca ggagcaacct 240

gggcatctaa gatgaaaaat atggaggggtt cagaccccac acatattgct gaaaggcatg	300
gtcacaaaga actcaagaaa atcttcgaag acttttcaat ccaagaaatt gacataaata	360
atgagcaaga aaatgattat gaagaggata ttgcctcatt ttccacatat attccttcca	420
cacagaaccc agcatttcat catgaaagca ggaagacata cgggcaagag tgcaaatgga	480
gctgaggcaa atgaaatgga aggggaaggn aaacagaatg ggntcaggca tggagaccaa	540
acacagccca ctaagagggtt ggcagtgaga gttctgaaa accagtatga tgacttgtn	600
gtgttcaatc cctggngct gattcaagaa aaataattcc acaaggggtgc tattcntngt	660
ttttacaaga cntcctt	677

<210> 316

<211> 843

<212> DNA

<213> Homo Sapiens

<400> 316

agcttttaac attcaattta tttgtggcat ttgtacatga aaattatatg acgataacat	60
tgcttttctat tctaagctag taaattgttt ctaagaaata atagattgat aaaattgcaa	120
gtcttaatac aaaggtaggt tatgaaaatg tatattaatt tgagatatag aaaagttttc	180
aaataataat gttttcaggg ttatatgcaa atagacacta aataagacaa ggtttctgca	240
aacatgatgt aacaataatg actggaactc tgaatgtgag aaattcagaa aatgaaccag	300
ctacttaaaa agcaaaaatg tgctaagtaa atttgtatgt tcatggttat tctaaggaga	360
ggaggaataa tctgttgagg ttagtgccct caagcagacc ccataacttt gctacaccgc	420
atttaacttc tctgtgctgt tttcttttaa ttttcaaaat ggaaatttagc tgtttcattg	480
gtgaagtgca ttgtaaaatg agagaatgtt caaataatgc aattactcta tggattctg	540
ttttaatagt aatataacca tatgaagcag gtataatgag aataaatttt gccataaaca	600
aattctgaaa tctgaanttt gtttctgctg tcatagtatg aattcgcttt aaagananca	660
ggcaatccaa attcaacttg ctacactgaa aacaaaatgt ccgtanatcg tgagttcata	720
taataacctc cttaatgatc ttctgacaca naaaccaat tcttttcaac ttgggggtcaa	780
caagaacctc ttgctgaatt ttcatataaa actatttctt gttggcagtt tctaccccc	840
gga	843

<210> 317

<211> 835

<212> DNA

<213> Homo Sapiens

<400> 317

acaagacacg cctgcgtagt ggtagtgccc tctgcagtc ccagtctagt actgaggacc	60
cgaaggatga gcctgcggag ctaaaaccag attctgagga cttatcctcc cagtcctcag	120
cttcaaaggc atctcaggag gatgccaatg aaatcaagtc taaacgggat gaagaagaac	180
gagaacgaga aaggagggag aaggagaggg aacgagaaa agaacgggag aaggagaagg	240
agagagaacg agagaagcag aagctaaaag agtcagaaaa agagagagat tctgctaagg	300
ataaagagaa aggcaaacat gatgatggac ggaaaaagga agcagaaatt atcaaacaat	360
tgaagattga actcaagaag gcacaggaga gccaaaagga gatgaaacta ttgctggata	420
tgtaccgttc tgccccaaag gaacagagag acaaagtcca gctgatggca gctgagaaga	480
agtctaaggc agagttggaa gatctaaggc aaagactcaa ggatctggaa gataaagaga	540
agaaaagagaa caaagaaaat ggctgatgaa ggatgccttg aggaagatcc gggcagtggg	600
gggacaagat agaataccta cagaagaagc taagccatgg gcaagcagga agaagaagca	660
ctcctctctg aaatgggatg tcacaaggcc aagcctttga agacatgcag gagcaaaaat	720
atccgntttg attgcagcaa nttgccggga anaanggatg atgccaaatt ttcaaagccc	780
aatgtcaaaa gccgttttca agttccaaat ccagnttcat naagnttgcc ttaaa	835

<210> 318

<211> 582

<212> DNA

<213> Homo Sapiens

<400> 318

caaaactgaat	cctgcttttaa	ttcaagcttg	nggagaacaa	agtcctacag	aaacattcca	60
nanaattttc	nggaaaagag	ggatcacaa	aaccctgtaa	aaaggagact	ganagtaatt	120
canagctcac	caagttcncn	ccgtatcaaa	ttccanaat	accacaaga	tttcttcacc	180
anctcantcc	tgactcaacc	tcttcaatct	ttanttcatt	agaagacaaa	gggtcanatt	240
attttaaatt	antcnantcc	caagaaattt	aaagacttga	agtagtagag	cattcaaaac	300
ttaaataact	ttaacaagaa	agccanctga	tcttaacaag	ttacnncngn	antaaatggg	360
aaatagactg	aatcanccta	nacataattt	cattagggnt	gcaaaccacc	cangggaaag	420
tagcacaaat	ataccanttt	gtaatccaca	ttcacaagaa	gtttgcnaca	caaatagaaga	480
aaactttgng	cccatagaca	acttatTTTT	taaaatatca	ctccccaaaa	gtagccatgt	540
ttccactttt	gggtcccctt	ccanatcaaa	aataccaact	tg		582

<210> 319

<211> 827

<212> DNA

<213> Homo Sapiens

<400> 319

gaagccattc	gatgttcac	agattggcca	tttcagccat	accttgtgtt	tgatgttgga	60
gatgtttcag	aaagacggga	taatgactca	tatataaatg	ttcaagaaat	aaaactgggtg	120
atggaaataa	ttaagcttat	taaagacaaa	agaaaggatg	ttagttttcg	aaacattggc	180
ataataactc	attacaaggc	ccagaagacg	atgattcaga	aggattttgga	caaagagttc	240
gatagaaaag	gaccagcaga	agtagacact	gtggatgcat	tccagggctcg	gcagaaggat	300
tgtgttattg	ttactgtgtg	cagagcaaat	agcatccaag	gttcaattgg	attcctggca	360
agtttgcaga	gattgaatgt	caccatcaca	cgagccaagt	acagcctctt	catcctcgga	420
catttgagga	ccctgatgga	aaaccagcat	tggaatcagc	tgattcagga	tgctcagaag	480
cgtggtgcca	ttattaagac	ctgtgacaaa	aactatagac	atgacgcagt	gaagattctg	540
aaactcaagc	ctgtgctgca	gagaagtctc	actcancctc	ctaccatagc	cccaaagggg	600
tccaaacccc	aaggggtgnt	tgcccaagca	ncaagctaga	cagttggatt	ttgccaaaga	660
caatcctggg	tgccggcttc	tccaatacca	aaacaaccct	ccggactccc	aagggaaaat	720
tacncctaac	ggtttacctt	caaagggacc	ctgaaaagac	ccncctgggt	caatgaccaa	780
cnttcanggg	nccccagaa	tggtgaaaa	agggatgggc	aatttag		827

<210> 320

<211> 598

<212> DNA

<213> Homo Sapiens

<400> 320

aaatTTTaaa	aggattttgt	tatttgcctat	acaaatatac	atttcaactt	ttacaacatt	60
cactccagtc	tgacctcctt	gtctatagaa	gactaagaga	tcaacatttc	cagtctctga	120
cttcaaggac	attattacgg	atacacaatg	ccctctgaaa	gcttttgcaa	atgacagaaa	180
atactgaaga	tgaccagagg	ctcaggtggt	aaggatgcat	ttccatggt	ttccaacagc	240
acacaaactc	cttacaaaaa	acaagcttat	ctagatggtc	ccacgagctg	gtcatcttca	300
gtttacaata	tgctgtggct	gctggcccat	gtcactgggc	tttctataaa	aagctttctt	360
ttcttgggaa	ctgctgtcct	cctgtctcaa	gtgtcctctt	gtccaccta	gagttcctcc	420
tggtgtgatg	ggctctggaa	ccacacttct	cctgtctccc	ttcactgaaa	gccctggcct	480
ctctcctgtg	acagagctcc	tcttccgggt	catcacattt	gctctgacac	gtgggnagcc	540
tcggggaaact	gggcanctgg	gaggntccgt	ttttttttgg	gaaggtttgt	tggtgccc	598

<210> 321

<211> 808

<212> DNA

<213> Homo Sapiens

<400> 321

gcataccac	catccacgag	gatgaggtgg	ccaagaccca	gaaggcagag	ggaggtggcc	60
gcctgcaggc	tctgcgttcc	ctgtctggca	ccccaaagtc	catgacctcc	ctatccccac	120
gttctctctc	ctcctcccc	tccccaccct	gttcccctct	catggctgac	cccctcctgg	180
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agggcaagca	gctgggcca	gctgtgaata	cggcccagg	gtgtggcctg	aaagtggcct	360
gtgtctcagc	cgccgtatcg	gacgagtcag	tggctggaga	cagtgggtgtg	tacgaggctt	420
ccgtgcagag	actgggtgct	tcagaagctg	ctgcatttga	cagtgcagaa	tcggaagcag	480
tgggtgcgac	ccgaattcag	attgccctga	agtatgatga	gaagaataag	caatttgcaa	540
tattaatcat	ccagctgagt	aacctttctg	ctctgttgca	ncaacaaaga	ccagaaagtg	600
aatatccgcg	tggctgtcct	tccttgcctc	gaaaagcaca	aactgcctgt	tccgggaccc	660
gggtctctga	cgctcaaac	actccaagt	ttcaatgaag	gtgttctggg	tatccatggt	720
ccctatccaa	accnttaac	aagaagacc	tttaanaag	tccaatgtcc	ngtnaccaac	780
cggacaaggg	agccaatctt	gggaaaaa				808

<210> 322

<211> 629

<212> DNA

<213> Homo Sapiens

<400> 322

agcaaaataa	atgtcactat	atcaagataa	agaataacat	taggtgtgaa	ctagcatagg	60
tgattcatgg	gaaacgaaat	ggcaaattcg	aaaggaattc	tgggaacccat	cgtactaggt	120
tacattgcct	ttttgcctgt	agagaacca	tgaggagagg	ggttctcagc	cttcccagtg	180
gaacccttct	cttagttgca	ctggcattgg	gggatctcat	tgtctggcct	aggtccaggc	240
agggcagctc	ctggggccca	agggcgggct	cactcaccag	ctgtcttcca	gtgtctgtgt	300
gctgtccttg	ccctcctgcc	tcttctccaa	ctccactgct	gtctgttcca	acagagcaag	360
acacagcgtc	cgtgtggca	ngccctgaag	caagggccat	gactcccact	ggcttgagct	420
ccctgtcttg	tttcttcaag	tattttgtan	ctgagaaagt	tgtaccaanc	gaatcnacct	480
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tccaaaatgg	ctcccgctcg	ttgggacana	catccnactt	tttaangcct	tccggggnaa	600
agggctgggn	taaggacatt	gggtncccc				629

<210> 323

<211> 798

<212> DNA

<213> Homo Sapiens

<400> 323

aacattttctg	tgatcaacat	tgcttactgc	gtttctactg	tcaacaaaat	gagcccaaca	60
tgacaactca	gaaaggacct	gaaaacttac	attatgatca	gggttgctag	acatctcgaa	120
ccaaaatgac	aggttcagca	ccacccctt	ctccaacacc	taacaaagag	atgaagaaca	180
aagcagttct	ttgcaaacct	ttaacaatga	caaaagctac	ttactgtaaa	cctcacatgc	240
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ctgtgcctgt	gtatatccca	gttcctatgc	acatgtacag	tcagaatatt	cctgttccta	360
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accagagac	acagtccagc	atgcctgatg	taccatatga	accagatttg	gatatcgaa	660
tagattttcc	cagagctgct	gaaggagcct	tgatatggga	aaatgaattt	ttattacca	720
ccngtttttg	ggcgaaagaa	tatgaaggaa	caagcccaaa	cctcgattct	aaaaaaaaag	780

ggagccaagg agaaaagg

798

<210> 324
 <211> 754
 <212> DNA
 <213> Homo Sapiens

<400> 324

aaaaggacac	taagggtttta	ataaggggaa	caaaaaattg	ttttcaccag	catagattca	60
cattacagta	caccaatatt	gacagcattc	tcttgtctat	ttttggtaca	gaagatggta	120
tctctctaca	taaccttgta	aggcttcagt	aactaaaatg	taaaacccaa	caaaacaaaa	180
ccccaaaaca	aaacaaaaac	cccagcctat	tagttttacag	tttattttta	aaattccgaa	240
agacactgca	agttctaaac	ttttagtagt	gctacccata	cacaaccatc	tggttaagaa	300
cccagtaaaa	gagccccctt	ccaaggaagc	tttgcaacag	tagagtgtgt	caatatggat	360
gtttcttact	acaagaaaaa	aattatacat	ggcacattct	cattcatatt	ctgtaatgta	420
aaaagttaca	aacataccta	atcaaataaa	taataataaa	aaaagaattt	gaatgtattt	480
gttaagtatc	ctaaaaccac	tacatagaat	aatggcaact	ttcactcaca	gattatttac	540
atggttaatac	ccagcgtggg	tacactgcta	caaaactcaa	aacagaagga	gtaaacttga	600
aatgttttcc	ataataaaga	tctagcanca	tgactatcct	aatgccgttt	tatcccgaat	660
gcttctggca	acgttccctt	ttaatccggt	gtctcatcca	attcaaaaan	tggcctttac	720
caaaaaatat	cctttttaca	gaaagaaacc	cggt			754

<210> 325
 <211> 854
 <212> DNA
 <213> Homo Sapiens

<400> 325

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caaaatgtca	ggaattggaa	ataaaagagc	agctggagaa	cctggcacct	ccatgcctcc	120
tgagaagaag	gcagctgttg	aagattcagg	gaccacagtg	gaaacaatta	agctaggagg	180
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gtttgatgaa	aacatccgta	tcatecttaa	acgttatgat	ctggagcagg	gcttggggaga	420
cctactcaca	gaacgaaaag	cccttgttgt	gcctgaacca	gaaccagact	ctgatagcaa	480
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caggaacgtg	tggagtcttc	ccgccgagcc	gtgtoccaga	ttgtgactgt	ttatgataaa	600
ttgcaagaaa	aagtggagct	cttatcccg	gaagctaaac	agtgggagat	aatctgatag	660
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acanggaatt	gacaagatct	tcctcaggaa	aaagcatcgc	aaccatgggc	tcaaggngtt	780
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tggaggtcca	anga					854

<210> 326
 <211> 760
 <212> DNA
 <213> Homo Sapiens

<400> 326

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cagaattttc	tggaaaagag	ggatcacaa	aaccctgtaa	aaaggagact	gagagtaatt	120
catagctcac	caagttctct	ccgtatcaaa	tttccagaat	acccacaaga	tttcttcacc	180
agctcagtc	tgactcaacc	tcttcaatct	ttatttcatt	agaagacaaa	gggtcatatt	240
atttaaaatt	attctagtct	caagaaattt	aaagacttga	agtagtagag	cattcaaaac	300

ttaaataact	ttaacaagaa	agccagctga	tcttaacaag	ttactctgct	agtaaatggg	360
aatagactg	aatcactcta	gacataat	cattagggct	gcaaaccacc	caggggagag	420
tagcacaatt	ataccatttt	gtaatccaca	ttcacaagaa	gtttgctaca	caaatagaaga	480
aaactttgtg	cccatagaca	acttat	taaaatatca	ctccccaaaa	gtagccatgt	540
ttccactttt	gttccctttt	ccacatcaaa	aataccaact	tgatttcttc	aggaggaatg	600
gacaatccaa	gtttatacaa	gtgggctggg	aaaaagaaaa	cactgaaaag	tctaaaagca	660
caagataaac	aaagcctggg	aagggaagac	agttaagagt	tatttgtttc	caantcaatc	720
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<210> 327

<211> 852

<212> DNA

<213> Homo Sapiens

<400> 327

caaagcagtt	ctttgcaaac	ctttaacaat	gacaaaagct	acttactgta	aacctcacat	60
gcagacccaa	tcttgtcaga	cagatgatac	ttggaggaca	gaatatgttc	cagtgcctat	120
ccctgtgcct	gtgtatatcc	cagttcctat	gcacatgtac	agtcagaata	ttcctgttcc	180
tactacagtt	cctgttccctg	tgccagttcc	tgtttttctg	cctgctccat	tggaacagcag	240
tgagaagatt	cctgcagcaa	ttgaggagct	aaaaagcaag	gtttcttcag	atgctcttga	300
tacagagttg	cttacaatga	cggatatgat	gagtgaagac	gaggggaaaa	cagagacaac	360
caacatcaac	agtgtaatga	ttgaaacaga	tataattggt	tcagaccttt	tgaagaactc	420
tgaccagag	acacagtcga	gcacatgtac	tgaccatata	gaaccaagat	ttggatatcg	480
aaatagattt	tccagagcgt	gctgaggagc	ttgatattga	aaatgaattt	ttattaccac	540
ctgttttttg	cgaagaatat	gaggaacagc	ccaagacctc	gatctaaaaa	aaaagggagc	600
caagagaaan	gctgtatcaa	ggataccaag	tctcatgatg	ataagtctga	caatttcaga	660
atgcagcatt	cctttcfaat	tatacgtatg	ggcgtaaatg	catgggnaac	accgggtcaa	720
aaactaagnn	acttgatga	aagatcctcc	gggnaattag	aatgagttaa	aatccttcna	780
aatccantna	agtttaaaag	agggtntaat	cccctcaaaa	ccanagctgg	ngccttaaaa	840
aggggttaaa	cc					852

<210> 328

<211> 799

<212> DNA

<213> Homo Sapiens

<400> 328

aaaaggacac	taagggttta	ataaggggaa	caaaaaattg	ttttcaccag	catagattca	60
cattacagta	caccaatatt	gacagcattc	tcttgtctat	ttttggtaca	gaagatggta	120
tctctctaca	taaccttgta	aggcttcagt	aactaaatg	taaaacccaa	caaaacaaaa	180
ccccaaaaca	aaacaaaaac	cccagcctat	tagttttacag	tttattttta	aaattccgaa	240
agacactgca	agttctaaac	ttttagtagt	gctacccata	cacaaccatc	tggttaagaa	300
cccagtaaaa	gagccccctt	ccaaggaagc	tttgcaacag	tagagttgtg	caatatggat	360
gtttcttact	acaagaaaaa	aattatacat	ggcacattct	cattcatatt	ctgtaattga	420
aaaagttaca	aacataccta	atcaaatata	taataataaa	aaaagaattt	gaatgtattt	480
gttaagtatc	ctaaaaccac	tacatagaat	aatggcaact	ttcactcaca	gattattttac	540
atggtaatac	ccagcgtggg	tacactgcta	caaaactcaa	aacagaanga	gtaaacttga	600
aatgttttcc	ataataaaga	tctagcaaca	tgactatcca	atgctgtttt	atcccagttg	660
cttctgcaac	gttcttttta	atccgtgtct	catccagttc	anaantgtcc	ttatcaanaa	720
taacctttac	tagaagaaac	cgtncagaca	tattttcaan	gggtttccgg	tccaattgaa	780
gttanacgtn	taccaaaca					799

<210> 329

<211> 978

<212> DNA

<213> Homo Sapiens

<400> 329

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agctgccc	gaaggacatt	atcaagtttc	tgcaggaaca	cggttcanat	tcgtttcttg	120
cagaacataa	attattagga	aacattaaaa	atgtggccaa	gacagctaac	aaggaccact	180
tggttacagc	ctataacat	ctttttgaaa	actaagcgtt	ttaagggtag	tgaaggtata	240
agtaaagtgt	ctgagcaagt	aaaaaatgtg	aagcttaaat	gaagataaac	ccaaagaaac	300
caagtctgaa	gagaccctgg	atgaggggtc	cccaaaatat	actaaatcct	gttctgaaaa	360
aggagagataa	aaccaacttt	cccaaaaagg	gagatgttgt	tactgctgg	tatacaggaa	420
cactacaaga	tgggactgtt	tttgatacta	atattcaaac	aagtgcagag	aagaagaaaa	480
atgccaagcc	tttaagtttt	aaggctcgag	taggcaaggt	tatcagagga	tgggatgaag	540
ctctcttgac	tatgagtaaa	ggagaaaagg	ctcgactgga	gattgaacca	gaatgggctt	600
acggaaagaa	aggacagcct	gatgccaaaa	ttcnccaaaa	tgcaaaactc	acttttgaag	660
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tgataaaact	tggccttgaa	gaaatttacn	caactagtta	gaacttgta	ctattgtaaa	780
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tgagagataa	atcccttatg	aatccctggg	ctaaaatact	ttcctacagc	tgtgtaaaaat	900
actgggtcaag	gagaactttt	tccttttacc	tcattgttga	aacttaagtg	gctcaataaa	960
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<210> 330

<211> 1017

<212> DNA

<213> Homo Sapiens

<400> 330

cgatcggcgg	agctcccacc	tccgcttaca	gctcgctgce	gccgtcctgc	cccgcgcccc	60
caggagacct	ggaccagacc	acgatgtgga	aacgctgggt	cgcgctcgcg	ctcgcgctgg	120
tggcggctgc	ctgggtccgc	gccaggaag	agctaaggag	caaatccaag	atctgtgtcca	180
atgtgttttg	tggagccggc	cggaatgtg	cagtcacaga	gaaaggggaa	cccacctgtc	240
tctgcattga	gcaatgcaaa	cctcacaaga	ggcctgtgtg	tggcagtaat	ggcaagacct	300
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gctatcagtc	caaccgtgat	gagctccgac	gtcgcatcat	ccagtggctg	gaagctgaga	480
tcattccaga	tggctggttc	tctaaaggca	gcaactacag	tgaatccta	gacaagtatt	540
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aacagaatga	aactgccatc	aatattacaa	cgtatccaga	ccaggagaa	aacaagtgtc	660
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tcagcttcca	agagtttctc	aagtgcctca	acccatcttt	caaccctcct	gagaagaagt	780
gtgccctgga	ggatgaaacg	tatgcagatg	gagctgagac	cgangtggac	tgtaacccgc	840
tgtgtctgtg	cctgtggaaa	ttgggtctgt	cagccatgac	ctgtgacnga	aagaatcaga	900
agggggccca	gaccagacn	gaggangaga	tgancngata	tgtccaggag	ctccaaagct	960
taggaaacag	cttgaaaaga	nccagagagg	gagccccc	agagattatg	aggaggc	1017

<210> 331

<211> 799

<212> DNA

<213> Homo Sapiens

<400> 331

cccagaaaga	tcatacagct	ttctgtaaaa	gaagatgtac	acctgaaaaa	ggcagaaaat	60
gcctggaagc	caagccaaaa	acgagacagc	caagccgatg	atcccga	cattaaaacc	120
caggagcttt	ttagaaaagt	tcgaagtatc	ttaaataaat	tgacaccaca	gatgttcaat	180
caactgatga	agcaagtgtc	aggacttact	gttgacacag	aggagcggct	gaaaggagtt	240

attgacctgg	tctttgagaa	ggctattgat	gaacccagtt	tctctgtggc	ttacgcaaac	300
atgtgtcgat	gtctagtaac	gctgaaagta	cccatggcag	acaagcctgg	taacacagtg	360
aatttccgga	agctgtctact	gaaccgttgc	cagaaggagt	ttgaaaaaga	taaagcagat	420
gatgatgtct	ttgagaagaa	gcagaaagaa	cttgaggctg	ccagtgtctcc	agaggagagg	480
acaaggcttc	atgatgaact	ggaagaagcc	aaggacaaag	cccggcggag	atccattggc	540
aacatcaagt	ttattggaga	actctttaa	ctcaaaatgc	tgactgaagc	catcatgcat	600
gactgtgtgg	tgaagctgct	aaagaacat	gatgaagaat	ccctggagtg	cctgtgtcgc	660
ctgtccacca	ccattggcaa	agacttggac	tttgaaaaaa	gccaaagcca	cgtatggacc	720
cagtacttta	atcagatgga	gaaaattgtg	aaaggaaaga	aaaacctcat	ctaggatcgg	780
gtcatgcttt	caggaggtt					799

<210> 332

<211> 881

<212> DNA

<213> Homo Sapiens

<400> 332

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caggagacct	ggaccagacc	acgatgtgga	aacgctggct	cgcgctcgcg	ctcgcgctgg	120
tggcgttcgc	ctgggtccgc	gccgaggaag	agctaaggag	caaatccaag	atctgtgccca	180
atgtgttttg	tggagccggc	cggaatgtg	cagtccacaga	gaaaggggaa	cccacctgtc	240
tctgcattga	gcaatgcaaa	cctcacaaga	ggcctgtgtg	tggcagtaat	ggcaagacct	300
acctcaacca	ctgtgaactg	catcgagatg	cctgcctcac	tggatccaaa	atccagggtt	360
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gctatcagtc	caaccgtgat	gagctccgac	gtcgcacatc	ccagtggctg	gaagctgaga	480
tcattccaga	tggctgggtc	tctaaaggca	gcaactacag	tgaaatccta	gacaagtatt	540
ttaagaactt	tgataatggt	gattctcgcc	tggactccag	tgaattcctg	aagtttgtgg	600
aacagaatga	aactgccatc	aatattacaa	cgtatccaga	ccaggagaac	aacaagttgc	660
ttaagygact	ctgtgttgat	gctctcattg	aactgtctga	tgaaaatgct	gantggaaac	720
ttagctttca	agaagtttct	caagngcctt	naaccatct	ttnaaccttc	ttgagaagaa	780
tgtgcccttg	gaggatgaaa	cgtatgcca	atggagcttg	aaancgaggt	ggactgtaan	840
ccgttggnet	gggncctggg	gaaaattggg	tcttgacaa	g		881

<210> 333

<211> 810

<212> DNA

<213> Homo Sapiens

<400> 333

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agaggcctgt	gtgtggcagt	aatggcaaga	cctacctcaa	ccactgtgaa	ctgcatcgag	120
atgcctgcct	cactggatcc	aaaatccagg	ttgattacga	tggacactgc	aaagagaaga	180
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caacgtatcc	agaccaggag	aacaacaagt	tgttagggg	actctgtgtt	gatgctctca	480
ttgaactgtc	tgatgaaaat	gctgattgga	aactcagctt	ccaagagttt	ctcaagtgcc	540
tcaaccatc	tttcaaccct	cctgagaaga	agtgtgcct	ggaggatgaa	acgtatgcag	600
atggagctga	gaccgangtg	gactgtaacc	cgtgtgtct	gtgcctgtgg	aaattgggtc	660
tgtcagccat	gacctgtgac	ngaaagaatc	agaagggggc	ccagacccag	acngaggang	720
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aggagcccc	caaagagatt	atgaggaggc				810

<210> 334

<211> 808
 <212> DNA
 <213> Homo Sapiens

<400> 334

cactttaatt	tctttattca	tcaatagtat	ccgaaaagga	agaatcagga	gttacaaaaa	60
caagttaa	gcaatataga	agcctactaa	atacaaatac	aagttcacaa	acacatatgc	120
aacagaaa	actgttttagatt	gtttcttgaa	gtttgactac	ttaaaaacat	aggtgtaaa	180
gaaagacatt	cagactgggc	cacgtgggct	tgtagcagg	cagaggaacc	ctgctttcca	240
aaaactgata	tagtccagag	tcacggcatg	tggaatgtt	tccatggaca	ctggatctta	300
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ggtcctcaga	tcatgtgatt	ctacggcata	gacgacagct	gccctattta	cacagaagct	540
gcagaactca	agaggaatgt	ggatttgctc	ttgggaagtt	caatgttgca	gggtaaagta	600
agtcttggt	gataaccatg	ttctaaatga	ctagtgaaga	gacactgngg	ttctctgctt	660
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atttcaaa	ctggaccaagtg	gaggtttg				808

<210> 335
 <211> 758
 <212> DNA
 <213> Homo Sapiens

<400> 335

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aggctaaa	atagaacaa	gaagagcaa	ggaaggtcca	gcaactcatg	accaaagaga	120
agagaagacc	aggtgtccag	agagtggacg	aaggtgggtg	gaacactgta	caaggggcca	180
agaacagtcg	ggtactggac	ccctcaaaat	tcctaaaaat	cactaagcct	acaattgatg	240
aaaaaattca	gctggtacct	aaagcacagc	taggcagctg	gggaaaaggc	agcagtgggtg	300
gagcaaaggc	aagtgtgact	gatgccttac	ggtcaagtgc	ttccagttta	aacagattct	360
ctgccctgca	acctccagca	ccctcagggt	ccacgccatc	cacgcctgta	gagtttgatt	420
ccgaaggac	cttaactagt	cgtggaagta	tgggcaggga	gaagaatgac	aagccccctt	480
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acaatcagtc	tcaagaagag	cagcggagag	agatgctgga	gaccgtgaag	cagctnacan	600
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aaaaccccga	aanttcagca	atgtcagctt	attgacaagg	gttgattatc	agaagaggac	720
tgganaggaa	gtccaaatct	atcatggtna	attttttc			758

<210> 336
 <211> 785
 <212> DNA
 <213> Homo Sapiens

<400> 336

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ctgagtcaat	ttctttttgt	ttttttaaat	atttgttcta	tgtattttaca	agccttaaag	120
ttgtcttaaa	gattttcaaga	gtattaagag	tacttttctc	agggtagcac	tttttttttt	180
tttaaacaa	tcttgaggtt	ctgtgggtcca	cagcatttcc	ttctgtttca	atgttatgta	240
cgttttgatt	actattgnga	ttttttaaat	tttctgaagc	aagctgagag	gcaggcagaa	300
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tctggactaa	atgtatatcc	ttaaaacaaa	catgaggngc	atcttgaagg	ggagggaat	420
ttattttctt	gctttttctat	tatacaagtt	gtttacagaa	actgcaaatt	aaaaaattac	480
actggcattt	gcagtcctta	aaataaatta	aaagttctca	actttttttt	ttttgctaaa	540

cattttttta	agtatgagtc	cttggtttaa	aagaaaagat	taaaacagaa	aatattttct	600
ataaatacnt	gnattttggg	tttaagggct	cccgccctaa	ggnttgaagg	ttacttttat	660
cccaggacc	tttttcctcc	atggaacccc	tttttttcnc	ttttcccttt	tcccacttcg	720
ngccnccent	nggggggttc	tggcaaaaaa	tggcccttgc	tgcnctgggg	aattggccaa	780
aaacc						785

<210> 337

<211> 643

<212> DNA

<213> Homo Sapiens

<400> 337

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agctgcccc	gaaggacatt	atcaagtttc	tgcaggaaca	cggttcanat	tcgtttcttg	120
cagaacataa	attattagga	aacattaaaa	atgtggccaa	gacagctaac	aaggaccact	180
tggttacagc	ctataaccat	ctttttgaaa	actaagcgtt	ttaanggtac	tgaangnta	240
nntaaagtgt	ctgancaagt	naaaaatgmn	aancttantg	aagataancc	caaagaaacc	300
aagtntgang	agaccctgga	tgaggggtcca	ccnaaatata	ctaaatctgn	tctgaaaaag	360
ggagataaaa	ccaactttcc	caaaaaggga	gatgttggtc	actgctggta	tacaggaaca	420
ctacaagatg	ggactgtttt	tgataactat	attcaaaca	gtgcaaagaa	naagaaaaat	480
gccaagcctt	taagttttta	ggtcggagta	cgcaaaagtt	atcanaggat	ggggatgaag	540
ctctcttgac	tatgagtaaa	ggagaaaagg	ctngactgga	aaatggaccc	aaaatggctt	600
accggaagaa	aaggagacagc	ctgatnccaa	aatttcccca	aat		643

<210> 338

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 338

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aagttctcct	tgaccagtat	tttacacagc	tgtaggaaaag	tatttttagac	cagggattca	120
taagggattt	atctctcaaa	agctgggacc	aagtaaaca	attttattaa	ctccttgaat	180
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gctgtccttt	ctttccgtaa	gccattcttg	gttcaatctc	cagtcgagcc	ttttctcctt	420
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cagtcctcat	ttgtagtgtt	cctgtatacc	agcagtgaac	aacatctccc	tttttgggaa	600
agttggtttt	atctcccttt	ttcagaacag	gatttagtat	attttggggg	accctcatcc	660
agggctctct	cagacttggg	ttctttgggt	ttatcttcat	ttaagcttca	cattttttac	720
ttgctcagac	actttactta	tactttcagt	acccttaaaa	ccgcttaagt	ttcaaaaaag	780
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<210> 339

<211> 758

<212> DNA

<213> Homo Sapiens

<400> 339

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cagtagctgt	cagagggaaa	gactgtgcag	taattgtcac	acagaagaaa	gtacctgaca	180
aattattgga	ttccagcaca	gtgactcact	tattcaagat	aactgaaaac	attggttgtg	240

tgatgaccgg	aatgacagct	gacagcagat	cccaggtaca	gagggcacgc	tatgaggcag	300
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ccgatatttc	tcaggtctac	acacagaatg	ctgaaatgag	gcctcttggt	tggtgtatga	420
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ttacatgcct	gtctactggg	ctatcaattg	atttcaaacc	ttcagaaaata	gaagttggag	660
tagtgacagt	tgaaaatcct	aaattcagga	ttcttacngg	aagcagagat	tgatgcttac	720
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<210> 340

<211> 840

<212> DNA

<213> Homo Sapiens

<400> 340						
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caacaagggtg	agcatcaatc	tctgcttctg	taanaatcct	gaatttagga	ttttcaactg	240
tcactactcc	aacttctatt	tctgaagggt	tgaaatcaat	tgatagaaca	gtagacaggc	300
atgtaattgc	agtttccact	gtctgttcaa	atgtccaatc	aaatttcttc	ttcacttttt	360
tttcaaggaa	gctgggtgac	tcagtttggt	taactcccgc	tgacgtggct	ttaaaccac	420
agtagtaacc	tgacggatca	cacttatata	cctgagggcc	ttgctcttca	tctataccaa	480
ttaaaatcat	acaacaacca	agaggcctca	tttcagcatt	ctgtgtgtag	acctgagaaa	540
tatcggaat	tcttttacac	agcatgtcca	caggaatctc	atagccatac	ttggatttcc	600
agtttagctgc	ctcatagccg	tgcccttctg	tacctgggat	ctgctgtcag	ctgcattccg	660
gtcatcacac	aaccaatggg	ttcagttatc	ttggaataag	tgaggtcact	gngctggaat	720
nccaataatt	tggcaggnac	ctttctttct	ggggngacaa	ttactggccc	agtcttttcc	780
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<210> 341

<211> 793

<212> DNA

<213> Homo Sapiens

<400> 341						
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aacagaaact	tggttanatt	gtttcttgaa	gtttgactac	ttaaaaacat	aggngtaaag	180
gaaagacatt	canactgggc	cncnggggct	tgntagcagg	cagaggaacc	ctgctttcca	240
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ttaggggaaa	naaccnttgg	gggtntcntt	ggnnttttaa	caaaattggg	gggncntttt	720
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<210> 342

<211> 906

<212> DNA

<213> Homo Sapiens

<400> 342

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cagtagctgt	cagagggaaa	gactgtgcag	taattgtcac	acagaagaaa	gtacctgaca	180
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ccgatatattc	tcagggtctac	acacagaatg	ctgaaatgag	gcctcttggg	tgttgtatga	420
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<210> 343

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 343

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tgcacatcac	tggcagagaa	ctgaggtcca	aaatagctga	aacctttgga	cttcaagaaa	180
attatatcaa	aattgtcata	aataagaagc	aactacaact	agggaaaacc	cttgaagaac	240
aaggcgtggc	tcacaatgtg	aaagcgatgg	tgcttgaact	aaaacaatct	gaagaggacg	300
cgaggaaaaa	cttccagtta	gaggaagagg	agcaaaatga	ggccaaactc	aaagaaaaac	360
aaattcagag	gaccaagaga	ggactagaaa	tactggcaaa	gagagcagca	gagacagtgg	420
tggatccaga	aatgacaccg	tacttagaca	tagctaacca	gacaggcaga	tcaatcagaa	480
ttcccccatc	agaaaagaaa	gcccttatgt	tagctatggg	atatcatgag	aagggcagag	540
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<210> 344

<211> 629

<212> DNA

<213> Homo Sapiens

<400> 344

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cgcatgatcc	atcctgtctt	cagtcagtgc	cttctggaag	ggagggaaag	tcttggatgc	180
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tcccactggg	cacacatcta	cagaggagt	cgtggcgag	tgaggacggg	tactgtctga	300
gccgacacac	agcgaactac	atacttttag	aaagagcctc	tgtcacatgg	ctagaacaac	360
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tctcttagct agcagtgagt tcagtatgac agcacagagt ctaaaaatat taattaaaaa	480
taaattgctt tggtagcat ttaaaccctt cccattcaat agaagatttc tgtaatgagg	540
aatgctgaat atatataaag cctgccactc aatctttgaa tttcngggg cgcaatttta	600
ctgaactaag anccctaaaa caactggcg	629

<210> 345

<211> 724

<212> DNA

<213> Homo Sapiens

<400> 345

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ctttcatttt aaaaagtatt atttaatttt tgggggacctt aattaaaatt taacatttaa	180
ccatgngtnn tttttttgta aacagtctac atgtcaacaa atggataagg gttacaaaag	240
gcaaatnctg acttcatttg tgttttaaac acgattatat gaatttttct tttttaatta	300
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tcagctccaa tggaaattnc tcatagcact tcttacagac tggcttcag tcaaaactcca	540
caaacttatt cttgantgtt aatttagtgt tgcaggtana acaggcaaag cagttcacgc	600
accaggcctt attaagagca gagaccccca tcaccttcta taacacgatt gcagtgaggaa	660
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<210> 346

<211> 907

<212> DNA

<213> Homo Sapiens

<400> 346

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tactgatgca gaaagacgat cagtgatgga tgcaacacag attgctggtc ttaattgctt	180
gcgattaatg aatgaaacca ctgcagttgc tcttgcatat ggaatctata agcaggatct	240
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tgggaagaaa tacaagctag acattaagtc caaaatccgt gcattattac gactctctca	480
ggagtgtgag aaactcaaga aattgatgag tgcaaatgct tcagatctcc ctttgagcat	540
tgaatgtttt atgaatgatg ttgatgtatc tggaaactatg aatagaggca aatttctgga	600
gatgtgcaat gatctcttag ctagagtgga gccaccactt cgtagtgtt tggaaacaaa	660
ccaagttaaa gaaagaagat atttatgcag tggagatagt tgggtgtgct acacgaatcc	720
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atgctgatga aactgcactc gaggtgggc cattgcantg ggccatctta tcgcctgctt	840
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<210> 347

<211> 711

<212> DNA

<213> Homo Sapiens

<400> 347

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ccagtttcaa	agtaaaactg	ttacgancat	nttactnnc	aaacttctca	tattcnccac	660
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<210> 348

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 348

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caatttggtt	cttagcttct	tcttggaagg	ctcgggtattc	atcctctacc	ttagcaatgg	420
catcctgtaa	tcgattggca	tcatttccgg	tatgagccag	atcttctctg	aagctactag	480
ccaaagtctc	tgctttttct	ttgtccagcc	tgacactctc	caggagggtcc	tgaatatcag	540
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<210> 349

<211> 832

<212> DNA

<213> Homo Sapiens

<400> 349

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aacaaaatta	ttttttataa	aagcaaaaaga	ataaagaata	tatacaaaaag	ggacctggaa	180
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gagggtgtgc	tatacataaa	cttcagtcac	ttttgcttgt	gcagaatcat	cccaatcttc	360
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ggtaagtcct	tccttctctt	tcctctgat	tatatacaac	atatctcctt	tcaagactat	600
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acatcangaa	aagaaaactc	aattcagaaa	tgaagaaaac	tggcaggtat	acaatacacc	720
cccagaacat	ctcaatatcc	ctggccagta	caattcaagt	gnactgggta	caggcccata	780
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<210> 350
 <211> 782
 <212> DNA
 <213> Homo Sapiens

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 tcaggctnat tctctcaca atntaaacct tgaggggata tgaagggaacc caactcngg 660
 aaangaaaaa tcaattcana aattgaagaa acctggcagg tatacaatac ccccccaggn 720
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 aa 782

<210> 351
 <211> 775
 <212> DNA
 <213> Homo Sapiens

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 cagtctttgt gcttgncttc aaccagtcct ttnttcagat tctttacccc cagaggtgtc 720
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<210> 352
 <211> 865
 <212> DNA
 <213> Homo Sapiens

<400> 352
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ccccccagag cattttttaa atatccctgg ncacaagtnc caattcaagg gnacctggtt      780
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<210> 353

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 353

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<210> 354

<211> 705

<212> DNA

<213> Homo Sapiens

<400> 354

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<210> 355

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 355

WO 99/04265

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cagatggccc cgggcggccc aggtcctnta ctgtgaagga gcaggagct gccgaggag      660
acgagcctca gtgcgggggtg gaaggctctt tgccttgctc accagggntc agccaagccc      720
tgagtggtgt ccccgctcgg ggaggggccc gccgagcggg caggagagagc cagtcctgtc      780
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<210> 356

<211> 750

<212> DNA

<213> Homo Sapiens

<400> 356

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accgcaatgg ggccctctatc cagcagttct gcatcaacct gcggcagctc tacggggaca      180
gccgcaagtt cctgctgctt ggtctgaggg ccttcatccc tgagaaggac agccagcact      240
tcgagaactt cctggagacc attggcgtga aggatggccg cggcatcatc actgacagct      300
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ccacggggcag ctctgatgac cggtcggcac cctcagaggg ggatgagtgg gaccgcatga      420
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gatggacagt ggatgggggg gcacccacac cttccgcgca gtcgtcatag gccttcccag      540
aaggagctgc ccagacctgc gtgtcagccc ttggtggtgg ccaggganag gcgcccgtg      600
agatggcccc gggcggggcc aagtcctcta ctgtgaagga acaggagct tgccgangga      660
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ccttgcaatg nggccccgct tcggggaagg                                     750

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<210> 357

<211> 725

<212> DNA

<213> Homo Sapiens

<400> 357

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ccccgagcgg ggacacactg cagggttggt ctganccctg gtggacaagg caaagagcct      180
tccacccccg actgaggttc gtgtccctcg gcagctccct gctccttcac agtanaggac      240
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acgcaggtct gggcagctcc ttctgggaag gcctatgacg actgcgcgga aggtgtgggt      360
gcccccccat ccaactgtcca tcatgtgag tccctgtcca tgctgcagcc cagcgccctca      420
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atggtctnca ggaagttctc gaantgctgg ctgnccttn tcagggatga anggccttan      660
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acttc                                                         725

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<210> 358
 <211> 813
 <212> DNA
 <213> Homo Sapiens

<400> 358
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 atgctgcaga tgatgatgaa gatgatgatg atcagttttc tgagggaaggat gatgaaacca 480
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 ggaaacctgc agtcaatata aagcaagggt aatgtttgaa ttttggaata aaaactcttg 600
 aggaaattaa gtcaaagaaa atgaaggaaa aatctaagaa gcaagggtgag ggttcttcag 660
 gagtttccag tcttttactt cacccttgag ccccgntcca ngtcctgaaa aagaaaatgt 720
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 atgagtctta ctgagagact ggggaacca aaa 813

<210> 359
 <211> 756
 <212> DNA
 <213> Homo Sapiens

<400> 359
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 tagaagagaa aaaacgtgcc atgcaagaga caaagataaa aggggaaaag gtagaacaga 180
 aaatagaagg gaaatgggta aatgaaaaga aagcacaaga agataaactt cagacagctg 240
 tcctaaagaa acaggagaa gagaagggaa ctaaagtgc agctaaaaga gaaaagctcc 300
 aagaagacaa gcctaccttc aaaaaagaag agatcaaaga tgaaaagatt aaaaaggaca 360
 aagaacccaa agaagaagtt aagagcttca tggatcgaaa gaagggattt acagaagtta 420
 agtcgcagaa tggagaattc atgaccacaa aacttaacaa tactgagaat actttcagcc 480
 gccctggagg gagggccagc gtggacacca aggaggctga gggcgcccc caggtggaag 540
 ccggcaaaaag gctggaggag cttcgtcgtc gtgcgggga gaccgagagc cgaagagttc 600
 gagaagctca aacagaagca gcaggaggcg gctttggagc tggaggaact caaggaaaaa 660
 ganggaggag agaaggaagg tcctgganga ggaagagcag aggaaggaaac aggaggaaaag 720
 ccgacgga aaccttcaag aggaggaaaga agaaga 756

<210> 360
 <211> 706
 <212> DNA
 <213> Homo Sapiens

<400> 360
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 gatcttctgt tgacttcana tngggttgg atcactgctc aaatacagag ttatgatgat 180
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cctaccttta agccagcagt ttnccttatt tggggngcc	ctgctgcant ggggggatga	660
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<210> 361
 <211> 726
 <212> DNA
 <213> Homo Sapiens

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gagcgagtga acatgccgcc cgcggtggac	cctgcggagt tcttcgtgct	180
gatggagcgt		
taccagcact accgncagac cgtgcgcgcc	ctcaggatgg anttcgtgct	240
cgaggtgcat		
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gccgagcacc gcnagctgat ggccctggaac	caggcggaga accggcgct	360
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cggatagcga ggctgcggca ggaggancgg	nagcaggagc agtgncaggc	420
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gcccgcgaag ccgaagaggt gcangcctgg	gcgcagcgca aggagcngna	480
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ggtggaagca		
gcattggact cccggaagaa ctacaactgg	gccatcacca gagagggct	600
ggtggtcagg		
ccacaacgca nggacttcta agggcccagt	aaggacagtg cccggcaggg	660
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<210> 362
 <211> 747
 <212> DNA
 <213> Homo Sapiens

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nattcacaga		
acatgctagt cagctngcag ttttacctcg	taaagatanc aganaattat	180
agncaaacca		
gtaaacangg aattnacttt tcaaaagatt	aaatccaaac tgancaaat	240
tntaccctaa		
aacttactcc atccaaatat tggataaaaa	gtcagcaggg atncattctn	300
ttctgaaactt		
tanattttnt anaaaaatat gtaatagnga	tcaggaggag ctnttgttca	360
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aaagcaangt taccttacca taggccttaa	ttcaaaacttt gatccatttc	420
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gactttgtaa cgcanatgtc acttttaatg	ccagccctgc cctggttagc	660
ncttctggag		
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<210> 363
 <211> 1227
 <212> DNA
 <213> Homo Sapiens

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ggagacatag		
gaccaccaa tgggtgccagc aaggaaatac	cagaattgga agaagaaaa	180
acaattccta		
ccaaagagcc tgagcagata aaatcagaat	acaaggaaga aagatgcaca	240
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aagatcgta	tgactacac	atggattaca	tacttgtaaa	ccgtgaagaa	aattcacact	300
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<210> 364

<211> 831

<212> DNA

<213> Homo Sapiens

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<210> 365

<211> 785

<212> DNA

<213> Homo Sapiens

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<210> 366
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 <212> DNA
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<400> 366
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 ataactttgg acagtccaga tgaaattgac atcaatgtgg atgaacttga taccctcgat 720
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 <211> 803
 <212> DNA
 <213> Homo Sapiens

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<210> 368
 <211> 809
 <212> DNA
 <213> Homo Sapiens

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<210> 369

<211> 826

<212> DNA

<213> Homo Sapiens

<400> 369

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<210> 370

<211> 783

<212> DNA

<213> Homo Sapiens

<400> 370

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cagacacttt	attctgagca	atccaatgca	tgatagaaaa	accttttagat	atataaaaga	180
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 <212> DNA
 <213> Homo Sapiens

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 tcttcccttt tga 793

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 <211> 804
 <212> DNA
 <213> Homo Sapiens

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<210> 373
 <211> 792
 <212> DNA
 <213> Homo Sapiens

<400> 373
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<210> 374

<211> 745

<212> DNA

<213> Homo Sapiens

<400> 374

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<210> 375

<211> 734

<212> DNA

<213> Homo Sapiens

<400> 375

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accacacaca ataaagacca tctctgcctc aggcattcgc ccccaaacct ccacctctc	240
tgtttacttt ccaccaagca gaagtttctg aatgggtccac tcacatgctg ccattgcgat	300
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<210> 376

<211> 822

<212> DNA

<213> Homo Sapiens

<400> 376

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<210> 377

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 377

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gctaactggg aaatactatt tacaagaaga ttcaacctaa tcaatatcac ttatcaaaag 540
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ttgcacaatt ttctgaacta tgagaaaaat ttaaaggatc cntaaagcnc ctggcaaaaa 780
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<210> 378

<211> 870

<212> DNA

<213> Homo Sapiens

<400> 378

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tttagcaacg taagtttaac cagtaagtgt cacaactgat caacagtact taaaaggaaa 360
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cccataaaag gatacncagt attttgctgn aaataccagg accacattta caatatatgc 720
aaaaaattag aatgcagngg taagntcctt anatttaagc cctcatatgn gncaacaggg 780
gaaaattcca tttattttta agaaaggaaa aanggagacn gggatataaa tactcggaga 840

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870

<210> 379

<211> 837

<212> DNA

<213> Homo Sapiens

<400> 379

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<210> 380

<211> 793

<212> DNA

<213> Homo Sapiens

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<210> 381

<211> 807

<212> DNA

<213> Homo Sapiens

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<210> 382

<211> 800

<212> DNA

<213> Homo Sapiens

<400> 382

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<211> 1203

<212> DNA

<213> Homo Sapiens

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WO 99/04265

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 aaaatcacat tactacaaaa tggggagaaa actgtttgcc tgggttagac acctgcacgc 1980
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<210> 385
 <211> 804
 <212> DNA
 <213> Homo Sapiens

<400> 385
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 cataaagaat ggcccttctg gataagcaca aagtcaagag acagcgattg gacagaattt 180
 gtgaaggtat ccgccccag atcatgaacg gccccctgca cccccgcccc ctggtggcgc 240
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<210> 386
 <211> 782
 <212> DNA
 <213> Homo Sapiens

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 gtctaccaca ggcaaacagt tttctcccca tttttagta atgtgatttt cctattagca 180
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 ctttttctct tagttcatct atttttact ggtccttggg cccaagtgt tctgagtgat 600
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 ga 782

<210> 387
 <211> 865
 <212> DNA
 <213> Homo Sapiens

<400> 387
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 tggtagacga gaaagcctta gcacaagctc tcaaggaggg caggatacga ggggcagccc 240
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 aggcagctgc cactgagatc cgccgagcca tcacaggtca catcccagaa agcttaagaa 420

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actgtgtgaa caaggaatta tctgtcacat cagcgccttg gtcagtaata gaccagcaag 480
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 tcagatacat ttgggaccna gagatagtga aaaatgatga acttagagaa aaaggaatat 780
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<210> 388

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 388
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 ancagtttca nggttcaactt ccttcccttg anccaggnc aggnccatttn gctttggggn 180
 aaattaaaat canaattcta aaagttganc anctttgttt tttttnaatn gactnanctn 240
 tanccacca ttacaactta nggacggcat gactngataa nganggactt gngtgagggt 300
 ttgagttttc aattaanctt tgnatcacat gaggnaatng ncagcattct tgagncnggt 360
 tatggaatag gcagatanaa ccctgtagta ccaanagttg gaaatnnggt aatngacaac 420
 gcactngcct taacatctc angtagagaa cttttacatt agngagangt ncttgaattt 480
 cananctcac caaattttta ttacttttta tngaaaactg cagngaangc taaaggtcta 540
 cgtttacaat aaacaaatcc agtancagta actcacactg aaccaaanca tacttctgat 600
 agccattatt tttcngcttg gggacaattt taaagntttt cttttggccc aaaaaccngg 660
 aatgtatccc aaacnaaggc tcaaaagagg cccatccttt tcaaacaaaa aagggcantg 720
 gattcncaaa aanactggng aatagaaca tgg 753

<210> 389

<211> 737

<212> DNA

<213> Homo Sapiens

<400> 389
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 gtggctatga caacgtggac atcaaggctg ccggcgagct cggaaattgcc gtgtgcaaca 180
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 acgaacataa ccaccacctc atcaatgact ttaacataaa gcagatgagg cagggagcat 600
 tccttgtaga cgcagcccggt ggccggcctg tggacgagaa agccttagca caagccctna 660
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 tgcttaaggg tccgttg 737

<210> 390

<211> 775

<212> DNA

<213> Homo Sapiens

<400> 390

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gtctaccaca	ggcaaacagt	tttctcccca	ttttgtagta	atgtgatttt	cctattagca	180
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gtgggctggt	tggganaagg	cccttgggaa	aggatgtgcc	actgtcggga	gggttgtgag	720
tcactgggat	gccttncagg	ggatgatccc	tttcatggct	tggcaggaaa	gtctt	775

<210> 391

<211> 776

<212> DNA

<213> Homo Sapiens

<400> 391

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tgcactgtgg	agatgcccct	cctgaaggac	ctggccactg	tggccttctg	tgacgcgcag	180
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gcagaaggtc	tacaccctgc	aggatttgct	gtatcagaac	cgactgcgct	ttctttcact	720
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<210> 392

<211> 909

<212> DNA

<213> Homo Sapiens

<400> 392

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tttttct	gtt	tgggaca	aat	ttaaagt	ttt	tctttt	gtca	caaaaac	agg	aatgtac	ccta	180
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aaaaaa	gtgg	gtttgt	ttcat	agacaat	ctg	acaagtt	acc	ataaaa	agt	tttctg	gaga	420
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cctcaag	gtc	ncagga	aatg	ggggat	tttc	ctcnta	aaaa	at	tttta	att	ttggggg	840
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909

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<210> 393
 <211> 769
 <212> DNA
 <213> Homo Sapiens

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 taaggaaaatg caacattatt cttcttgaac ccttttagct caagactttc cactcaataa 480
 aatagcagag gatctgaaac tgagaaaata tatttgagta caaacagctt gtgaaactta 540
 atactttttt tttttttttg catcatcana gggttttact gaacttacaa ccgacttgcc 600
 cgctcagtat gccagttcan atgtgaaagg cgctttnttg tcagcagcct gnactggctt 660
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<210> 394
 <211> 813
 <212> DNA
 <213> Homo Sapiens

<400> 394
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 ccagagatgg caataaaact gactctcaac atc 813

<210> 395
 <211> 762
 <212> DNA
 <213> Homo Sapiens

<400> 395
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<210> 396

<211> 822

<212> DNA

<213> Homo Sapiens

<400> 396						
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<210> 397

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 397						
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cggngaccac	accgggccct	gtcaggcttt	aactcgant	ctttacgggg	taatcgnntg	780
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<210> 398

<211> 751

<212> DNA

<213> Homo Sapiens

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<400> 398
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<210> 399

<211> 800

<212> DNA

<213> Homo Sapiens

<400> 399
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 tgnngcangcc cacaagctga cggcgatgac ctncctnacc agcttcttct ncttgagccc 660
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 aaccttttt gacagntacc 800

<210> 400

<211> 810

<212> DNA

<213> Homo Sapiens

<400> 400
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 ttccagaaga aaggagaaac tttcttcagc aattgtacaa atttatggaa gatagaggta 180
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 aggaaaaaga agttacatta aaaaaccnga agacaatgaa aatctgggcc gaccaagatg 720
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810

caaatctgga tncnatgaat gggattaagc

<210> 401
 <211> 860
 <212> DNA
 <213> Homo Sapiens

<400> 401
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 aaaagacctc tgaccgatca tcagtgcctgg agatggagaa acgggagagg cgagccttgg 240
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<210> 402
 <211> 779
 <212> DNA
 <213> Homo Sapiens

<400> 402
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 tacaggcgcc cgccaccag cctggctaatt tttttgtatt tttagtagag attgggtttc 180
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 cagcttctag tttaaacagc atgtggtgtt tcagagggag gacctggag agctacatgt 360
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 aactgaata tcactggcaa ccctaaaatg atgaggattt aatgacttgc aactcaagt 480
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<210> 403
 <211> 1443
 <212> DNA
 <213> Homo Sapiens

<400> 403
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 actgaatctc aaaaagattt ggaaataacc aaagaaaatc tggctcaagc agttgaacac 180
 cgaaaaagg cacaagcaga attagctagc ttcaaagtcc tgctagatga cactcaaagt 240
 gaagcagcaa gggctcctagc agacaatctc aagttgaaaa aggaacttca gtcaaataaa 300

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agagaaaaag	tccacttgga	agagacaatt	ggagagattc	aggttacttt	gaacaagaaa	480
gacaaggaag	ttcagcaact	tcaggaaaac	ttggacagta	ctgtgacca	gcttgacgcc	540
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aaatgggaga	ggaagttag	tgatgcgatt	caaagcaaag	aagaagaaat	tagactcaaa	660
gaagataatt	gcagtgttct	aaaggatcaa	cttagacaga	tgtccatcca	tatggaagaa	720
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aaaanggaaa	catttagnca	aaaggcncag	ttggattcct	tggtnaaatc	ctgncttctn	1380
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<210> 404

<211> 819

<212> DNA

<213> Homo Sapiens

<400> 404

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gaacatgaca	agcagatttg	ggagtccaag	gccagacag	agggtccagct	tcagcagaag	180
gtctgtgata	ctctacaggg	ggaaaacaaa	gaacttttgt	cccagctaga	agagacacgc	240
cacctatacc	acagtcttca	gaatgaatta	gctaagttgg	aatcagaact	taagagtctc	300
aaagaccagt	tgactgattt	aagtaactct	ttagaaaaat	gtaaggaaca	aaaaggaaac	360
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caactggaga	ctgatcttca	ggcctccaga	gaactgacca	gtaggctgca	tgaagaaata	480
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gctattgctg	aactgcgtca	gcaacatgat	aaagaaatta	aagagctgga	aaacctgctg	600
tnccaggagg	aagaggagaa	tattggttta	gaagaggaga	acaanaangc	ttgtgggttaa	660
aacccaatca	gcttatggga	acacttgaaa	accatcaaaa	nggaaacatt	tagncaaaag	720
gcncagttgg	attccttggg	naaatcctgn	cttctnttcc	aaatggatcc	gagaaccgcn	780
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<210> 405

<211> 761

<212> DNA

<213> Homo Sapiens

<400> 405

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ttaggganag	gctaggcagt	gaacacatca	tgtatgcaat	ganaaaaata	ccaactggta	180
ggatggggga	ggggagggga	ggcagggaat	aggcncaa	ggaattctat	cctggctgtc	240
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agggcanaga	caatggggct	gaaaaactgt	aataactgnc	actaacagca	aagtanctta	360
gtnccttcaag	aggtcaggag	ttgcagtgtg	gtgttanacc	agtcanactc	ctggctgaaa	420

gtcaatgcct aatattggct cccagnggcc cctgagcact gtctcagggt ccacattcca	480
ggaatnttca natnttcctg gaatgacaag aattggaacc ctgctgncca tagacacttc	540
tccctgccct ttggtgaaag gaaagacttt gggcccttt aataccttan tatcccattgt	600
gatcaagggc caaaagccaa aggggattct tatccttata gcctaagacc ctgaaattct	660
tcccttccca attatatctg gaaattggcc aggggaanaa aaatgctgnc cttcccatgn	720
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<210> 406

<211> 758

<212> DNA

<213> Homo Sapiens

<400> 406

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attcctcagt atctttttaca ggaccacaaa agatcagggt cctgcaaaat ctcaacaaat	120
attaggtcca acaaaccaaa tgtgattctc agattaagca gaagcgttca ggctcagggc	180
agtagaagaa agcagactcg ccagtcctctg cagctccaac ctgtcctcgt atcacctctg	240
tttttgagg cactttccgt gaagagtgg agagaagacc tgtaaatggg aagactgttc	300
cactggaatt gatgttctga tgtagagggt gagagaattc caagttttga ggggagtgggt	360
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gtcccatcca ctgngctcta accggctgga tctgctcctc ggccacagga gagagcattt	660
ttcagcagcc actctttggc cncggtcttt cttccagcag cttcctttaa atcattcctt	720
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<210> 407

<211> 778

<212> DNA

<213> Homo Sapiens

<400> 407

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actgaatctc aaaaagattt ggaataaacc aaagaaaatc tggctcaagc agttgaacac	180
cgcaaaaagg cacaagcaga attagctagc ttcaaagtcc tgctagatga cactcaaagt	240
gaagcagcaa gggctctagc agacaatctc aagttgaaaa aggaacttca gtcaaataaa	300
gaatcagtta aaagccagat gaaacaaaag gatgaagatc ttgagcgaag actggaacag	360
gcagaagaga agcacctgaa agagaagaag aatatgcaag agaaactgga tgctttgcgc	420
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aaatgggaga ggaagtttag tgatgctgatt caaagcaaag aagaagaaat tagactcaaa	660
gaagataatt gcagtgtcta aaggacactt agacagatgt ctttctatg gaagaattaa	720
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<210> 408

<211> 752

<212> DNA

<213> Homo Sapiens

<400> 408

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aaaccaaang ngattntnaa attaancaaa ancgttcagg ctcagggcag taaaaaaaag 180
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ntttccgnga anagttggan anaaaacctg taaanggnaa aactgttcca ntggaaatnga 300
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<210> 409

<211> 736

<212> DNA

<213> Homo Sapiens

<400> 409

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agatcaagtc caatatcgat gccctgctga gccgcttggg gcagatcgct gcggagcaaa 180
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cagccagtgc catgtcctct gcaggtggag ttactggcct actccttccc atgaaccctt 660
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<210> 410

<211> 766

<212> DNA

<213> Homo Sapiens

<400> 410

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ctaccctctg gcctgggcag tgcanacagg gagggctcat ggggaaggag taggccagta 180
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cctggggcag cgatgccctt cacctgctgg nggccattgc tcctgtcagg ctgcttactg 360
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<210> 411

<211> 812

<212> DNA

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<213> Homo Sapiens

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<210> 412

<211> 857

<212> DNA

<213> Homo Sapiens

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 gaagaagatg aggagaagat tcagaatgaa gattatcatc acgagcttcc agatggagat 180
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 actcaaaact caaatggccc gaagtctgat gtatgaaaac tgatgtaaag gaatacactt 720
 tcagaaataa aaagcacagt gctgcttctg gagacatgcn gacaagnctt tttttgctga 780
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 tcctggcnaa agtctta 857

<210> 413

<211> 790

<212> DNA

<213> Homo Sapiens

<400> 413
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 agcanatgan atgtctntca catgtatatt naattattca tgctttttca atagtctntt 180
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 cgtgtntaca gggccaggaa cgtaatgaat ccatgttaac ttaatttcat ttaaaattnc 540

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attttagtaa gtcnncnaac agaaagatcc atgcggttga acagtgtgcc tgncttgac	600
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catagnggct acagggcana atctttttca aaagcaattt tctgggccct aaatctacag	720
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<210> 414
 <211> 1063
 <212> DNA
 <213> Homo Sapiens

<400> 414	60
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nggcnttgac tctgnnnngc gacntnttgc tagtcttcag gntcctact acaggctttg	180
taatganctn nacttgnctt gagacagcct angggagacc acggatgntc tattannngn	240
gcangctggn ctatngcaan ntgggnctna nnetgnanaa tcannngcng ccatgnnaga	300
tnaatagaag ctcatnntgt cataaatggn ccatgactta taaatnaagt ggactggata	360
tcttatgaca gnagcnatnt angcttngtg ngngttaa gcttcacct nnggangata	420
agaggncnac cttgtntnan ctntgcnge tagnaagancc agaganannt gccntgggag	480
attcatggcc natgatagta tatnatctct tacaccanac atgccttgct gnacncaaa	540
tctggacata cacgntttcc ccatctcaga cttcnttgca gcagctgctt nccnacnta	600
cccatgaacg acanntgctt acgntanagc ntgaacnath tgatgagctt cntcagccca	660
gacctcatca tttcgagaag cacatgtccc tgcgtttcaa cctatggatg agggaaagnc	720
ctngngctta aagctcttga aaatccttta cacnngaanc nttctgcata gcttnaatca	780
ctctgagntg cccacatngn gtnttggaag gcttcggnt annatgggtc cgggacctnc	840
aacccttcg tttgaatnct nacntgaccg ganagggtnt gcctgggttc cttnggccnc	900
gaacttaacc ntcacaattn ggntgngant tcntggtaac ggcntaatct nccccaggaa	960
ttggccgctg cttcnacggg aattaanggg aatctttccc atcccnctta nnaccagtta	1020
ggngccntt tttcaatntt cngactcccg gagcttttaa aaaccggggg ccttaggttn	1063
cttggatggc nttgggggtn gcccccttta gggaattaaa ggg	

<210> 415
 <211> 824
 <212> DNA
 <213> Homo Sapiens

<400> 415	60
gtttgattnt aacaaaaant attatgcaca aatnacnag gntanagact ctncatctn	120
anatnaaaat ancagttata attacacaca taatataggt acctataca atgattccaa	180
taaatatcac aggaaataca ntgcattttc aagntgnana gacnaatact tntcattca	240
cagngnttga catanganag cctatttaca tancnatctg tataaagtca tgctctnant	300
ancaggntat ncagngctgn gccancacaa tgnnttnaga angtaagaa cgggncaaac	360
cactnntggn gctggggatc tgganaagcc acctgnanaa gcttactct gagcangact	420
cannaatgnc ttgngccctt taggtggcac tggctgtgga agtggttaag ctgctgctga	480
actcaattcg tggactgnag aattaggaat ggganccagg cggttnggat gaccattgcc	540
cactcnanca natnccaaag nnetnagaan gggaacnctc caancctgct tnatggngat	600
taancatnct tcttcttttg cttaccccat ggattananc acancagcna gtacngactt	660
ggntttaccc ncttcngttg gaaataagga ttcttgatng actaaannnc agctggtnaa	720
aacntaactn tccctcaatt tagcnttatt ntatgaancc ggggcctant nctntgttca	780
aaaangngnt ttttaagttcc ggtaatecta ccgnaatta nttgggggct ntgaattcan	824
cnccttana anatttnggn ttaccatttn aatccaaagg ccac	

<210> 416
 <211> 838
 <212> DNA

<213> Homo Sapiens

<400> 416
 ctcaaaagtg gaaaatatgt acaatctgta atgagctttt tcctgaaaaat gtctatatgtg 60
 tgcacttcga aaaagaacat aaagctgaga aagtcaccagc agtagccaac tacattatga 120
 aaatacacaa ttttactagc aaatgcctct actgtaatcg ctatttaccac acagatactc 180
 tgctcaacca tatgttaatt catggtctgt cttgtccata ttgccgttca actttcaatg 240
 atgtggaaaa gatggccgca cacatgcgga tggttcacat tgatgaagag atgggaccta 300
 aaacagattc tacttttgagt tttgatttga cattgcagca gggtagtcac actaacatcc 360
 atctcctggt aactacatac aatctgaggg atgccccagc tgaatctggt gcttaccatg 420
 cccaaaataa tcctccagtt cctccaaagc cacagccaaa gggttcaggaa aaggcagata 480
 tcctgtataa aagttcacct caagctgcag tgccctataa aaaagatggt gggaaaaacc 540
 tttgtcctct ttgcttttca atcctaaaag gaccatatac tgatgcactt gcacatcact 600
 tacgagagag gcaccaagtt attcagacgg tcacccagtt tgagaaaaag ctnacctaca 660
 aatgnatcca ttggcttggt gngnatacca gcaacatgga ncggctnaac tatcacttct 720
 gnatctagnt cactggangg gccgtttggn aagganccca aatggggccag gataagacaa 780
 aaggcnccct ttnggggttaa tcagncttcc aagtctngca cctgtgnaac gcacttac 838

<210> 417

<211> 880

<212> DNA

<213> Homo Sapiens

<400> 417
 aagcacataa cagcaattta tttagatgct taaaatgaat acaaagggaa aataaagatc 60
 acaaaattat acatactaca acagtgtgtc atatattaga tggataaaat gaatccacca 120
 tgatggtggt gaactaaaga taaaactaaa tatccaaaat gcagcactca ttggtttgct 180
 gcttcaaac aacacacttt tatacagatc taaaagggtg caaaattagt agctgcaaag 240
 tcaattcttg catgtgattt tagcttaaaa gatttcagaa aacagatctg aaataccagt 300
 ttttgttttt gacagctgta atgtcaagga tattcagaac aagaaaaatc ctataatata 360
 agagagtcca gatataatc ttacgtggct ggcctctggt gcaagattgt acaaggttat 420
 gtgcaaaaaac taagtctgtc caaaaagtcc atactagcgc agttttgagc ttttgctagg 480
 taaaactagat agagcgttta ttacacagca agggcaacac taaaaaaga aatctatgat 540
 gggcacacag taacaggatc atgagcatca cttgaatagg tctaaaagac tgtcaaata 600
 acatttcaac tattcagaat gaatacatga aaaaaaatcg cttttcccaa aggtctacta 660
 tacncattan actgggagct tgnatgttgg gccctacact accatgggga attangttta 720
 acacttntta aaaacatttg gccaatcatt tcncagangg gaaagaaatg ttgaaaaggc 780
 cgataaaata aacccttggtg ttttctcggg gggattcatg gagtcacccg ccttaatggg 840
 ttttcacatt taagttaccc gggcttggtg aaaaaagggt 880

<210> 418

<211> 763

<212> DNA

<213> Homo Sapiens

<400> 418
 agaagatggc ggaagcggaa ttttaaggacc atagtacagc tatggatact gaaccaaacc 60
 cgggaacatc ttctgtgtca acaacaacca gcagtaccac caccaccacc atcaccactt 120
 cctcctctcg aatgcagcag ccacagatct ctgtctacag tggttcagac cgacatgctg 180
 tacaggtaat tcaacaggca ttgcatcggc cccccagctc agctgctcag taccttcagc 240
 aaatgtatgc agcccaacaa cagcacttga tgctgcatac tgacagctctt cagcagcagc 300
 atttaagcag ctcccagctt cagagccttg ctgctgttca ggcaagtttg tccagtggaa 360
 gaccatctac atctcccaca ggaagtgtca cacagcagtc aagtatgtcc caaacgtctg 420
 tagaaattct tatggactgg aatcttcttc aaggcttact ttgttcctgg gatgcagtgg 480
 tgcataagaag atagggcatt gactcactca gacctggctt gccagcatg cattgcaaca 540

ataatgtgca agttattaaa gacatgagtg aattcgtgac agattgtcag aaaagaaaca	600
agagttttct acaacaaaaa actggcttat ggaacatata cttctgcttg agttgaatgt	660
gttggggctg agtgtaagaa aatgcaagct gcaaatctgg cttacatgtg gaaccaaagc	720
tggaatgng tgctttaaan gcaacttgta aaattggatt tcc	763

<210> 419

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 419	
ggactatttta cttttaaatgt aattatcaat acagtcggtt taaatctacc attttgttgt	60
tggttttcta tttgtttcat ttgttctctc ttcccttttt tcacctcttc aggattattt	120
tggattcact acttttttta nagngtcgtt ttaccactac tattggccta ttacctgtat	180
ctcttttttt taatggcatt tctctaggat ttacaatatg catcttttagc ttatagtatc	240
ttgaaatagt agngtaacac ttcacaaata gagtaaaaac cttataatct tccatttttc	300
ccttccttct tttgtgctat tgatgacnca tatttactcc tacagatatt ataaacaaat	360
tgatatacnc acattatcat ttttgcttta catactcaat tatcttttaa ataaaaataa	420
aattgaggag aaaatccggt atattatcta cacatttact gtttccagca cttttcattt	480
ctttgngtag attcaaatct ctgncatctt ccttttgccc aaagaacttc ttttcattct	540
tcttatagtt caggtctgct ggcaaccaat tagctcagcc tttggtttgc taaaaaagtt	600
catatattat cttgattttc aaatggnatt taagctctat ataggaattc ttaggtgact	660
ttaatccctt catcattggg aagangtcat aaagggttg caaaggacta gaaatctgct	720
tacatttttt natttggtta tctttcttac cca	753

<210> 420

<211> 799

<212> DNA

<213> Homo Sapiens

<400> 420	
gaaaaacgct ttgataccaa gaattaaaaa tgcttgtcta caaacatctt cccttgcggt	60
tcgtgtaaat tcattagtgt gcttaggaaa gattttggaa tacttgata agtggtttgt	120
acttgatgat atcctaccct tcttacaaca aattccatcc aaggaacctg cggctcctcat	180
gggaatttta ggtatttaca aatgtacttt tactcataag aagttgggaa tcaccaaaaga	240
gcagctggcc ggaaaagtgt tgccctcatct tattccctg agtattgaaa acaatcttaa	300
tcttaatcag ttcaattctt tcatttccgt cataaaaaga atgcttaata gattggagtc	360
tgaacataag actaaactgg agcaacttca tataatgcaa gaacagcaga aatctttgga	420
tataggaaat caaatgaatg tttctgagga gatgaaagt acaaatattg ggaatcagca	480
aattgacaaa gtttttaaca acattggagc agacctctg actggcagtg agtccgaaaa	540
taaagaggac gggttacaga ataaacataa aagagcatca cttacacttg aagaaaaaca	600
aaaattagca aaagaacaag agcaggcaca gaagctgaaa agccagcagc ctcttaaacc	660
ccaagtgcac acacctgttg ctactgttaa acagactaag gacttgacag acacactgat	720
ggataaatatg tcatccttga ccagccttcc tggtagtacc cctaaatctt ctgcttcaag	780
tctttcactt ctggtcctt	799

<210> 421

<211> 770

<212> DNA

<213> Homo Sapiens

<400> 421	
gttcaatatg ggggacattc tggctcatga atctgaatta cttggactag tgaaagagta	60
tttagatttt gctgaatttg aagacacctt gaaaacattt tcaaaagaat gcaaaataaa	120
aggaaaacca ttgtgtaaaa cagtaggcgg atctttcaga gactccaaat cattgacaat	180

tcagaaggat	cttgtcgtcg	catttgacaa	cggagaccag	aagggtgttct	tcgatctgtg	240
ggaggagcac	atttcaagtt	ccatccgaga	tggggactcc	tttgcccaga	agctggaatt	300
ctatctccac	atccattttg	ccatctatct	tttgaagtac	tctgtgggga	gaccggacaa	360
agaggagctg	gatgaaaaga	tttctacttt	caaaacctac	ctggagacca	aaggggcagc	420
cttgagccag	accacagagt	ttcttccttt	ctatgccctt	ccttttggtc	ccaaccctat	480
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atataaggag	aatgggacan	agtaacaaag	aaatcttgca	gcagcttcac	cagcagctgg	660
ntgaagcttg	aaccgtaggt	caatgacata	cctcaaacgg	naccataaga	tccaggcccg	720
actaccacaa	tctcantgga	gtcacagcan	aactggtggg	attctcttga		770

<210> 422

<211> 733

<212> DNA

<213> Homo Sapiens

<400> 422

caaaaangaan	gctttatttt	gaattttaaa	aatacataca	tcttacactg	taatcaaaac	60
aaagcttaag	aaagtcaatt	cccgtctcct	ttagccctga	cttacactgg	gtaccctgtt	120
ctgtggccgc	cgggggtgac	ggncccttgc	aggggtcat	ccccgtcca	ctgcacatta	180
gccagccct	tccgccttgt	cttccccgng	ttggtcatga	tcccaggtga	ctccgnggtc	240
anaagcttct	ctcctgagag	ttctccgagc	tggggctgga	tcagttcgtc	tttgteccana	300
tcggcttcca	tgatgtcatg	gncctcttca	tcattcttcat	cttcatcatc	atcagattca	360
agaacaccat	ctggtagctc	ttcggaaatt	agctgcttga	tgatgaattc	tatctggcgg	420
atcatttcag	cattgccttc	tttgatgaag	cagcgtagga	tgtcttccat	tcccattgct	480
cttgcttcct	cacgaatgga	tggancagaa	aggatgctgt	acagagctcc	attcacatac	540
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tgccaccttg	gcacacatgg	tcttccctgn	gctgcggagg	gcagaggttc	atggagcaaa	660
agccaccgag	tactccaacg	gggnagccag	acagggcagn	cagggctcct	tcanaacatc	720
aaccagccc	gaa					733

<210> 423

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 423

catctgtcca	gggtgcatcg	agccgggagg	gctcaccagc	caggagcagc	acgccactcc	60
actccccctc	gcccatccgt	gtgcacaccg	tggctgcagag	gcctcagcag	cccatgaccc	120
atcgagaaac	tgcacctgtt	tcccagcctg	aaaacaaaacc	agaaagtaag	ccaggcccag	180
ttggaccaga	actccctcct	ggacacatcc	caattcaagt	gatccgcaaa	gaggtggatt	240
ctaaacctgt	ttcccagaag	ccccacctc	cctctgagaa	ggtagagggtg	aaagttcccc	300
ctgctccagt	tccttgtcct	cctcccagcc	ctggcccttc	tgtgttcccc	tcttccccca	360
agagtgtggc	tacagaagag	agggcagccc	ccagcactgc	ccctgcagaa	gctacacctc	420
caaaaccagg	agaagccgag	gctcccccaa	aacatccagg	agtgtctgaa	gtggaagcca	480
tcctggagaa	ggtgcagggg	ctggagcagg	ctgtagacaa	ctttgaaggc	aagaagactg	540
acaaaaagta	cctgatgata	gaagagtatt	tgaccaaaga	gctgctggcc	ctggattcag	600
tggaccccga	gggacgaagc	cgatgtgcgt	caggccagga	gagacggtgt	caggaaggtt	660
cagaccatct	tggaaaaaact	tgaacagaaa	gccattgatg	tccangtcaa	gtccaggtct	720
atgaacttca	agccaagcaa	ccnttgaagc	agatcaagcc	cctggaggca	atcatggaaa	780
aggggtgccgt	ggcagcaaga	caagggcaag	aaaaatgctt	ggaaatggcn	gaagatcccc	840
acacnggaaa	ccagcaggcc	cg				862

<210> 424

<211> 859

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<212> DNA

<213> Homo Sapiens

<400> 424
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cagatattcc tatggctcct ggcacatttt actctctcta aagtcaggta ttttaattat 120
gagatgaaga aaatcatctc attaaaatgg caacatttct gataaatgtt tcatatttat 180
gtgatgggta attgactccc catctacccc tccagtccag agctacaaaa gacagtgcac 240
aaccacagct aacagggtgg gggggtgccc aagtagacag ggctgcagaa caagcaacgg 300
ggttaaactt ctcaaacaac aagcaacttc tttatttgta cagagtaaga atatagaaga 360
aaagcatcat tttctttttt agccctttta ttagtggttt gctccacccc aagttactgc 420
ataccaagca gctaataaaa accaactgac ttaaagtctc tgaaatgcat gcaacttaaa 480
attccctaaa gcacacatcg gttccgagtc tgatttttac agggcagagg ctacgggtgct 540
gttgggttac caggggtgtc tggcatgctg ctgggggttg aagtcgctgc tgctgnggct 600
tctggctgct ggggttctgt gtggggatct ttctgcattt ccagcatttt tcttggcctt 660
ggctgctgcc acggnaccca tcttcatgaa tgccctgcaa tggctggacc tgnctcaaa 720
gttgctgggg ctggagttca ttagacctgg accttgcccc tgggacatca aagggtttt 780
tggcgaaggt tttccaaga agggcctgga accttcctgg acanccgntt tttctgggccc 840
tggaacgnc attgggggtt 859

<210> 425

<211> 837

<212> DNA

<213> Homo Sapiens

<400> 425
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tgatactttg aaaaggctcac agctttttac agcagaaagc ctacaggcca gcaaagaaaa 180
ggaagctgat cttagaaaaag aatttcaggg acaagaagca attttacgaa aaactatagg 240
aaaattaaag acagagttac agatgggtaca ggatgaagct ggaagtcttc ttgacaaatg 300
ccaaaagctt cagacggcac ttgccatagc agagaacaat gttcagggtt tcaaaaaaca 360
gcttgatgat gccaaaggag gagaaatggc cctattaagc aagcacaag aagtggaaag 420
tgagctagca gctgccagag aacgtttaca acagcaagct tcagatcttg tcctcaaagc 480
tagtcatatt ggaatgcttc aagcaactca aatgaccag gaagttacaa ttaaagattt 540
agaatcagaa aaatcgagag tcaatgagag attatctcaa cttgaagagg aaagagcttt 600
tttgccaagc caaaacccaa agtctggatg aagagcagaa gcnacagatt ctaagaactg 660
ggagaagaaa gtaaatgaac caagagactc agcaggaata ttatgaaagg gaacttaaaa 720
anctgcaagt agaattggaag aagaggggct taattaacga nggccattct aagacttttg 780
gaagaattag cttggaacnc cttttggcaa ttgaacttgt cncaggtaat gccattt 837

<210> 426

<211> 724

<212> DNA

<213> Homo Sapiens

<400> 426
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atcacaggaa atacagtgc ttttcaagtt ggagagacaa atactttctc attcacagt 180
tttgacatag gaaagcctat ttacataaca atctgtataa agtcatgctc ttagtaacag 240
tctatacaga gctgtgcca cacaattctt tcagaatgtg aagtaccggg caaaccactc 300
ctggcgctgg ggatctggag aagccactgg agaagcttca ctctgagcag gactcaaaaa 360
tgtcttgggc cctttagggtg gcaactggctg tggagtggt ttgctgctgt tgaactcaat 420
atcgtggact ggagaattag gaatgggatc caggcggtta ggatgtccat tgcccactcc 480

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accagattcc agagcactta nattgggaac actcacaac ctgtttgttg gtgatttacc 540
attcttcttc ttttgcttag ccaatggatt aataacacca acagtaggac ttgagttaaa 600
cactttggtg aaagttagtt tctcgaattg actaattcca gctgataaaa cttattatcc 660
tcaattagtt tctttatgan ctgggcctct ttctgtaagc atggccttta attctggaat 720
catc 724

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<210> 427
 <211> 981
 <212> DNA
 <213> Homo Sapiens

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<400> 427
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tagatgatga tagntncaat gaanctgnga ncatanatta angaaacana naacantncn 180
aaaggtccac aaatctggtc ctatgaaaag agtaaaatta ccaagactng gtgaaaganc 240
ccannaaaaan ncanagagag anagagagag agagaganac anagagagag aganaaaggg 300
aaggcacacn taancnatat cagcaataaa angggnnact ttantacana ttctgcaanc 360
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gatgccgata tgtttgaaaa cttaaatgaa acggaaaaat tccttgaaga accacaantt 480
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ggttncagaa ccactcccc antaccnaaa tttataattg ctcaagttcc tgatataaaa 600
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catangattt tgggaanggn ccaacttggg gccttngtaa ctttttaaaag aaatngggaa 900
ttctttgntn aanaattcct ncncccaaaag aaaacccctt tggcccccana agttntttna 960
aatgggggaaa tttncccaaa c 981

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<210> 428
 <211> 655
 <212> DNA
 <213> Homo Sapiens

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<400> 428
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ttttattcat ccaagaaata ttcattagag aaattggcat gggatttttt tttcattgta 180
atgtccttgt caggtatcaa ggctttttca gctgataaa gcatattaag aaatgcttcc 240
tcttttccta ttctctggaa aagattgtgt aatattgctg ttactacttc ctgtaatgtt 300
tggtgaaatt cacaattgaa gacatctggg cctagcgtgt tctttgtagg aagaatatta 360
agaaagaatt ccatttcttt aaaagttacg agcacagttg gccttcaga tctatggatc 420
ccacatgagt tccagattca accaattgtg tattaataat atttgggaaa aaaagccaca 480
agaaataata caactatata aaataatata atttttaaaa tacaatataa caacgattta 540
cacagaatgt nccattatgt taggnattat aagtaactca gaggntattt aaagnatgtg 600
agaggnnatg gataggctat atgccaataa ctttgccant cttatantca gggaa 655

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<210> 429
 <211> 788
 <212> DNA
 <213> Homo Sapiens

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<400> 429
gagcagcaga gatttttctg gtgagaatta attaccagta acagttcaat atggggggaca 60

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ttctggctca tgaatctgaa ttacttggac tagtgaaaga gtatttagat tttgctgaat	120
ttgaagacac cttgaaaaca ttttcaaaag aatgcaaaat aaaaggaaaa ccactgtgta	180
aaacagtagg cggatctttc agagactcca aatcattgac aattcagaag gatcttgtcg	240
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ttgccatcta tcttttgaag tactctgtgg ggagaccgga caaagaggag ctggatgaaa	420
agatttccta cttcaaaacc tacctggaga ccaaaggggc agccttgagc cagaccacag	480
agtttcttcc tttctatgcc ctctcttttg ttcccaacc tatggtgcac cctcattta	540
aagaactctt ccaggattcc tggactccag agttaaagtt gaagttggaa aagtttctag	600
ctttaatatc taaagccagc aacacgccna agcttttaac aatatataag gagaatggac	660
aaagtaccaa gaaatcttgc agcagcttca ccacagctgg ttgaagctga acgtaggta	720
gngccttctt taaacgggac aattaagaat ccaggccgac taccacaatc ttantggggg	780
tcccagca	788

<210> 430

<211> 655

<212> DNA

<213> Homo Sapiens

<400> 430

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aaagcttaan aaagtcaatt cccgnttccct ttanccctga cttacnctgg gtncccgttt	120
ntggggccnc cggggngac gggcctttgc aggggctcat ccccgnctcca ctggacatta	180
nccagccctt tccgcttgg ctctcccgng ttggtcatga nccccaggtn ctccngggtc	240
aaaagcttnt ntcccgaaag ttctccganc tggggctgga tcanttcgtc tttgnccaaa	300
ncggnntcca tgatgncatg ggcctnttca tcatcttcat tttcatcatc atcanattca	360
anaacnccat ntggnanctt ttccggaattt aactgcttga tgangaattc tatntggngg	420
ancatttcag cattgccttn tttgaagaac cancgtagga nggtttccat tcccattggg	480
nttgnttccct cacgaatgga tggaaacanaa aggatgctnt acananctcc attcacatac	540
ggntgnatnt catggnnttct atggccaana anaatcccaa aggcctttgag cccaggntcg	600
gcccttggca caaatgttnt tcttggtctc cgaaggccaa ggttcattga ccaaa	655

<210> 431

<211> 844

<212> DNA

<213> Homo Sapiens

<400> 431

ggaagaagga agaggtaact ataactaccc aatattgcag ccatggagtc catgcttaat	60
aaattgaaga gtactgttac aaaagtaaca gctgatgtca ctagtgtgt aatgggaaat	120
cctgtcacta gagaatttga tggttggtcga cacattgcca gtggtggcaa tgggctagct	180
tggaagattt ttaatggcac aaaaaagtca acaaaagcagg aagtggcagt ttttgcctt	240
gataaaaaac tgattgacaa gtatcaaaaa tttgaaaagg atcaaatcat tgattctcta	300
aaacgaggag tccaacagtt aactcggctt cgacaccctc gacttcttac tgtccagcat	360
cctttagaag aatccaggga ttgcttggca tttgtacag aaccagtttt tgccagtta	420
gccaatgttc ttggttaactg ggaaaatcta ccttccccta tatctccaga cattaaggat	480
tataaacttt atgatgtaga aaccaaatat ggtttgtctc aggtttctga aggattgtca	540
ttcttgcata gcagtgtgaa aatgggtgca tggaaatata actcctgaaa atataatttt	600
gaataaaagt ggagcctgga aaataatggg ttttgatttt tngntatcat caaccaatcc	660
ttctgaacaa gagcctaaat ttcttgttaa agaatgggac ccaaatttac cttcattgng	720
tcttncaaat cctgaatatt tggcttctga atcctacttt ctgngaactt gtgaaaccag	780
ccagtggata tgggattcct ttaggaactg gtatggaatg ccgggatttt aataaaaggg	840
gaaa	844

<210> 432

<211> 807
 <212> DNA
 <213> Homo Sapiens

<400> 432
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 ctttttcttt catgtgtaaa aacaaccatg tgaggtatgt tacaggtcaa aagaaaaaca 120
 aaactacttc cttattcagt gtaaaggagg cttataagca ttccaaaata aaaacaaaca 180
 aaaaccagac aagtacatag tctatttcca tttcctttta tacatcctct ctatatatca 240
 cacatttagc aataggagaa tagagaacta attcaaatgc aagggaatct tttttgtaga 300
 ttctgttgac agatgctcct taacctaaac attttctact ctaaacataa cggacttaat 360
 tgtcttcagt acgtgaaata attttaaggt gatctagtag tttgaaaatt tcattcactt 420
 aagaacactt aagctgaaaa atagcactat ttttcagagg caatttctca acagaaaaag 480
 gcaatggtaa cagttcaatt gatggaaatg gttgaaataa aatacctgaa gtagaaaaaa 540
 ggtgtaggaa caattttgta aaaacatagc accattacct caacgaatga acaaatttta 600
 catactggat ttttttcaa tgacttattt tcatatttag tagttcaagg tctataagct 660
 ggtatattaa gcttttcttc tggtaagag ntcaacactt acatcatggg attttacnaa 720
 attaaaaacc aattttctta ataaaccgng gctcctaaaa tggtagcaag gaaaaattct 780
 tcaataccta atttaattcc ataagga 807

<210> 433
 <211> 866
 <212> DNA
 <213> Homo Sapiens

<400> 433
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 acacctcttt ggcactagtt cagaatgggt atgtgtcggg cccctctgcc atactcagaa 180
 caccagaaaag cacaaaaacc ggtcctgttt gtcagccacc agtgagtcag agccgctccc 240
 tgttttcttc tgteccgtcc aagccaccaa tgtctctgga gcctcaaaat gggacgtatg 300
 caggaccagc gccagcattc cagccatttt tcttcaactg agcatttcca tttaatatgc 360
 aagagctggg actcaagggt agaattcaga acccatctct tcgagaaaaat gatttcattg 420
 aaattgaact ggaccgacag gagctcacct accaagagtt gctcagagtg tgtgtctgtg 480
 agctgggtgt taatccagat cangtggaga ngatcagaaa gttacccaat actctgttaa 540
 ggaaggacaa ggatgttgtc cgactccaag atttccagga gctggaactg gttctgatga 600
 taagtgaata taattttctg ttcanaaatg ctgcattccac actgactgaa aggccttgct 660
 ataacaggag agcttcaaaa actgacttac taatgcacag ggacttttat cactggagta 720
 ttatgacagt gngcatcacc ttntggggccc aaggaccaag ccatttgtct aaaaggcctc 780
 aaaatgcccc ggganggcct ctggtggcca tggcattagt atatactaac catcattctg 840
 gccaggtatg gaagcccctg gacccc 866

<210> 434
 <211> 764
 <212> DNA
 <213> Homo Sapiens

<400> 434
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 gaaaatgaaa gtggagaaca tggaacagca atatttgnrc tcttctcata ggatgcagtt 180
 acacacacat atgactggaa tcaacttcaga gtaaaaaaaa agtgggctgg gtgcagtggc 240
 tcacacctgt aatcccagca ctttgggagg ccaaggacag gagcatcact taaggccaga 300
 agtttgagac cagcctgggc cacatagtga gacctgtct ctatgggcgg ggtgggggtg 360
 gggggcattg taaaaaagca gttgttcttt tanaaggcat cagagagccc tntagtgacc 420

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acgaagggga gttaatgcag agatgactcg agacagagaa gcagtcatga gtgtttacaa 480
aggaaaaagt gagggaggga aagctctttt ggtaaacagc atattttacaa ttagttaact 540
gnattctttaa atactttttaa cctgagtaac atttataaat atgttatagg aaacctcaca 600
gtcacaaagtc acactagaat ccatctgtcc agtatctggg ctttccccac accagaatcc 660
atctgtccag tatctgggct ttcccagatc ttctcttctt cataagttcc caanggcagc 720
anaagtgtga agcatgcaca ccaaggaaaa acgcattcca gccc 764

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<210> 435
 <211> 834
 <212> DNA
 <213> Homo Sapiens

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<400> 435
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agataaagaa cagtgttcta cccatggttt acagagcact agaagctcct tccattcaga 120
tccaggagct ctgtctaaac atcattccaa cctttgcaaa tcttatagac taccatcca 180
tgaaaaacgc tttgatacca agaattaaaa atgcttgtct acaaaccatct tcccttgagg 240
ttcgtgtaaa ttcattagtg tgcttaggaa agattttgga atacttggat aagtggtttg 300
tacttgatga taccctaccc ttcttacaac aaattccatc caaggaacct gcggtcctca 360
tggaattttt aggtatttac aaatgtactt ttactcataa gaagttggga atcaccaaaag 420
agcagctggc cggaaaagtg ttgcctcatc ttattccctt gagtattgaa aacaatctta 480
atcttaatac gttcaattct ttcatctccg tcataaaaaga aatgcttaat agattggagt 540
ctgaacataa gactaaactg gagcaacttc atataatgca agaacagcag aaatcttttg 600
atataggaaa tcaaatgaat gtttctgagg agatgaaagt tcaaatattg ggaatcagca 660
aattggcaaa gtttttaaca acattggagc agacctntg actggcagtg agtccgaaaa 720
taaagangac gggttacaga ataaccttaa aagagcatcc ttaccacttg gaggaataac 780
caaaatttgc caaagaaccc aggaccggcn ccgaagctgg aaaagccgca ggct 834

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<210> 436
 <211> 812
 <212> DNA
 <213> Homo Sapiens

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<400> 436
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aaatatagtt taattcttac aaatcttctt ttgaaaatgc aattcatata tgctgcaacc 120
tcagaagttt gaatttgaaa tgaaatatga aggtagtagt caggggaagtc acatcagagt 180
gccttgctcaa atatccaaac aaatcagcac atacctcttc cttgatacag gaggaataaa 240
gtgattctaa atatatccaa gtgaatgcag aaaaatacat tactatttga ggcagaccat 300
gctaaaatat aatttacaat gattagtttg cacttaagat ggtaataaac gcatttaaac 360
caatgaaatg aagggttaagt tgaattttgt agtatttgct cagtctctgt actaaacaat 420
agttcatctg aaaagtttgg aaaaagcaaa taacctgata cttctcttta tgcttatcat 480
tttctcactg tcatctttaa tgcaaacaaa tcaatacagc atcaagattt ttacatatt 540
aaaatgaaga ctaatgactc atagactgng taccatatag tacttaatag atgagcttgc 600
aatgaccatc acctcaattt tttaaataac accaagatcc acaagccaaa ataaacattt 660
gattaaaaag ttatggtatt caagataact cagtttctt tttctctttg agattgggna 720
anggctgggt ctttaaaaaa ccctggaaaa gggagttggg taaagaggga aaaaaatcct 780
tcaangcttt taaaaaaact tcnactgggt ta 812

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<210> 437
 <211> 842
 <212> DNA
 <213> Homo Sapiens

<400> 437

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agagcaaagc	cccaacttgc	cctccactgg	tgatgtcaca	cccacccatg	aagagcctgc	120
ctctagggtt	gttgaatgtt	gggtcacgaa	gatctcaacc	tggccaaaga	agagaaccca	180
gaaagatcat	cacagtttct	gtaaaagaag	atgtacacct	gaaaaaggca	gaaaatgcct	240
ggaagccaag	ccaaaaacga	gacagccaag	ccgatgatcc	cgaaaacatt	aaaaccagg	300
agcttttttag	aaaagttcga	agtatcttaa	ataaattgac	accacagatg	ttcaatcaac	360
tgatgaagca	agtgtcagga	cttactgttg	acacagagga	gcggctgaaa	ggagtatttg	420
acctgggtctt	tgagaaggct	attgatgaac	ccagtttctc	tgtggcttac	gcaaacatgt	480
gtcgatgtct	agtaacgctg	aaagtaccca	tggcagacaa	gcctggtaac	acagtgaatt	540
tccggaagct	gctactgaac	cgttgccaga	aggagtttga	aaaagataaa	gcagatgatg	600
atgtctttga	gaagaagcag	aaagaacttg	aggctgccag	tgctccagag	gagaggacaa	660
ggcttcatga	tgaactggaa	gaagccaagg	acaaaagccc	ggcggagatc	cattggcaac	720
atcaagttta	ttggagaact	cttttaaact	caaaatgctt	gacttgaagc	catcattgca	780
tgactgtgtg	gtgaagctgc	ttaagaaccn	ttgatgaaga	atccctggaa	tggcctgtgt	840
cg						842

<210> 438

<211> 678

<212> DNA

<213> Homo Sapiens

<400> 438

aaactngcan	tgntgtntt	tattttgtnc	tttatatttt	caaagngaaa	agaaatanna	60
ctgagncaat	ntctttttgt	ntttttaaan	atttgtntca	tgtatttaca	ngccttaaag	120
nngctctaaa	gatntcaaga	gnattaanag	nactttnttc	agggnagcac	tnnttttttt	180
ttaaacantt	nttggngttc	tgtggnccac	annatttctt	tntgtntcaa	ngtnatgtat	240
gtnttgatna	cnatngngat	nttttaaan	ttntgaanca	agctgagagg	cnngcanaaa	300
gatntgancg	cnmaaaaaaa	aaaatctttn	ttaccttgn	caccccaaac	tttttcaaat	360
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tatttctctg	cttttctatn	atacangtng	ttacanaaaa	ctgngaatta	naaaattaca	480
ctggnatttg	cngaccttaa	aataaattaa	aagtntcaa	ctnttttttt	ttttgntaaa	540
cnttttttta	agnatgannc	cntgggttaa	aagaaaagnt	ttaaaccgaa	aatattttct	600
ataaataata	cctggatttt	ggnnttaggg	cccccgccct	aaggnttgna	ggttactttt	660
ntccnangac	ctttttcc					678

<210> 439

<211> 826

<212> DNA

<213> Homo Sapiens

<400> 439

gaccctttac	caacaaatga	aatgatgat	gatatatgca	agaaaccctg	tagtgtagca	60
cctaagtata	ttccactgg	ttctagtact	aacctaatta	atgaaataaa	tggagttagc	120
gaaaaattat	cagccacgga	gagcattgtg	gaaatagtaa	aacaggaagt	attgccattg	180
actcttgaat	tggagattct	cgaaaatccc	ccagaagaaa	tgaactgga	gtgtatccca	240
gtcccatca	ccccttcac	agttccttcc	tttcttcaa	ctcctccaac	tcctccagct	300
tctcctctc	acaactccag	cattgttctt	gctgctgcca	ctactgttag	ttctccgagt	360
gctgccatca	cagtccagag	agtcctagag	gaggacgaga	gcataagaac	ttgccttagt	420
gaagatgcaa	aagagattca	gaacaaaata	gaggtagaag	cagatgggca	aacagaagag	480
atthttggatt	ctcaaaactt	aaattcaaga	aggagccctg	tcccagctca	aatagctata	540
actgtaccaa	agacatggaa	gaaacaaaaa	gatcggaacc	gaaccactga	agagatgtta	600
gaggcagaat	tggagcttaa	agctgaagag	gagctttcca	ttggcaaagt	acttgaatct	660
gaccaggata	aatgagcca	ggggtttcat	cctgaaagag	acccctntgg	cctaaaaaaa	720
gtgaaaagct	gtggaagaaa	atggagaaga	actgagccag	accgtaatgg	ggcctgaaag	780
ggttctgang	gtgaaggaat	agatgcttaa	ttcangcttc	cccaga		826

<210> 440
 <211> 689
 <212> DNA
 <213> Homo Sapiens

<400> 440
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 agagtacttt tctcagggtg gcaacttttt ttttttaaac aattcttgga gttctgtggt 120
 ccacagcatt tcttctgttt tcaatgttat gtatgttttg attactattg tgatttttta 180
 aattttctga agcaagctga gaggcaggca gaaagatttg atgccaaaaa aaaaaaatc 240
 tttctttacgt tgttcacccc aaactttctc aaatctggac taaatgctat accttaaac 300
 aaacatgagg tgcattctga aggggaggga aatttatttc tctgcttttc tattatacaa 360
 gttgtttaca gaaactgcaa attaaaaaat tacactggca ttgagctcc ttaaaaaaaa 420
 ttaaaagtgc tcaacttttt ttttttgcta aacatttttt taagtatgag tccttgttta 480
 aaaagaaaag attaaaacag aaaaatatttt ctataaataa tacatgtatt ttggtttttag 540
 tgctcccgcc ctaaggtttg aagtttactt ttatccagta cctttttcct ccatgatcac 600
 ctttttttct ctttccctn ttccactcgg gcacacgtgg ggggtttctg cnanaattgg 660
 ccttgctgca ctgngaattgg gcnaaaacc 689

<210> 441
 <211> 883
 <212> DNA
 <213> Homo Sapiens

<400> 441
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 caagtacgcc ggtgtatcag tcagcaccta tcatagtgcc tacgcagcaa cagccgcctc 120
 cagccaagag agagaaaaaa actataagaa ttcgggatcc aaaccaggga ggtaaagaca 180
 taacagagga gattatgtct ggaggtggca gcagaaatcc tactccacc ataggaagac 240
 ccacgtccac acctactcct cctcagcagc tgcccagcca ggtccccgag cacagccctg 300
 tggtttatgg gactgtggag agcgtcatc ttgctgccag caccctgtc actgcagcta 360
 gcgaccagaa gcaagctcaa atagctataa ctgtaccaa gacatggaag aaacaaaaag 420
 atcggaacccg aaccttgaa gagatgtag aggcagaatt ggagcttaa gctgaagagg 480
 agctttccat tgacaaaagta cttgaatctg aacaagataa aatgagccag gggtttcac 540
 ctgaaagaga cccctctgac ctaaaaaaag tgaaagctgt ggaagaaaat ggagaagaag 600
 ctgagccagt acgtaatggt gcttgagagt gtttcttgag ggtgaaggaa tagatgctaa 660
 ttcaggcttc acagatagtt ctgggtgatgg gggtacattt ccatttaaac cagaatnctg 720
 gaagcctact ggtacttgaa ggtaagaaca gtatgaccag ggagtttctg gtggactttc 780
 cagttcatgc ctggctgnat tccaaaancc naaggcctg gcttctatta anggatgngg 840
 ttnttgacag gatcaaccaa ncccaaatgg ccaatgggga act 883

<210> 442
 <211> 777
 <212> DNA
 <213> Homo Sapiens

<400> 442
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 ttttctataa ataatacatg tattttgggt ttatgtctcc cgcctaagg tttgaagttt 120
 acttttatcc agtacctttt tcttccatga tcaccttttt ttctctttcc cctctcccac 180
 tcgtgcacac gtgggggttt ctgcgagaat tggccttgct gcaactgtgat tggcgaagac 240
 gtgaaacttt ttaaaaaaat acttaaatg tttcttttgt ttcattttgt gtatttgag 300
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 gatttcagag ccacgccctt cccattctgc tctgcagggt ccttgctgct ctcccatttg 420
 tagaaggcat cctcgagat cacctcctcg tcatatagac aatcaaaaaa catccgcagc 480

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tccttctctg	natctgagtc	taggtacttg	agtaagatcg	gcactctctg	cttgaaacag	600
cagtgtccac	ttcttgaang	tagaagaagt	cggctattaa	tagctggttt	acaaacagca	660
gtcatttaaa	gctctaagga	atggtaggtg	aactcntctg	ggatttcggc	taagaataag	720
ccctttancc	aggccaaaga	acctgggtcan	tcaattcgct	tttggccctc	caataaa	777

<210> 443

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 443

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taaagcagat	gatgatgtct	ttgagaagaa	gcagaaagaa	cttgaggctg	ccagtgtctc	120
agaggagagg	acaaggcttc	atgatgaact	ggaagaagcc	aaggacaaag	cccggcggag	180
atccattggc	aacatcaagt	ttattggaga	actctttaa	ctcaaatgc	tgactgaagc	240
catcatgcat	gactgtgtgg	tgaagctgct	aaagaaccat	gatgaagaat	ccctggagtg	300
cctgtgtcgc	ctgctcacca	ccattggcaa	agacttggac	tttgaaaaag	caaagccacg	360
tatggaccag	tactttaatc	agatggagaa	aattgtgaaa	gaaagaaaaa	cctcatctag	420
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gagagtggac	gaaggtgggt	ggaacactgt	acaagggggc	caagaacagt	cgggtactgg	660
accctcctcaa	antcctaaaa	atcactaagc	ctacaattga	tgaaaaaant	cactggacct	720
aaagccagct	aggcagctgg	ggaaaaggca	gcagtgggtg	accaangcaa	gtgaaactga	780
gcentacggc	aagtgtcttc	agttaaacag	atctntgncc	tgaaccttca	gaaccttang	840
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<210> 444

<211> 756

<212> DNA

<213> Homo Sapiens

<400> 444

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taaagttgct	ctaaagattt	caagagtatt	aagagtactt	ttctcagggg	agcacttttt	180
ttttttttaa	caattcttgg	agttctgnng	nccacagcat	ttccttctgn	ttcaatgnta	240
tgatgttttt	gattactatt	gggatttttt	aaattttctg	aagcaagctg	anaggcaggc	300
ngaaagattt	gatgccnaaa	aaaaaaaaa	aatctttntt	accttgggtca	ccccaaactt	360
tntcaaactt	ggactaaatg	ctatacctta	aaacaaacnt	gaggggcatn	ttgaaggggga	420
gggaaattta	tttctctgnt	tttctattat	acnagttgnt	taccgaaact	gnaaatttaa	480
aaattaccct	ggcntttgca	ggccttaaaa	taaattaaaa	gntctcaact	tttttttttt	540
gccaaacatt	tttttaagta	tgagnccctg	nttaaaaaaga	aaagattnaa	nccgaaaata	600
ttttctataa	ataatacntg	nattttgggt	ttaaggctcc	cgccttaang	nttgaagggt	660
acttttatcc	nagnnccctt	tttccctcca	tgaanacccc	tttttttcnc	ctttcccttc	720
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<210> 445

<211> 783

<212> DNA

<213> Homo Sapiens

<400> 445

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<210> 446

<211> 866

<212> DNA

<213> Homo Sapiens

<400> 446

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<210> 447

<211> 789

<212> DNA

<213> Homo Sapiens

<400> 447

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gatctttgct taataagaag aaaaaagagg caaggagaaa acgaagagaa agaaattttg 240
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gtaaagatga tgtggcacct gaaagtgggt atactacagt gaagaaacct gaatcaaaga 360
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WO 99/04265

789

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<210> 448
 <211> 820
 <212> DNA
 <213> Homo Sapiens

<400> 448
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 cctgcctcag cctccctagt agctgggatt acagggtgcc accaccatgc ccaattaatt 180
 tttgtatttt tgggtacagac aggggtttcac catggtggcc aggatgggtct cgatctcgtt 240
 gaccttggtga tccgcctgcc tgggcctccc aaagtgtctgg gattacaggc gtgagccacc 300
 gcccctggac tacttatgga ggttttaaaa aatcttttaa gtccaggcct gacgtttaga 360
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<210> 449
 <211> 936
 <212> DNA
 <213> Homo Sapiens

<400> 449
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 aggtgaaaaga gttgatgtgc cagattgaag catcagctaa ggaacatgaa gcagagataa 180
 ataagttgaa cgagctaaaa gagaacttag taaaacaatg tgaggcaagt gaaaagaaca 240
 tccagaagaa atatgaatgt gagttagaaa atttaaggaa agccacctca aatgcaaacc 300
 aagacaatca gatatgttct attctcttgc aagaaaatac atttgtagaa caagtagtaa 360
 atgaaaaagt caaacactta gaagatacct taaaagaact tgaatctcaa cacagtatct 420
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<210> 450
 <211> 806
 <212> DNA
 <213> Homo Sapiens

<400> 450
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 agaatagtgt ggcattttaa taaaatttgc taaatgaatg aaaaatccaa aataaatcat 180

gaagccattt ataaatcaca ccaatcttgc ttgggttaaa caatagaaag taacactttt	240
gaaagagaag gcaaacaggt gttagagggg caagaatgtg agctcgagga aaagacagct	300
acgaactgtg tttttaacaa ctcatattt ggctactata tttcccaatc tattctaaca	360
ctaacaagaa tctgtctaata taattgtgac aacatctgca aaaccatagt tacctatttt	420
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<210> 451

<211> 909

<212> DNA

<213> Homo Sapiens

<400> 451

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tgagagagag agtattaaga gggaaataca gaattccctt ctacatgtct acagactgtg	180
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aaccagagct agacatctca gaccaaaaaa gaatagatat tatggtggga atgggatatt	360
cacaagaaga aattcaagaa tctcttagta agatgaaata cgatgaaatc acagctacat	420
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<210> 452

<211> 672

<212> DNA

<213> Homo Sapiens

<400> 452

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aaaccacagg cntgaactgn aaacctgtct taactatgaa ctggncctaa ggttaattct	180
tannngccat tcantatttc nntccttggg aactgtaatg ttntagcacc ggatgatctc	240
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ttnanacnca taccgtcnan tttcanaccn acccagacgg nangcacatg gngatggggc	360
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tttccatcag tggtnagga aaacacttta aatgcaactn anttccacat cananncact	600
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ggaatgnccc cc	672

<210> 453

<211> 834
 <212> DNA
 <213> Homo Sapiens

<400> 453

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<210> 454
 <211> 703
 <212> DNA
 <213> Homo Sapiens

<400> 454

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aggcttggct	nccgaatgtc	gcatttgggg	gacgaaaaag	gtgcttccgc	tgcttgaaa	660
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<210> 455
 <211> 825
 <212> DNA
 <213> Homo Sapiens

<400> 455

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ctgcagatgc aaaccaggca gaaggccatg aatcgaattt cattgcccag ttggccttcc	660
agaacacacc agggaaaaaca cacagagttt taaggaggaa cctgggcagg cttgacaatt	720
gaacgttnca tgggtgatca caattgaacg tgtgcacaag aagctganga cttgtggaat	780
ccggacaggc attgccaacc aggggccagc ttaacaagcc ccagg	825

<210> 456

<211> 740

<212> DNA

<213> Homo Sapiens

<400> 456

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gaaaaccccc ctttatactt	740

<210> 457

<211> 726

<212> DNA

<213> Homo Sapiens

<400> 457

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cagaactcct gtgggggtctc tttaaaatgc taacaccagc gttaaaagac ttgggggcaag	180
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<210> 458

<211> 870

<212> DNA

<213> Homo Sapiens

<400> 458

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ataaaagaaa aaggcaagcc acttatgtg aacccaagaa caaacaaggg aatggcattt	180
actttacaag aacgacaaat gcttggtctt caaggacttc tacctccaa aatagagaca	240

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gaccagaa	ac gagatcgcac	ccacagttga	tganctgatg	gatgagttta	tgaagcttt	780
actgacag	at atggccggaa	cacctttatt	cagttcgaag	acnttgga	aa tcataangcc	840
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<210> 459

<211> 761

<212> DNA

<213> Homo Sapiens

<400> 459

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gagaacaaaa	ccccagaaaa	cacccttaaa	actgaagaca	ttatctcttc	ttggctgaaa	660
aaagggggtc	cctggagcac	angaaaaggt	ttatcaaggg	aggcttctat	tcngtaatca	720
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<210> 460

<211> 876

<212> DNA

<213> Homo Sapiens

<400> 460

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cactctttta	gaacttggat	tttggcatcg	acatggattc	aaggatttgc	attgtggggc	180
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atgctctagg	ggaggccatc	aatgaataca	aggggtgctgt	gatcggtgtc	agccatgatg	600
cccgactcat	cacagaaacc	aattgccagc	ttgtgggttg	tggaggaaca	gagtggttagc	660
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catgggcagc	cnggccccga	naagtgaagc	tttnccttcc	agaagtntcc	gagagaacat	780
aattgggggg	gcctaaaann	cctctggggg	cttcccttct	tttgaanaat	gctntggnc	840
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<210> 461

<211> 689
 <212> DNA
 <213> Homo Sapiens

<400> 461
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 ggcagcaact cctttccttt atttcttccc cttgtaaagg gaaattcaag ttcagcagca 180
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 ggataatggc aaaggcctca gaagctcacc tccagctctg agcttcaaca gctgtttgta 300
 ccagtgaagtc agcattaaat ccaccagaaa agaacagcac cacccaaaga ctggggggca 360
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 acaataggcc acataaactt ggctggatgg aacctcaca taaggtggtc acctcttgtt 480
 tgtttagggg gatgccaagg ataaggccag ctcagttata tgaagagaag cagaacaaac 540
 aaagtctttc agagaaatgg atgcaatcag aagtggtatc cccgncaca tcaaggtcac 600
 actccacctt catgtgcttg aaatgggttc caggtcagct gcaggccan aggcagtctt 660
 canaaggaag gggagaccac agaggactt 689

<210> 462
 <211> 840
 <212> DNA
 <213> Homo Sapiens

<400> 462
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 tgttacggct cggaggcacc aagcaagatt accttatgct ggctactttg gatgagaatg 180
 aggaagtgat agatggaggc aaaaaaggag caatcgatga ccttcagcaa ggtgaattgg 240
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 atgaaccagc tgaaaaagaa aattccagca aaaaagaagt aaaaatacct aaaataaata 360
 ataaaaatac agcagaaagt caaaggacat cagttaataa ggtgaaaaat aagaataggc 420
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 aggtgacagg atggcagcca ttgattcttc ttattcagga tgatgccctg tcacaccact 780
 ttcagnttgt agnaaactct tggggaaccc ttggtaaaaa ggaanggcna caaaacagca 840

<210> 463
 <211> 784
 <212> DNA
 <213> Homo Sapiens

<400> 463
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 tttgcatctc tggtgtgtag ccagtcatca cgttcagcct cccatctaag ctgtttgaga 180
 cttgcattat ctttgttagc catggcattc atgccaatgt tatcaaatct ggatcccata 240
 tttcatcca atagatggcc aaactcttca gcagatacaa ataggctgga atcatttaag 300
 tttcttttct ttttcttggt cccttgaaat gagccagcaa agtcaaaatc atctgtacct 360
 tttctcttgc ttttcttagt actgactttg gagtggactt caagttcttg aacactctca 420
 ctttcatcat ctaacacatc catgaatgtt cctccatctt catcaacttc agcaaattct 480
 tcatcatcca tacttcctaa agaaacttca tcgtcatcca ggttaccaag ttcattatca 540
 ctaccttctg aatcttcatc taatgtgtta tccttagctc cttttggtct ctttttcacg 600

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gtcaatcagc	tcttcaaatt	ctttcatcat	ccacgtcctt	ctaatacttt	cttcaatctg	720
catccccgtt	tttggnnttct	cttttaanca	gcaacttttt	ttatnaaacc	ctgggggaaa	780
aaac						784

<210> 464

<211> 850

<212> DNA

<213> Homo Sapiens

<400> 464

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ctgagggccc	aggcaaggag	aaggagctgc	ctggacagac	cctgcactgg	gggcccagg	120
ccacagaagc	cgcaggctcg	ggtctgcagc	ccctgaagct	ggactaccgc	gccctggccg	180
ccgtgcccag	cgttggcagc	gtgcagaggg	taccgtctgg	agcagctgga	gggaagatgg	240
ctgaatctcc	ctgtccccct	agtggccagc	agccgccctc	cccgccttct	ccggatgagc	300
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ccctccggga	gcggcagaag	tactttgagc	tggaggtgcg	cgtgcccag	gccgagggcc	480
cccctaagcg	cgtgtccctg	gtgggtgctg	acgacctgcg	gaagatgcag	gaggagggaag	540
ccagaaaact	acagcagaag	agagcgcaga	tgctgcggga	ggcggcagaa	gctggggccg	600
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caccctgggc	cagcccagc	cccacttaag	gcagaacccg	gcgtcccccc	ggccctggaa	720
gtggcgcccc	ggtgcggaag	gncaaaagct	gaacggggcc	ancaggaacc	ggttgccctt	780
canagtncgg	gacccaccgg	gacccancg	tgccctggtc	ccttgcccaa	cttcggggcc	840
ctggaaggcc						850

<210> 465

<211> 759

<212> DNA

<213> Homo Sapiens

<400> 465

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tcactagtta	cagtctcgcc	gaggtctcgg	ctggggtggg	gcagttagtt	agtcacaggc	120
cagaactcct	gtggggtctc	tttaaaatgc	taacacccag	gttaaaagac	ttggggcaag	180
ggtggtgctg	gagctggcag	ggccccacc	ccaagtctgg	gggaggtgcc	tgctcctcta	240
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tgccacatct	tcaggggcca	cagcgccggg	tgagggcctg	cccagaagca	ccagagccac	360
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ggagcttttg	canggggaca	aggcaacgct	tcgggtgccc	ggtgggttcc	ggacttttga	720
acgcgccaan	ccggttcctt	gngggcgccc	cgtttcaac			759

<210> 466

<211> 1240

<212> DNA

<213> Homo Sapiens

<400> 466

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gcactggaag	tacaggtcca	gggtatagct	tccacacta	tggatttcct	acttatgggt	120

ggattacttt	ccatcctgga	actactaaat	ctaagtctgg	gatgaagcat	ggaaccatgg	180
acactgaatc	taaaaaggac	cctgaagggt	gtgacaaaag	tgatgacaaa	aacactgtaa	240
acctctttgg	gaaagttatt	gaaaccacag	agcaagatca	ggagcccagc	gaggccaccg	300
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atctagccat	gatgagcaat	agcctgcat	gtttgctgct	gctgttggcc	gctggggctg	900
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<210> 467

<211> 885

<212> DNA

<213> Homo Sapiens

<400> 467

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gtacaggtcc	agggatatagc	ttcccacact	atggatttcc	tacttatggg	gggattactt	120
tccatcctgg	aactactaaa	tctaagtctg	ggatgaagca	tggaaacctg	gacactgaat	180
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ggaaagtatt	tgaaccacac	gagcaagatc	aggagcccag	cgaggccacc	gttgggaatg	300
gtgaggtcac	tctaactgtat	gcaacaggaa	caaaagaaga	gagtgtctga	gttcaggata	360
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atgatctgta	ccagacgccc	ttgcacttgg	cagtgtatcac	taagcaggaa	gatgtggtgg	660
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tttgaccta	gcttgcccaa	agaaggacat	gataaagttc	tcaagtatct	tacttaagcn	780
caaaaanggc	agcactactt	tnntgaccac	ccccacggg	ggacggtctt	gaatgccatt	840
catttaagcc	atgatgagcc	ataagcctgg	catggtttgc	tgctg		885

<210> 468

<211> 748

<212> DNA

<213> Homo Sapiens

<400> 468

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atcaagtgc	tctcatttta	aaatatctct	tttcttaacc	cttaatttga	atgcaaaatg	120
atgtgtggt	cagaaggaat	gccagggtgg	gaccgtgata	cctttaatga	caataggaac	180
gtagcagagg	gacaacagca	atgacaacag	aaagcagctg	tgatccagca	gcagctggca	240
aagcttagta	agcaacctca	tccccagatg	catccgctca	gccagtgttg	tgattgctag	300
atactatctg	taagtgaacc	aaactaaaat	tcatttatga	accaagaaaag	gaagccaagt	360
tgaaaaggtc	tcgagttaaa	tcgagaatga	ttcaggcggg	ccggctctct	gagcaccttt	420

ggatgcactt cagcttctgt cttgtggaaa cgcgtggaat tttagggctt tggtttacac	480
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ctcgnctatt tgctgccttg tggaggcagg cgaaanaagc agcgagtggg ccctgaaaag	720
gnnggcnttc actgggctgg aaggcttg	748

<210> 469

<211> 770

<212> DNA

<213> Homo Sapiens

<400> 469

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atcaagtgc tctcatttta aaatatctct tttcttaacc ctttaattga atgcaaatg	120
atgctgtggt cagaaggaat gccagggtggc gaccgtgata cttttaatga caataggaac	180
gtagcagagg gacaacagca atgacaacag aaagcagctg tgatccagca gcagctggca	240
aagcttagta agcaacctca tcccagatg catccgctca gccagtgttg tgattgctag	300
atactatctg taagtgaacc aaactaaaat tcattttatga accaagaaag gaagccaagt	360
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agctgagttt gcgggaaagg atgtnttcca cgcgccttnt cgcanacact ggactgnct	660
tgggagctcn gctattttgc ttgcccttgt ggangcaggc caaanaagc caacgaatgg	720
ggccctgaaa agngggcct tcanctgggc ttggaagctt gcctnggatc	770

<210> 470

<211> 892

<212> DNA

<213> Homo Sapiens

<400> 470

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agcgccatct cactgctgtg caggatgaga atggggacag tgtcttacac ttagcaatca	180
tccaccttca ttctcaactt gtgagggatc tactagaagt cacatctggt ttgatttctg	240
atgacattat caacatgaga aatgatctgt accagacgcc cttgcacttg gcagtgatca	300
ctaagcagga agatgtggtg gaggatttgc tgagggtctg ggccgacctg agccttctg	360
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ccttctatga cctggatgac tcttgggaaa atgcaggaaa aggattgaag gagttggnct	840
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<210> 471

<211> 759

<212> DNA

<213> Homo Sapiens

<400> 471

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atgctgtggt cagaaggaat gccaggtggc gaccgtgata cttttaatga caataggaac	180
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<210> 472

<211> 852

<212> DNA

<213> Homo Sapiens

<400> 472

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tgggtaactc tgttttgac cctaacttgc caaagaaggg cattgataaa ggtcttcaag	780
tatcttactt cagcccaaaa anggcagcac tacttntttg accaccccaa cgggggacgg	840
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<210> 473

<211> 804

<212> DNA

<213> Homo Sapiens

<400> 473

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atgctgtggt cagaaggaat gccaggtggc gaccgtgata cttttaatga caataggaac	180
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atactatctg taagtgaacc aaactaaaat tcatttatga accaagaaag gaagccaagt	360
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aatcatgggg cattttgttg agagttagca gtgaggcacc acttgggtcaa gagactcggg	600
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tcggaactcg nctatttct gnttctgtga agcaggcnaa nanaagcanc gaantggggc	720
cctgaaaagn gggctcttcac ttggnctgga aggcttgccc tgggatcnc ttnaatgggc	780

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804

<210> 474
 <211> 819
 <212> DNA
 <213> Homo Sapiens

<400> 474
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 gttgtcaact atccaaaaga taacaaaaga aaaatggatg agacagatgc ttcacagca 360
 gtgaaagtga aaagagcagt ccagaaaaca tccgatttaa tagtggtggg tctcccatgg 420
 aaaacaaccg aacaggacct gaaagagtat tttagtacct ttggagaagt tcttatgggtg 480
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<210> 475
 <211> 721
 <212> DNA
 <213> Homo Sapiens

<400> 475
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 acaaggtttc aaaagtccag acagccttct ggttccatat cacaggcctt gcgttcatag 660
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<210> 476
 <211> 442
 <212> DNA
 <213> Homo Sapiens

<400> 476
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 angcacacca cangctcagn ccatgtntn agcccatcag nttcagttna catngccaca 240
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<210> 477
<211> 878
<212> DNA
<213> Homo Sapiens

<400> 477
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<210> 478
<211> 768
<212> DNA
<213> Homo Sapiens

<400> 478
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ttcaaaatct tcttagggta aaataaatac ccgtatctat gcagtaccat aaacatgtta 180
ataaaaggcc actcaacatt gaaagccttc tatgaccagt aactgaaatt tacacaagtg 240
taaagaaggg attaaacat gccgttgaca agttaactta cccctgggct ccttgaaggc 300
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gacgccggcc tnggatgcc gtgatgacca attcttgaat gagaaagcat gtagaccgna 720
tttctatgag cagaaatatt tacnggccta ctttcaatgg aagngctt 768

<210> 479
<211> 815
<212> DNA
<213> Homo Sapiens

<400> 479
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ttcatcagca	gtgaaagtga	aaagagcagt	ccagaaaaca	tccgatttaa	tagtggtggg	420
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tcttatgggt	caggtcaaga	aagatcttaa	gactgggtcat	tcaaaggggt	ttggctttgt	540
tcgttttacg	gaatatgaaa	cacaagtga	agtaatgtca	cagcgacata	tgatagatgg	600
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cagaaaagtg	tttgtggggg	cgctgtacag	angacatgac	tgangataan	cttcnggagt	720
tcttttttta	ataccgggat	gtgatggatg	cttcatttcc	caaccatttc	agggcctttg	780
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<210> 480

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 480

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cttcaaaatc	ttcttaggt	aaaataaata	cccgatcta	tgcagtacca	taaacatgtt	180
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gtaaagaagg	gattaaacca	tgccgttgac	aagttaactt	acccctgggc	tccttgaagg	300
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tgctgagtaa	tagtgcaagt	gcattttagg	tgcggtcacc	cagacttatt	caaaactaga	420
tttcaaaaga	aaaaaaaaa	ttttcacttt	ggccaatgca	agaacaaata	ccaattaagt	480
ctgggtatca	ggtgtcaatg	catgacaggt	gatgaatcca	tttgacttga	gacaactttt	540
caaataagtt	tatttgaagc	aaaataaact	actgccaaaga	aactttatga	aaagttccat	600
cttcaaaagg	ggtcaaaaaa	ggggaattaa	ctgctatgaa	ttccttgcat	tcanggctgc	660
aaaacaaaga	ccccatatta	tttaaaatcc	agtttattta	agaatttncc	accntggaca	720
acttcttatt	aaaaaggcct	tccaggccca	nggaccacag	aaactgnang	ccaacangc	780
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<210> 481

<211> 1127

<212> DNA

<213> Homo Sapiens

<400> 481

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gagaatccga	agaagaaaat	ctcaataaat	ctgaataaag	tcaagtgtt	gagattgcac	180
ttaaacggaa	cttgctgtg	aatttcgagg	tgcccgga	gagtggcca	ccccacatga	240
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agaagatttc	aaagaaaaat	gccgccatag	ctgttcttga	ggagctgaag	aagttaccgc	360
ccttgctgct	agttgaacga	gtaaagccta	gaatcaaaaa	gaaaacaaaa	ccccatagtc	420
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tcaaagtccc	gcaggcgag	cccaccaaac	ccgactcaa	gtcagaggag	aagacaccca	720
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aataacatct cttcaggcca cgtaccccat ggacctctca cgagaccctn tgagcaactg 1080
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<210> 482
<211> 773
<212> DNA
<213> Homo Sapiens

<400> 482
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cccagatcca gcaggcaaaa aaggagaagg agccagagta cacgctcctc acagagcgag 180
gctccccgcg ccgcagggag tttgtgatgc aggtgaaggt tggaaaccac actgcagaag 240
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ttaagaata acatctcttc aggccacgta cccatggag ctctcacgag accctntgag 720
caactggact atctttncag agtccaggga ttncagggtg aataccaaga ctt 773

<210> 483
<211> 794
<212> DNA
<213> Homo Sapiens

<400> 483
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ggcaagtgg gaggggacca acctagcagt agnggcattt ganaataaat tancaaaaaa 180
atttagtatt accattnatt gatgacaaac acttaagttt tacttacatt ccatggggag 240
aaaaattcca gcgtaaaaaa tgaatggaag cagtacttaa ctgcagggc taccaggctt 300
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caaaagcaac acagntgtat acagaaacgt aggtcattct tttcagccct aanggagatg 420
taattaacag tatcgagcac tntggaaaa cactctgcag gtttatatgg actacatgga 480
gatcatatcc tgtagtgtag tgaaagctaa gtcctcaaga gccatatgta tagatncaca 540
atgtttttta ataattctta aaacagagat caaagttcat ttaagnctg tttgcattac 600
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atnggccaat ttatncaact gngggggaga cttattcaag ggttttgaaa gtccagggaac 720
tggtttcaag ctggaaccca ggggggcccc acaatttggc attcnctgga aactggccct 780
ggggttaagc caaa 794

<210> 484
<211> 788
<212> DNA
<213> Homo Sapiens

<400> 484
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tcagtgccgt tgaaacacga ggtataaatg accaaggatt gtacagagtt gtgggggtga 120
gttcaaaggt ccagagactt ctgagtatgt tgatggatgt aaaaacatgc aatgagggtg 180
acctggagaa ttctgcagat tgggaagtga agacaataac aagtgccttg aaacagtatt 240
tgaggagtct tccagagcct ctcatgacct atgagttaca tggagatttc attgttccag 300

ccaaaagcgg	cagcccagaa	tctcgtgtta	atgcgatcca	tttcttggtta	cacaaactgc	360
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actccaagca	gaacctgatg	actgtggcaa	acttaggagt	gggtgttgga	ccaactctga	480
tgaggccaca	ggaagaaact	gtcgtgcct	catggacttg	aagtttcaga	atattgttgt	540
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tgagcccacc	tgctgtcag	catcaccccc	aaatgcgcca	ccaangcagt	cnaagagaca	660
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<210> 485

<211> 430

<212> DNA

<213> Homo Sapiens

<400> 485

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agtgcagtga	gtgtgggggtc	ctgcagggtg	ccgtctagga	agggcaggct	tgagacgcgc	180
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tttanaatcg	nagcagcang	tgctcagga	ggagaggag	ccnnngtggc	tctggtggcg	360
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<210> 486

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 486

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tttgtacttc	tggaattggt	acttctatac	cggtgccctt	ggcaggaagt	gcccttctcc	180
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tgctgtttc	tggagaagaa	tcacagttga	caccagaaa	agtcttncca	aatttnctga	780
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<210> 487

<211> 728

<212> DNA

<213> Homo Sapiens

<400> 487

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cagggtgcctg	ccaccacgcc	tggctaattt	ttgtattttt	ggtagagacg	gggtttcacc	180

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<211> 844
 <212> DNA
 <213> Homo Sapiens

<400> 490

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aaggtgaagg gaaaagcaag aagatttcaa agaaaaatgc cgccatagct gttcttgagg	180
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<210> 491
 <211> 825
 <212> DNA
 <213> Homo Sapiens

<400> 491

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<210> 492
 <211> 946
 <212> DNA
 <213> Homo Sapiens

<400> 492

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gagaatccga agaagaaaat ctcaataaat ctgaaataag tcaagtgttt gagattgcac	180
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gctggaaaatc tttccatggg ggccgaggtc ncccagcttt taggagttat canggcctnt	900
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<210> 493

<211> 804

<212> DNA

<213> Homo Sapiens

<400> 493	
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gtaagagaaa gcccaatccn ggaatggagt tcntccattt tcagactaac cctgggcncn	720
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<210> 494

<211> 856

<212> DNA

<213> Homo Sapiens

<400> 494	
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<210> 495

<211> 757

<212> DNA

<213> Homo Sapiens

<400> 495

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<210> 496

<211> 1759

<212> DNA

<213> Homo Sapiens

<400> 496

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accaggaaga gcagctgaca gtgaattcaa aggcattaga gattcttgac aagatttctc	180
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<210> 497
 <211> 842
 <212> DNA
 <213> Homo Sapiens

<400> 497
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 <211> 707
 <212> DNA
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<210> 499
 <211> 772
 <212> DNA
 <213> Homo Sapiens

<400> 499
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<210> 500

<211> 787

<212> DNA

<213> Homo Sapiens

<400> 500

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<210> 501

<211> 886

<212> DNA

<213> Homo Sapiens

<400> 501

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<210> 502

<211> 626

<212> DNA

<213> Homo Sapiens

<400> 502

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<210> 503

<211> 884

<212> DNA

<213> Homo Sapiens

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<210> 504

<211> 612

<212> DNA

<213> Homo Sapiens

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<210> 505

<211> 2215

<212> DNA

<213> Homo Sapiens

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<211> 742

<212> DNA

<213> Homo Sapiens

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<211> 735

<212> DNA

<213> Homo Sapiens

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<210> 508

<211> 666

<212> DNA

<213> Homo Sapiens

<400> 508

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<210> 509

<211> 818

<212> DNA

<213> Homo Sapiens

<400> 509

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cgctcaccct ggctgcagtg ggtgctgcct ccaagacct gagccaccg cagcagatgg	180
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<210> 510

<211> 651

<212> DNA

<213> Homo Sapiens

<400> 510

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<210> 511

<211> 712

<212> DNA

<213> Homo Sapiens

<400> 511

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<210> 512

<211> 850

<212> DNA

<213> Homo Sapiens

<400> 512

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ctgtggggac	tggctggaag	ctgctggcag	ggtggagtgg	gctggggccc	cggcagattc	180
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 <212> DNA
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877

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<210> 515
 <211> 685
 <212> DNA
 <213> Homo Sapiens

<400> 515
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<210> 516
 <211> 790
 <212> DNA
 <213> Homo Sapiens

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<210> 517
 <211> 747
 <212> DNA
 <213> Homo Sapiens

<400> 517
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 taccagggca gtattcagtgc tcaggtgaga tgggttggcc tcaggttggg acgctgcttt 180
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<210> 518
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 <212> DNA
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<400> 518
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cttctgagga agaaatagat gctcctaagc ccaagaagat gaagaaagaa aaggaaatga 240
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<210> 519
 <211> 789
 <212> DNA
 <213> Homo Sapiens

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<400> 519
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<210> 520
 <211> 827
 <212> DNA
 <213> Homo Sapiens

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<210> 521

<211> 710

<212> DNA

<213> Homo Sapiens

<400> 521
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<210> 522

<211> 638

<212> DNA

<213> Homo Sapiens

<400> 522
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<211> 833

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<210> 526
 <211> 746
 <212> DNA
 <213> Homo Sapiens

<400> 526	60
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<211> 842

<212> DNA

<213> Homo Sapiens

<400> 529

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<211> 815

<212> DNA

<213> Homo Sapiens

<400> 530

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 <212> DNA
 <213> Homo Sapiens

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 <212> DNA
 <213> Homo Sapiens

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 <211> 678
 <212> DNA
 <213> Homo Sapiens

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<210> 534

<211> 789

<212> DNA

<213> Homo Sapiens

<400> 534

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<210> 535

<211> 802

<212> DNA

<213> Homo Sapiens

<400> 535

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<210> 536

<211> 901

<212> DNA

<213> Homo Sapiens

<400> 536

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<211> 761

<212> DNA

<213> Homo Sapiens

<400> 537

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<211> 869

<212> DNA

<213> Homo Sapiens

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<211> 760
<212> DNA
<213> Homo Sapiens

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<211> 729
<212> DNA
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<210> 542
 <211> 830
 <212> DNA
 <213> Homo Sapiens

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<400> 542
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tgggcccagc cctggatgcg gaccatgcc ccttgagca gttctttgta gtgatggagc 180
actgcctcaa acatgggctg aaagttaaga agagttttat tggccaaaat aaatcattct 240
ttggtccttt ggagctgggt gagaaacttt gtccagaagc atcagatata gcgactagt 300
tcagaaatct tcagaaatta aagacagctg tgggaagagg ccgagcgtgg ctttatcttg 360
cactcatgca aaagaaactg gcagattatc tgaagtgct tatagacaat aaacatctct 420
taagcgagtt ctatgagcct gaggccttaa tgatggagga agaagggatg gtgattgttg 480
gtctgctggg gggactcaat gttctcgatg ccaatctctg cttgaaagga gaagacttgg 540
attctcaggt tggagtaata gatttttccc tctaccttaa ggatgtgcag gatcttgatg 600
gtggcaagga gcatgaaaga attactgatg tccttgatca aaaaaattat gtggaagaac 660
ttaaccggc acttgagctg caccagttgg ggatctttca acccaagata gatggcttgg 720
gaaaagacta actcaaagct tcagaagagc ntttagctgc accagaccga attttgetcc 780
tttcaagaaa nacagcacn gttaagaaaa ccaaatggaa ttaatttcag 830

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<210> 543
 <211> 733
 <212> DNA
 <213> Homo Sapiens

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<400> 543
gaaaaataaa tgattttatt gcagggccaa tgataggtag tcacaagggc atgaaatggc 60
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gcatgaatca ggtttttaga aggaaggtag gagaggaaaa ctactcacta gcagaactga 180
actgctgtaa aatagggttaa attctttgaa aagtgaaaaa tgatagtagc aaaatcatga 240
agttgtatct gaaccagagc cgtgatgtaa ccaagtaaga tggaagtttc catccagagg 300
agttaattcc gaacaagtca cagaaagggtg anagctgccg gttccggcac gctgtcttct 360
ggagtgccag tgaccgggca agaaatttga ttctttcctt tgattctctt gggaaagaac 420
acatttccca agcccctgga gaccacaggg gtttggcact gtccgtgagg ctgtgctcct 480
gaggacggac gttcaggagg ccgtggagg agcagcgctg caggagcagg gtgtggcagc 540
tgtcgcacac tcgcaccggc ttggggtagg anggcagggc tagctcggtg ctggancang 600
tgttgcaaaa naatgtggc acagntncgg cagtgggtgc tttntccggg aaaagggaga 660
acttcttnt cacacttggc tacagnngng gncgctttcg ncatcttttt ancccaggcg 720
nnggcccttt caa 733

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<210> 544
 <211> 852
 <212> DNA
 <213> Homo Sapiens

<400> 544
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 agaaattgag aatagaactg gatgaaagca aacaacactt ggaacaggag cagcagaagg 180
 cagccctggc cagagaggag tgcctgagac taacagaact gctgggCGaa tctgagcacc 240
 aactgcacct caccagatct gaaatagctc aactcagtca agaaaaaagg tatacatatg 300
 ataaattggg aaagttacag agaagaaatg aagaattgga ggaacagtgt gtccagcatg 360
 ggagagtaca tgagacgatg aagcaaaggc taaggcagct ggataagcac agccaggcca 420
 cagcccagca gctggtgcag ctctcagca agcagaacca gcttctcctg gagaggcaga 480
 gcctgtcgga agaggtggac cggctgcgga cccagttacc cagcatgcca caatctgatt 540
 gctgacctgg atggaacaga gtgaaataaa tgaattacaa agagatattt acattcatct 600
 ggtttagact taatatgccca caacgcacca cgacctccc aggggtgacac cgcctcagcc 660
 tgcagtgggg ctggtcctca tcaacgcggg cgctgtcccc gcacgcagtc gggctggagc 720
 tggagtctga ctctagctga gcagactcct ggtgtatgtt ttcagaaatg gcttgaagtt 780
 atgtgtttaa atctgctcat tcgtatgcta ggttatacat atgattttca ataaatgaac 840
 tttttaaga aa 852

<210> 545

<211> 414

<212> PRT

<213> Homo Sapiens

<400> 545
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 20 25 30
 Tyr Gln Arg Thr Cys Glu Asp Leu Lys Glu Gln Leu Lys His Lys Glu
 35 40 45
 Phe Leu Leu Ala Ala Asn Thr Cys Asn Arg Val Gly Gly Leu Cys Leu
 50 55 60
 Lys Cys Ala Gln His Glu Ala Val Leu Ser Gln Thr His Thr Asn Val
 65 70 75 80
 His Met Gln Thr Ile Glu Arg Leu Val Lys Glu Arg Asp Asp Leu Met
 85 90 95
 Ser Ala Leu Val Ser Val Arg Ser Ser Leu Ala Asp Thr Gln Gln Arg
 100 105 110
 Glu Ala Ser Ala Tyr Glu Gln Val Lys Gln Val Leu Gln Ile Ser Glu
 115 120 125
 Glu Ala Asn Phe Glu Lys Thr Lys Ala Leu Ile Gln Cys Asp Gln Leu
 130 135 140
 Arg Lys Glu Leu Glu Arg Gln Ala Glu Arg Leu Glu Lys Glu Leu Ala
 145 150 155 160
 Ser Gln Gln Glu Lys Arg Ala Ile Glu Lys Asp Met Met Lys Lys Glu
 165 170 175
 Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu Ser
 180 185 190
 Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys Glu
 195 200 205
 Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu Ala
 210 215 220
 Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr Gln
 225 230 235 240
 Leu Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His Arg
 245 250 255

Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln Glu
 260 265 270
 Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu
 275 280 285
 Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu
 290 295 300
 Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Ser
 305 310 315 320
 Glu Ile Ala Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu
 325 330 335
 Gly Lys Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln
 340 345 350
 His Gly Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp
 355 360 365
 Lys His Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys
 370 375 380
 Gln Asn Gln Leu Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp
 385 390 395 400
 Arg Leu Arg Thr Gln Leu Pro Ser Met Pro Gln Ser Asp Cys
 405 410

<210> 546

<211> 2885

<212> DNA

<213> Homo Sapiens

<400> 546

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tcgagacgac	ttccccctcc	gcaaaacagc	ctctgaaccc	aacttgaaag	tgcggtcaag	240
gctaaaacag	aaggtggctg	agcggagaag	cagtcctcctc	ctgcgtcgca	aggatgggac	300
tggtattagc	acctttaaga	agagagctgt	tgagatcaca	ggtgccgggc	ctggggcgctc	360
gtccgtgtgt	aacagcgcac	ccggctccgg	ccccagctct	cccaacagct	cccacagcac	420
catcgctgag	aatggcttta	ctggctcagt	ccccaacatc	cccactgaga	tgctccctca	480
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gcggatccga	ggtcgcaaa	ccacgctaga	tgagatccag	acagtgcact	ctgaatacca	1680


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cccaggccgg cagaggagcc catggagcag gagcctgccc tgtgacgccc cggcccccat 2820
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aattt

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<210> 547

<211> 897

<212> PRT

<213> Homo Sapiens

<400> 547

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Glu Phe Leu Leu Ser Lys Ser Lys Glu Pro Thr Pro Gly Gly Leu Asn
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His Ser Leu Pro Gln His Pro Lys Cys Trp Gly Ala His His Ala Ser
      20           25           30
Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Pro Pro Gly Thr Pro Pro
      35           40           45
Ser Tyr Lys Leu Pro Leu Pro Gly Pro Tyr Asp Ser Arg Asp Asp Phe
      50           55           60
Pro Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Val Arg Ser Arg
      65           70           75           80
Leu Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg
      85           90           95
Lys Asp Gly Thr Val Ile Ser Thr Phe Lys Lys Arg Ala Val Glu Ile
      100          105          110
Thr Gly Ala Gly Pro Gly Ala Ser Ser Val Cys Asn Ser Ala Pro Gly
      115          120          125
Ser Gly Pro Ser Ser Pro Asn Ser Ser His Ser Thr Ile Ala Glu Asn
      130          135          140
Gly Phe Thr Gly Ser Val Pro Asn Ile Pro Thr Glu Met Leu Pro Gln
      145          150          155          160
His Arg Ala Leu Pro Leu Asp Ser Ser Pro Asn Gln Phe Ser Leu Tyr
      165          170          175
Thr Ser Pro Ser Leu Pro Asn Ile Ser Leu Gly Leu Gln Ala Thr Val
      180          185          190
Thr Val Thr Asn Ser His Leu Thr Ala Ser Pro Lys Leu Ser Thr Gln
      195          200          205
Gln Glu Ala Glu Arg Gln Ala Leu Gln Ser Leu Arg Gln Gly Gly Thr

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      210              215              220
Leu Thr Gly Lys Phe Met Ser Thr Ser Ser Ile Pro Gly Cys Leu Leu
225              230              235              240
Gly Val Ala Leu Glu Gly Asp Gly Ser Pro His Gly His Ala Ser Leu
      245              250              255
Leu Gln His Val Leu Leu Leu Glu Gln Ala Arg Gln Gln Ser Thr Leu
      260              265              270
Ile Ala Val Pro Leu His Gly Gln Ser Pro Leu Val Thr Gly Glu Arg
      275              280              285
Val Ala Thr Ser Met Arg Thr Val Gly Lys Leu Pro Arg His Arg Pro
      290              295              300
Leu Ser Arg Thr Gln Ser Ser Pro Leu Pro Gln Ser Pro Gln Ala Leu
305              310              315              320
Gln Gln Leu Val Met Gln Gln Gln His Gln Gln Phe Leu Glu Lys Gln
      325              330              335
Lys Gln Gln Gln Leu Gln Leu Gly Lys Ile Leu Thr Lys Thr Gly Glu
      340              345              350
Leu Pro Arg Gln Pro Thr Thr His Pro Glu Glu Thr Glu Glu Glu Leu
      355              360              365
Thr Glu Gln Gln Glu Val Leu Leu Gly Glu Gly Ala Leu Thr Met Pro
      370              375              380
Arg Glu Gly Ser Thr Glu Ser Glu Ser Thr Gln Glu Asp Leu Glu Glu
385              390              395              400
Glu Asp Glu Glu Glu Asp Gly Glu Glu Glu Asp Cys Ile Gln Val
      405              410              415
Lys Asp Glu Glu Gly Glu Ser Gly Ala Glu Glu Gly Pro Asp Leu Glu
      420              425              430
Glu Pro Gly Ala Gly Tyr Lys Lys Leu Phe Ser Asp Ala Gln Pro Leu
      435              440              445
Gln Pro Leu Gln Val Tyr Gln Ala Pro Leu Ser Leu Ala Thr Val Pro
      450              455              460
His Gln Ala Leu Gly Arg Thr Gln Ser Ser Pro Ala Ala Pro Gly Gly
465              470              475              480
Met Lys Asn Pro Pro Asp Gln Pro Val Lys His Leu Phe Thr Thr Ser
      485              490              495
Val Val Tyr Asp Thr Phe Met Leu Lys His Gln Cys Met Cys Gly Asn
      500              505              510
Thr His Val His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser
      515              520              525
Arg Leu Gln Glu Thr Gly Leu Leu Ser Lys Cys Glu Arg Ile Arg Gly
      530              535              540
Arg Lys Ala Thr Leu Asp Glu Ile Gln Thr Val His Ser Glu Tyr His
545              550              555              560
Thr Leu Leu Tyr Gly Thr Ser Pro Leu Asn Arg Gln Lys Leu Asp Ser
      565              570              575
Lys Lys Leu Leu Gly Pro Ile Ser Gln Lys Met Tyr Ala Val Leu Pro
      580              585              590
Cys Gly Gly Ile Gly Val Asp Ser Asp Thr Val Trp Asn Glu Met His
      595              600              605
Ser Ser Ser Ala Val Arg Met Ala Val Gly Cys Leu Leu Glu Leu Ala
      610              615              620
Phe Lys Val Ala Ala Gly Glu Leu Lys Asn Gly Phe Ala Ile Ile Arg
625              630              635              640
Pro Pro Gly His His Ala Glu Glu Ser Thr Ala Met Gly Phe Cys Phe
      645              650              655

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Phe Asn Ser Val Ala Ile Thr Ala Lys Leu Leu Gln Gln Lys Leu Asn
 660 665 670
 Val Gly Lys Val Leu Ile Val Asp Trp Asp Ile His His Gly Asn Gly
 675 680 685
 Thr Gln Gln Ala Phe Tyr Asn Asp Pro Ser Val Leu Tyr Ile Ser Leu
 690 695 700
 His Arg Tyr Asp Asn Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Glu
 705 710 715 720
 Glu Val Gly Gly Gly Pro Gly Val Gly Tyr Asn Val Asn Val Ala Trp
 725 730 735
 Thr Gly Gly Val Asp Pro Pro Ile Gly Asp Val Glu Tyr Leu Thr Ala
 740 745 750
 Phe Arg Thr Val Val Met Pro Ile Ala His Glu Phe Ser Pro Asp Val
 755 760 765
 Val Leu Val Ser Ala Gly Phe Asp Ala Val Glu Gly His Leu Ser Pro
 770 775 780
 Leu Gly Gly Tyr Ser Val Thr Ala Arg Cys Phe Gly His Leu Thr Arg
 785 790 795 800
 Gln Leu Met Thr Leu Ala Gly Gly Arg Val Val Leu Ala Leu Glu Gly
 805 810 815
 Gly His Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser
 820 825 830
 Ala Leu Leu Ser Val Lys Leu Gln Pro Leu Asp Glu Ala Val Leu Gln
 835 840 845
 Gln Lys Pro Asn Ile Asn Ala Val Ala Thr Leu Glu Lys Val Ile Glu
 850 855 860
 Ile Gln Ser Lys His Trp Ser Cys Val Gln Lys Phe Ala Ala Gly Leu
 865 870 875 880
 Gly Arg Ser Leu Arg Gly Ala Gln Ala Gly Glu Thr Glu Glu Ala Glu
 885 890 895
 Met

<210> 548
 <211> 1298
 <212> DNA
 <213> Homo Sapiens

<400> 548
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 tgatggagag agaaagcatc naaagcttct ggaagcaatc agttcccttg atggaaaagaa 180
 taggcggaaa ttggctgana ggtctgaggc tagtctgaag gtgtcagagt tcaatgtcag 240
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 gttacctctg aacaaagaag agattgaacg gatccacaga gaatagcatt caataaaacg 420
 cacaagtcct ctccaaatgg gacctgtcgc tcctgaagaa ccggcaggca gacgagctgg 480
 tttttccctt ggagaaagag gagccagcca ttgctcccat tgaacatgtg ctgagtggtc 540
 ggaaggcaag aactcccctg gagcaggaaa ttttcaacct cctccataag aacaagcagc 600
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 angccaaggc tcgaagagag aagaaaatcn aaagttaaaa gtatcacaaa gtcgtgaaga 780
 aaggaaaggc caagaaagcc ctaaaagagt ttgagcagct gcggaagggt aatccagctg 840
 ccgactaga agaacgaaga aaaggagaaa gaaggaggag gagaaagaag aagaacaagg 900
 agaagaagaa agaagaaggg agaaggagaa gaaaagaagg agaaggagaa aaggaagaag 960

gagaaagaaa aggagaagga aaaggaaaag aaggagaaga aagaagaact aagaagaagg 1020
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 aggaaagaag aggaagaact nagaagaaga aagaggagga aagaagaag aagaataagg 1140
 aacnagaaag aaggagaaga aagaataaga agaggaagaa gaaaaagaag aaaagaagaa 1200
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 agaaagtata agaaggaaga agaagaaaga aggaaaaa 1298

<210> 549
 <211> 236
 <212> PRT
 <213> Homo Sapiens

<400> 549
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 Ser Gln Glu Glu Leu Ala Asp Leu Pro Lys Asp Tyr Leu Leu Ser Glu
 20 25 30
 Ser Glu Asp Glu Gly Asp Asn Asp Gly Glu Arg Lys His Lys Leu Leu
 35 40 45
 Glu Ala Ile Ser Ser Leu Asp Gly Lys Asn Arg Arg Lys Leu Ala Arg
 50 55 60
 Ser Glu Ala Ser Leu Lys Val Ser Glu Phe Asn Val Ser Ser Glu Gly
 65 70 75 80
 Ser Gly Glu Lys Leu Val Leu Ala Asp Leu Leu Glu Pro Val Lys Thr
 85 90 95
 Ser Ser Ser Leu Ala Thr Val Lys Lys Gln Leu Ser Arg Val Ser Lys
 100 105 110
 Thr Val Glu Leu Pro Leu Asn Lys Glu Glu Ile Glu Arg Ile His Arg
 115 120 125
 Glu Ile Ala Phe Asn Lys Thr His Lys Ser Ser Pro Asn Gly Thr Leu
 130 135 140
 Ser Ser Val Leu Lys Asn Arg Gln Ala Glu Gln Leu Val Phe Pro Leu
 145 150 155 160
 Glu Lys Glu Glu Pro Ala Ile Ala Pro Ile Glu His Val Leu Ser Gly
 165 170 175
 Trp Lys Ala Arg Thr Pro Leu Glu Gln Glu Ile Phe Asn Leu Leu His
 180 185 190
 Lys Asn Lys Gln Pro Val Thr Asp Pro Leu Leu Thr Pro Val Glu Lys
 195 200 205
 Ala Ser Leu Arg Ala Met Ser Leu Glu Glu Ala Lys Met Arg Arg Ala
 210 215 220
 Glu Leu Gln Arg Ala Arg Ala Leu Gln Ser Tyr Tyr
 225 230 235

<210> 550
 <211> 2236
 <212> DNA
 <213> Homo Sapiens

<400> 550
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 ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180
 gtgctgcaa tgtaccacca gaccatggac gtggccgtgc tcgtgggaga cctgaagctg 240
 gtcacatcatg aaccagccg tctgcctctg tttgatgcc ttcggccgct gatccactg 300

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ctgatccccg tgaagagctc tcctgatgag cccctcactt ggcagtatgt ggatcagttt 660
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ggcggggact ggatcgacct tgtggttgcc gctgcccc caaaggagta tgacgatgag 1740
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ctccggcccc acctcgtgaa cacaaagcct cggaccagcc ttgagagagg ccacatgaca 1860
cacaccagat ggcattcctt ggacctgaat ctatcaccca ggaatctcaa actccctttg 1920
gccctgaacc agggccagat aaggaacagc tcggggcact tttttgaagg ccaatgtgga 1980
ggaaagggag cagccagccg tttgggagaa gatctcaagg atccagactc tcattccttt 2040
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taagacccca ctggagtctc tctctctcca tccctctcct ctgccctctg ctctaattgc 2160
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<210> 551

<211> 652

<212> PRT

<213> Homo Sapiens

<400> 551

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Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
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Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
      20             25            30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
      35             40            45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
      50             55            60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
      65             70            75            80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
      85             90            95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
      100            105            110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu

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<210> 552
<211> 2162
<212> DNA
<213> Homo Sapiens
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-286-

aa

2162

<210> 553
 <211> 403
 <212> PRT
 <213> Homo Sapiens

<400> 553
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 Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
 20 25 30
 Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
 35 40 45
 Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
 50 55 60
 Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
 65 70 75 80
 Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
 85 90 95
 Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
 100 105 110
 Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
 115 120 125
 Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
 130 135 140
 Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
 145 150 155 160
 Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
 165 170 175
 Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
 180 185 190
 Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
 195 200 205
 Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
 210 215 220
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu

370 375 380
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
 385 390 395 400
 Lys Pro Lys

<210> 554
 <211> 1789
 <212> DNA
 <213> Homo Sapiens

<400> 554
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 aaagagcaac taaagcataa agaatttctt ctggctgcta atacttgtaa ccgtgttggt 180
 ggtctttgtt tgaaatgtgc tcagcatgaa gctgttcttt cccaaaccca tactaatggt 240
 catatgcaga ccactgaaag actggttaaa gaaagagatg acttgatgct tgcactagtt 300
 tccgtaagga gcagcttggc agatacgag caaagagaag caagtgttta tgaacagggtg 360
 aaacaagttt tgcaaatata tgaggaagcc aattttgaaa aaaccaaggc tttaatccag 420
 tgtgaccagt tgaggaagga gctggagagg caggcggagc gacttgaaaa agaacttgca 480
 tctcagcaag agaaaagggc cattgagaaa gacatgatga aaaaggaaat aacgaaagaa 540
 agggagtaca tgggatcaaa gatgttgatc ttgtctcaga atattgcccc actggaggcc 600
 caggttgaaa aggttacaaa ggaaaagatt tcagctatta atcaactgga ggaaattcaa 660
 agccagctgg cttctcggga aatggatgtc acaaagggtg gtggagaaat gcgctatcag 720
 ctgaataaaa ccaacatgga gaaggatgag gcagaaaagg agcacagaga gttcagagca 780
 aaaactaaca gggatcttga aattaaagat caggaaatag agaaattgag aatagaactg 840
 gatgaaagca aacaacactt ggaacaggag cagcagaagg cagccctggc cagagaggag 900
 tgccctgagac taacagaact gctgggagaa tctgagcacc aactgcacct caccagacag 960
 gaaaaagata gcattcagca gagctttagc aaggaagcaa aggcccaagc ctttcaggcc 1020
 cagcaagag agcaggagct gacacagaag atacagcaaa tggaaagcca gcatgacaaa 1080
 actgaaaatg aacagtattt gttgctgacc tcccagaata catttttgac aaagttaaag 1140
 gaagaatgct gtacattagc caagaaactg gaacaaatct ctcaaaaaac cagatctgaa 1200
 atagctcaac tcagtcaaga aaaaaggat acatatgata aattgggaaa gttacagaga 1260
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 gactcctggt gtatgttttc agaaatggct tgaagttatg tgtttaaatc tgctcattcg 1740
 tatgctagggt tatacatatg attttcaata aatgaacttt ttaaagaaa 1789

<210> 555
 <211> 493
 <212> PRT
 <213> Homo Sapiens

<400> 555
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 20 25 30
 Tyr Gln Arg Thr Cys Glu Asp Leu Lys Glu Gln Leu Lys His Lys Glu
 35 40 45

Phe Leu Leu Ala Ala Asn Thr Cys Asn Arg Val Gly Gly Leu Cys Leu
 50 55 60
 Lys Cys Ala Gln His Glu Ala Val Leu Ser Gln Thr His Thr Asn Val
 65 70 75 80
 His Met Gln Thr Ile Glu Arg Leu Val Lys Glu Arg Asp Asp Leu Met
 85 90 95
 Ser Ala Leu Val Ser Val Arg Ser Ser Leu Ala Asp Thr Gln Gln Arg
 100 105 110
 Glu Ala Ser Ala Tyr Glu Gln Val Lys Gln Val Leu Gln Ile Ser Glu
 115 120 125
 Glu Ala Asn Phe Glu Lys Thr Lys Ala Leu Ile Gln Cys Asp Gln Leu
 130 135 140
 Arg Lys Glu Leu Glu Arg Gln Ala Glu Arg Leu Glu Lys Glu Leu Ala
 145 150 155 160
 Ser Gln Gln Glu Lys Arg Ala Ile Glu Lys Asp Met Met Lys Lys Glu
 165 170 175
 Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu Ser
 180 185 190
 Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys Glu
 195 200 205
 Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu Ala
 210 215 220
 Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr Gln
 225 230 235 240
 Leu Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His Arg
 245 250 255
 Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln Glu
 260 265 270
 Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu
 275 280 285
 Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu
 290 295 300
 Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Gln
 305 310 315 320
 Glu Lys Asp Ser Ile Gln Gln Ser Phe Ser Lys Glu Ala Lys Ala Gln
 325 330 335
 Ala Leu Gln Ala Gln Gln Arg Glu Gln Glu Leu Thr Gln Lys Ile Gln
 340 345 350
 Gln Met Glu Ala Gln His Asp Lys Thr Glu Asn Glu Gln Tyr Leu Leu
 355 360 365
 Leu Thr Ser Gln Asn Thr Phe Leu Thr Lys Leu Lys Glu Glu Cys Cys
 370 375 380
 Thr Leu Ala Lys Lys Leu Glu Gln Ile Ser Gln Lys Thr Arg Ser Glu
 385 390 395 400
 Ile Ala Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly
 405 410 415
 Lys Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His
 420 425 430
 Gly Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp Lys
 435 440 445
 His Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln
 450 455 460
 Asn Gln Leu Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp Arg
 465 470 475 480
 Leu Arg Thr Gln Leu Pro Ser Met Pro Gln Ser Asp Cys

485

490

<210> 556
 <211> 1306
 <212> DNA
 <213> Homo Sapiens

<400> 556
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 cggcaaagga gaaaagaaat tgcccagaag gcagcagagg aaaatgagag ataccggaag 240
 gagatggaac agattgtaga ggaggaagag aagtttaaga agcaatggga agaagactgg 300
 ggctcaaagg aacagctact cttgcctaaa accatcactg ctgaggtaca cccagtaccc 360
 cttcgcaagc caaagtatga tcagggagtg gaacctgagc tcgagcccg c agatgacctg 420
 gatggaggca cggaggagca gggagagcag gatttccgga aatatgagga aggctttgac 480
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 aagaaggagg gatccttaga cctggccctg gaaggcggtg tggactcccc cattgggaag 600
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<210> 557
 <211> 328
 <212> PRT
 <213> Homo Sapiens

<400> 557
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 20 25 30
 Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu Lys Phe Lys Lys
 35 40 45
 Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu Leu Leu Pro Lys
 50 55 60
 Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg Lys Pro Lys Tyr
 65 70 75 80
 Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp Asp Leu Asp Gly
 85 90 95
 Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys Tyr Glu Glu Gly
 100 105 110
 Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile Met Gly Lys Asp
 115 120 125
 Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu Asp Leu Ala Leu
 130 135 140

Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val Val Ser Ala Val
 145 150 155 160
 Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile Val Lys Gly Asp
 165 170 175
 Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp Tyr Thr Leu Ala
 180 185 190
 Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln Gly Gly Asp Trp
 195 200 205
 Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu Tyr Asp Asp Glu
 210 215 220
 Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln Ile His Ala Leu
 225 230 235 240
 Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr Lys Pro Arg Thr
 245 250 255
 Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp His Pro Trp Asp
 260 265 270
 Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu Ala Leu Asn Gln
 275 280 285
 Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu Gly Gln Cys Gly
 290 295 300
 Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu Lys Asp Pro Asp
 305 310 315 320
 Ser His Ser Phe Pro Leu Ala Gln
 325

<210> 558
 <211> 2289
 <212> DNA
 <213> Homo Sapiens

<400> 558
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 ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180
 gtgctgcgaa tgtaccacca gacctggac gtggccgtgc tctgtggaga cctgaagctg 240
 gtcacatg aaccacagccg tctgcctctg tttgatgcca ttcggccgct gatccactg 300
 aagcaccagg tggaaatga tcagctgacc ccccgccgct ccaggaaagct gaaggagggtg 360
 cgtctggacc gtctgcaccc cgaaggcctc ggcctgagtg tgcgtggtgg cctggagttt 420
 ggctgtgggc tcttcatctc ccacctcatc aaaggcggtc aggcagacag cgtcgggctc 480
 caggtagggg acgagatcgt ccggatcaat ggatattcca tctcctcctg taccatgag 540
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 ctgatecccg tgaaaagctc tctgatgag cccctcactt ggagtagtgg ggatcagttt 660
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 gaacctgagc tcgagcccgc agatgacctg gatggaggga cggaggagca gggagagcag 1380
 ccacaggaga tgttgaagag gatggtggtt tatcaagaca gcattcaaga caagatttcc 1440

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<210> 559

<211> 481

<212> PRT

<213> Homo Sapiens

<400> 559

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 20          25          30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
 35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
 50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
 65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
 85          90          95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
100          105          110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
115          120          125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
130          135          140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145          150          155          160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
165          170          175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
180          185          190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
195          200          205
Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
210          215          220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
225          230          235          240
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
245          250          255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys

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	260		265		270										
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Val	Ala	Ala	Ala	Gly	Arg	Glu	Leu	Phe	Met	Thr	Asp	Arg	Glu	Arg	Leu
	290		295		300										
Ala	Glu	Ala	Arg	Gln	Arg	Glu	Leu	Gln	Arg	Gln	Glu	Leu	Leu	Met	Gln
305			310		315									320	
Lys	Arg	Leu	Ala	Met	Glu	Ser	Asn	Lys	Ile	Leu	Gln	Glu	Gln	Gln	Glu
			325		330									335	
Met	Glu	Arg	Gln	Arg	Arg	Lys	Glu	Ile	Ala	Gln	Lys	Ala	Ala	Glu	Glu
			340		345									350	
Asn	Glu	Arg	Tyr	Arg	Lys	Glu	Met	Glu	Gln	Ile	Val	Glu	Glu	Glu	Glu
			355		360									365	
Lys	Phe	Lys	Lys	Gln	Trp	Glu	Glu	Asp	Trp	Gly	Ser	Lys	Glu	Gln	Leu
	370		375		380										
Leu	Leu	Pro	Lys	Thr	Ile	Thr	Ala	Glu	Val	His	Pro	Val	Pro	Leu	Arg
385			390		395									400	
Lys	Pro	Lys	Tyr	Asp	Gln	Gly	Val	Glu	Pro	Glu	Leu	Glu	Pro	Ala	Asp
			405		410									415	
Asp	Leu	Asp	Gly	Gly	Thr	Glu	Glu	Gln	Gly	Glu	Gln	Pro	Gln	Glu	Met
			420		425									430	
Leu	Lys	Arg	Met	Val	Val	Tyr	Gln	Asp	Ser	Ile	Gln	Asp	Lys	Ile	Ser
			435		440									445	
Gly	Asn	Met	Arg	Lys	Ala	Leu	Thr	Pro	Thr	Leu	Cys	Ser	Pro	Gln	Ser
	450		455		460										
Arg	Ser	Trp	Gly	Arg	Met	Ser	Gly	Ser	Tyr	Ala	Ser	Arg	Arg	Arg	Asp
465			470		475									480	
Pro															

<210> 560

<211> 2409

<212> DNA

<213> Homo Sapiens

<400> 560

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gtgctgcgaa	tgtaccacca	gaccatggac	gtggccgtgc	tcgtgggaga	cctgaagctg	240
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aagcaccagg	tggaatatga	tcagctgacc	ccccggcgct	ccaggaagct	gaaggagggtg	360
cgctctggacc	gtctgcaccc	cgaaggcctc	ggcctgagtg	tgcgtggtgg	cctggagttt	420
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caggtagggg	acgagatcgt	cgggatcaat	ggatattcca	tctcctcctg	tacctatgag	540
gaggtcatca	acctcattcg	aaccaagaaa	actgtgtcca	tcaaagtgag	acacatcggc	600
ctgatccccg	tgaaaagctc	tcctgatgag	cccctcactt	ggcagtatgt	ggatcagttt	660
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cagcgtgagc	tgcagcggca	ggagcttctc	atgcagaagc	ggctggcgat	ggagtccaac	1080
aagatcctcc	aggagcagca	ggagatggag	cggcaaaagg	gaaaagaaat	tgcccagaag	1140

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gcagcagagg aaaatgagag ataccggaag gagatggaac agattgtaga ggaggaagag 1200
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accatcactg ctgaggtaca cccagtaccc cttcgcaagc caaagtatga tcagggagtg 1320
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<210> 561
 <211> 521
 <212> PRT
 <213> Homo Sapiens

<400> 561

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Ile	Glu	Asn	Asp	Ala	Glu	Lys	Asp	Tyr	Leu	Tyr	Asp	Val	Leu	Arg	Met
			20					25					30		
Tyr	His	Gln	Thr	Met	Asp	Val	Ala	Val	Leu	Val	Gly	Asp	Leu	Lys	Leu
		35					40					45			
Val	Ile	Asn	Glu	Pro	Ser	Arg	Leu	Pro	Leu	Phe	Asp	Ala	Ile	Arg	Pro
		50				55					60				
Leu	Ile	Pro	Leu	Lys	His	Gln	Val	Glu	Tyr	Asp	Gln	Leu	Thr	Pro	Arg
65				70					75					80	
Arg	Ser	Arg	Lys	Leu	Lys	Glu	Val	Arg	Leu	Asp	Arg	Leu	His	Pro	Glu
			85					90					95		
Gly	Leu	Gly	Leu	Ser	Val	Arg	Gly	Gly	Leu	Glu	Phe	Gly	Cys	Gly	Leu
			100					105					110		
Phe	Ile	Ser	His	Leu	Ile	Lys	Gly	Gly	Gln	Ala	Asp	Ser	Val	Gly	Leu
		115					120					125			
Gln	Val	Gly	Asp	Glu	Ile	Val	Arg	Ile	Asn	Gly	Tyr	Ser	Ile	Ser	Ser
		130				135					140				
Cys	Thr	His	Glu	Glu	Val	Ile	Asn	Leu	Ile	Arg	Thr	Lys	Lys	Thr	Val
145				150					155					160	
Ser	Ile	Lys	Val	Arg	His	Ile	Gly	Leu	Ile	Pro	Val	Lys	Ser	Ser	Pro
			165					170					175		
Asp	Glu	Pro	Leu	Thr	Trp	Gln	Tyr	Val	Asp	Gln	Phe	Val	Ser	Glu	Ser
			180					185					190		
Gly	Gly	Val	Arg	Gly	Ser	Leu	Gly	Ser	Pro	Gly	Asn	Arg	Glu	Asn	Lys
		195				200						205			

Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
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 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
 370 375 380
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
 385 390 395 400
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
 405 410 415
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Thr Phe Cys Pro
 420 425 430
 Ser Pro Gln Pro Pro Arg Gly Pro Gly Val Ser Thr Ile Ser Lys Pro
 435 440 445
 Val Met Val His Gln Glu Pro Asn Phe Ile Tyr Arg Pro Ala Val Lys
 450 455 460
 Ser Glu Val Leu Pro Gln Glu Met Leu Lys Arg Met Val Val Tyr Gln
 465 470 475 480
 Asp Ser Ile Gln Asp Lys Ile Ser Gly Asn Met Arg Lys Ala Leu Thr
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 Pro Thr Leu Cys Ser Pro Gln Ser Arg Ser Trp Gly Arg Met Ser Gly
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 Ser Tyr Ala Ser Arg Arg Arg Asp Pro
 515 520

<210> 562

<211> 1445

<212> DNA

<213> Homo Sapiens

<400> 562

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gaaagctgaa	tgaggttcag	agcttctctg	aagctcaaac	agaaatgggtg	aggacgcttg	180
agcggaaagt	agaagcaaaa	atgatcaagg	aggaaagcga	ctaccacgac	ctggagtcgg	240
tggttcagca	ggtggagcag	aacctggagc	tgatgaccaa	acgggctgta	aaggcagaaa	300
accacgtcgt	gaaactaaaa	caggaaatca	gtttgctcca	ggcgcagggtc	tccaacttcc	360
agcgagagaa	tgaagccctg	cgggtgcggcc	agggtgccag	cctgaccgtg	gtgaagcaga	420
acgccgacgt	ggccctgcag	aacctccggg	tggtcatgaa	cagtgcacag	gcttccatca	480

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agcaactggt ttccggagct gagacactga atcttgttgc cgaaatcctt aaatctatag 540
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gcatgaagct ccgtgtatac cctgaggtca ccaccgctcg atctaaatgt gcagttgtgt 660
ccttaaatat gcagtcttca cccagagtaa agtgttgatc gcaagagtcc agtgtcgtgc 720
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tccgccgatg ctcagggtc cctctggctc ccgggtcact cttgtggccc cagtgggtgg 1080
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ctcagagggg cggcgatgag cactaaatgc ttttttgant attttcctat agattttttt 1380
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<210> 563
 <211> 192
 <212> PRT
 <213> Homo Sapiens

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<400> 563
Pro Ala Gly Ser Pro Ser Ala Asp Phe Ala Val His Gly Glu Ser Leu
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Gly Asp Arg His Leu Arg Thr Leu Gln Ile Ser Tyr Asp Ala Leu Lys
 20           25           30
Asp Glu Asn Ser Lys Leu Arg Arg Lys Leu Asn Glu Val Gln Ser Phe
 35           40           45
Ser Glu Ala Gln Thr Glu Met Val Arg Thr Leu Glu Arg Lys Leu Glu
 50           55           60
Ala Lys Met Ile Lys Glu Glu Ser Asp Tyr His Asp Leu Glu Ser Val
 65           70           75           80
Val Gln Gln Val Glu Gln Asn Leu Glu Leu Met Thr Lys Arg Ala Val
 85           90           95
Lys Ala Glu Asn His Val Val Lys Leu Lys Gln Glu Ile Ser Leu Leu
100          105          110
Gln Ala Gln Val Ser Asn Phe Gln Arg Glu Asn Glu Ala Leu Arg Cys
115          120          125
Gly Gln Gly Ala Ser Leu Thr Val Val Lys Gln Asn Ala Asp Val Ala
130          135          140
Leu Gln Asn Leu Arg Val Val Met Asn Ser Ala Gln Ala Ser Ile Lys
145          150          155          160
Gln Leu Val Ser Gly Ala Glu Thr Leu Asn Leu Val Ala Glu Ile Leu
165          170          175
Lys Ser Ile Asp Arg Ile Ser Glu Val Lys Asp Glu Glu Glu Asp Ser
180          185          190

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<210> 564
 <211> 1226
 <212> DNA
 <213> Homo Sapiens

<400> 564


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ctgggcccgcg agggcgcgag cttgggagcg gagcccagggc cgtgccgcgc ggcgccatga      60
agggcaagga ggagaaggag ggcggcgcac ggctggcgcg tggcggggga agccccgaga      120
agagcccagag cgcgcaggag ctcaaggagc agggcaatcg tctgttcgtg ggccgaaagt      180
accgggagggc ggcggcctgc tacggccgcg cgatcacccg gaaccgcgtg gtggccgtgt      240
attacaccaa ccgggccttg tgctacctga agatgcagca gcacgagcag gccctggccg      300
actgccggcg cgccctggag ctggacgggc agtctgtgaa ggcgcacttc ttcctggggc      360
agtgccagct ggagatggag agctatgatg aggccatcgc caatctgcag cgagcttaca      420
gcctggccaa ggagcagcgg ctgaacttcg gggacgacat ccccagcgct cttcgaatcg      480
cgaagaagaa gcgctggaac agcattgagg agcggcgcat ccaccaggag agcgagctgc      540
actcctacct ctccaggctc attgccgcgg agcgtgagag ggagctggaa gagtgccagc      600
gaaaccacga gggatgatgag gacgacagcc acgtccgggc ccagcaggcc tgcattgagg      660
ccaagcacga caagtacatg gcggacatgg acgagctttt ttctcagggtg gatgagaaga      720
ggaagaagcg agacatcccc gactacctgt gtggcaagat cagcttttag ctgatgcggg      780
agccgtgcat cacgcccagt ggcattcacct acgaccgcaa ggacatcgag gaggacctgc      840
agcgtgtggg tcattttgac ccggtgaccg ggagccccct gaccaggaa cagttcatcc      900
ccaacttggc tatgaaggag gttattgacg cattcatctc tgagaatggc tgggtggagg      960
actactgagg ttccctgccc tacctggcgt cctggtccag gggagccctg ggcagaagcc      1020
cccgccccc aaacatagtt tatgtttttg gccaccccg cgcgttcccc caagttctgc      1080
tggtggactc ttgactgttt cccctctcag catcgctttt gctgggcccgt gattgtcccc      1140
tttgtgggct ggaaaagcag gtgagggtgg gctgggctga ggccattgcc gccactatct      1200
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<210> 565

<211> 303

<212> PRT

<213> Homo Sapiens

<400> 565

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Met Lys Gly Lys Glu Glu Lys Glu Gly Gly Ala Arg Leu Gly Ala Gly
 1              5              10              15
Gly Gly Ser Pro Glu Lys Ser Pro Ser Ala Gln Glu Leu Lys Glu Gln
      20              25              30
Gly Asn Arg Leu Phe Val Gly Arg Lys Tyr Pro Glu Ala Ala Cys
      35              40              45
Tyr Gly Arg Ala Ile Thr Arg Asn Pro Leu Val Ala Val Tyr Tyr Thr
      50              55              60
Asn Arg Ala Leu Cys Tyr Leu Lys Met Gln Gln His Glu Gln Ala Leu
      65              70              75              80
Ala Asp Cys Arg Arg Ala Leu Glu Leu Asp Gly Gln Ser Val Lys Ala
      85              90              95
His Phe Phe Leu Gly Gln Cys Gln Leu Glu Met Glu Ser Tyr Asp Glu
      100             105             110
Ala Ile Ala Asn Leu Gln Arg Ala Tyr Ser Leu Ala Lys Glu Gln Arg
      115             120             125
Leu Asn Phe Gly Asp Asp Ile Pro Ser Ala Leu Arg Ile Ala Lys Lys
      130             135             140
Lys Arg Trp Asn Ser Ile Glu Glu Arg Arg Ile His Gln Glu Ser Glu
      145             150             155             160
Leu His Ser Tyr Leu Ser Arg Leu Ile Ala Ala Glu Arg Glu Arg Glu
      165             170             175
Leu Glu Glu Cys Gln Arg Asn His Glu Gly Asp Glu Asp Asp Ser His
      180             185             190
Val Arg Ala Gln Gln Ala Cys Ile Glu Ala Lys His Asp Lys Tyr Met
      195             200             205
Ala Asp Met Asp Glu Leu Phe Ser Gln Val Asp Glu Lys Arg Lys Lys

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      210              215              220
Arg Asp Ile Pro Asp Tyr Leu Cys Gly Lys Ile Ser Phe Glu Leu Met
225              230              235              240
Arg Glu Pro Cys Ile Thr Pro Ser Gly Ile Thr Tyr Asp Arg Lys Asp
      245              250              255
Ile Glu Glu His Leu Gln Arg Val Gly His Phe Asp Pro Val Thr Gly
      260              265              270
Ser Pro Leu Thr Gln Glu Gln Phe Ile Pro Asn Leu Ala Met Lys Glu
      275              280              285
Val Ile Asp Ala Phe Ile Ser Glu Asn Gly Trp Val Glu Asp Tyr
      290              295              300

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<210> 566
 <211> 1857
 <212> DNA
 <213> Homo Sapiens

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<400> 566
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tagtggccgg ccggccgctc tcatcccccg taaggagcag agtcctttgt actgaccaag      180
atgagcaaca tctacatcca ggagcctccc acgaatggga aggtttttatt gaaaactaca      240
gctggagata ttgacataga gttgtgggtcc aaagaagctc ctaaagcttg cagaaatttt      300
atcccaactt tgtttggaag cttattatga caataccatt tttcatagag ttgtgcctgg      360
tttcatagtc caaggcggag atcctactgg cacagggagt ggtggagagt ctatctatgg      420
agcgccattc aaagatgaat ttcattcacg gttgcgtttt aatcggagag gactggttgc      480
catggcaaat gctggttctc atgataatgg caccactttt ttcttcacac tgggtcgcgc      540
agatgaactt aacaataaagc ataccatctt tggaaagggt acaggggata cagtatataa      600
catgttgcca ctgtcagaag tagacattga tgatgacgaa agaccacata atccacacaa      660
aataaaaagc tgtgaggttt tgtttaatcc ttttgatgac atcattccaa gggaaattaa      720
aaggctgaaa aaagagaaac cagaggagga agtaaaagaaa ttgaaaccca aaggcacaaa      780
aaatttttagt ttactttcat ttggagagga agctgaggaa gaagaagagg aagtaaactc      840
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acatctcagt tctgttccag ttgtagaaag tgaaaaaggt gatgcaccag atttagttga      960
tgatggagaa gatgaaagtg cagagcatga tgaatatatt gatggtgatg aaaagaacct      1020
gatgagagaa agaattgccca aaaaattaaa aaaggacaca agtgcgaatg ttaaatcagc      1080
tggagaagga gaagtggaga agaaatcagt cagccgcagt gaagagctca gaaaagaagc      1140
aagacaatta aaacgggaac tcttagcagc aaaacaaaaa aaagtagaaa atgcagcaaa      1200
acaagcagaa aaaagaagtg aagaggaaga agccctcca gatggtgctg ttgccgaata      1260
cagaagagaa aagcaaaagt atgaagcttt gaggaagcaa cagtcaaaga agggaaacttc      1320
ccgggaagat cagacccttg cactgctgaa ccagtttaaa tctaaactca ctcaagcaat      1380
tgctgaaaca cctgaaaatg acattcctga aacagaagta gaagatgatg aaggatggat      1440
gtcacatgta cttcagtttg aggataaaag cagaaaagtg aaagatgcaa gcatgcaaga      1500
ctcagataca tttgaaatct atgatcctcg gaatccagtg aataaaagaa ggagggaaga      1560
aagcaaaaag ctgatgagag agaaaaaaga aagaagataa aatgagaata atgataacca      1620
gaacttgctg gaaatgtgcc tacaatggcc ttgtaacagc cattgttccc aacagcatca      1680
cttaggggtg tgaaaagaag tatttttgaa cctgttgtct ggttttgaaa aacaattatc      1740
ttgttttgca aattgtggaa tgatgtaagc aaatgctttt ggttactggt acatgtgttt      1800
tttcctagct gaccttttat attgctaaat ctgaaataaa ataactttcc ttccaaa      1857

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<210> 567
 <211> 372
 <212> PRT
 <213> Homo Sapiens

<400> 567

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Met Ala Asn Ala Gly Ser His Asp Asn Gly Thr His Phe Phe Phe Thr
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Leu Gly Arg Ala Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys
      20      25      30
Val Thr Gly Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp
      35      40      45
Ile Asp Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys
      50      55      60
Glu Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys
65      70      75      80
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys Pro
      85      90      95
Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu Ala Glu
      100     105     110
Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met Lys Gly Lys
      115     120     125
Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro His Leu Ser Ser
      130     135     140
Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala Pro Asp Leu Val Asp
145     150     155     160
Asp Gly Glu Asp Glu Ser Ala Glu His Asp Glu Tyr Ile Asp Gly Asp
      165     170     175
Glu Lys Asn Leu Met Arg Glu Arg Ile Ala Lys Lys Leu Lys Lys Asp
      180     185     190
Thr Ser Ala Asn Val Lys Ser Ala Gly Glu Gly Glu Val Glu Lys Lys
      195     200     205
Ser Val Ser Arg Ser Glu Glu Leu Arg Lys Glu Ala Arg Gln Leu Lys
      210     215     220
Arg Glu Leu Leu Ala Ala Lys Gln Lys Lys Val Glu Asn Ala Ala Lys
225     230     235     240
Gln Ala Glu Lys Arg Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala
      245     250     255
Val Ala Glu Tyr Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys
      260     265     270
Gln Gln Ser Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu
      275     280     285
Leu Asn Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro
      290     295     300
Glu Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met
305     310     315     320
Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp Ala
      325     330     335
Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg Asn Pro
      340     345     350
Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met Arg Glu Lys
      355     360     365
Lys Glu Arg Arg
      370

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<210> 568

<211> 1537

<212> DNA

<213> Homo Sapiens

<400> 568

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caccaaccag atccgcctaa ccaatgtggc cgtggtacgg atgaagcgtg ccgggaagcg 180
cttcgaaatc gcttgctaca aaaacaaggt cgtcggctgg cgagcgcgcg tggaaaaaga 240
cctcgatgaa gttctgcaga ccactcagt gtttgtaaag gtttctaaag gtcaggttgc 300
caaaaaggaa gatctcatca gtgcgtttgg aacagatgac caaactgaaa tctgtaagca 360
gattttgact aaaggagaag ttcaagtatc agataaagaa agacacacac aactggagca 420
gatgtttagg gacattgcaa ctattgtggc agacaaatgt gtgaatcctg aaacaaagag 480
accatacacc gtgaccccta ttgagagagc catgaaggac atccactatt cggtgaaaac 540
caacaagagt acaaaacagc aggcctttgga agtgataaag cagttaaaag agaaaatgaa 600
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aaagaaaagc tcaagccact gatcaaggtc atagaaagtg aagattatgg ccaacagtta 720
gaaatcgatg gtcgtattga cccgggctgc ttccgagaaa ttgatgagct aataaaaaag 780
gaaactaaa gcaagggttc tttggaagta ctcaatctga aagatgtaga agaaggagat 840
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aagatgcaaa gtccagagtg gcattttgct actctgtctc atgccttgat agctttccaa 1140
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ttattagggg tatgtctata caacaaaagg gggggtcttt cctaaaaaag aaaacatatg 1260
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aagcttggtg gatgttcctg attatttgag gaacagatat aggaaaattg tgccggaatt 1380
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ataaaaccaa ttttatgttt attaaactta aaaaaaa 1537

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<210> 569

<211> 210

<212> PRT

<213> Homo Sapiens

<400> 569

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Ala Ala Arg Arg Ser Val Val Thr Ala Arg Arg Trp Trp Pro Ser Gly
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Trp Thr Ala Arg Val Ser Pro Gly Ser Pro Ala Ser Gly Ser Leu Asn
20      25      30
Ser Arg Asp Val Asp Leu His Pro His Gln Pro Asp Pro Pro Asn Gln
35      40      45
Cys Gly Arg Gly Thr Asp Glu Ala Cys Arg Glu Ala Leu Arg Asn Arg
50      55      60
Leu Leu Gln Lys Gln Val Val Gly Trp Arg Ser Gly Val Glu Lys Asp
65      70      75      80
Leu Asp Glu Val Leu Gln Thr His Ser Val Phe Val Asn Val Ser Lys
85      90      95
Gly Gln Val Ala Lys Lys Glu Asp Leu Ile Ser Ala Phe Gly Thr Asp
100     105     110
Asp Gln Thr Glu Ile Cys Lys Gln Ile Leu Thr Lys Gly Glu Val Gln
115     120     125
Val Ser Asp Lys Glu Arg His Thr Gln Leu Glu Gln Met Phe Arg Asp
130     135     140
Ile Ala Thr Ile Val Ala Asp Lys Cys Val Asn Pro Glu Thr Lys Arg
145     150     155     160
Pro Tyr Thr Val Ile Leu Ile Glu Arg Ala Met Lys Asp Ile His Tyr

```

165 170 175
 Ser Val Lys Thr Asn Lys Ser Thr Lys Gln Gln Ala Leu Glu Val Ile
 180 185 190
 Lys Gln Leu Lys Glu Lys Met Lys Ile Glu Arg Ala His Met Lys Leu
 195 200 205
 Arg Phe
 210

<210> 570
 <211> 1211
 <212> DNA
 <213> Homo Sapiens

<400> 570
 accatctttg gaaagggttac aggggtatatac agtatataac atgttgcgac tgtcagaagt 60
 agacattgat gatgacgaaa gaccacataa tccacacaaa ataaaaagct gtgagggttt 120
 gtttaatcct tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaaacc 180
 agaggaggaa gtaaagaaat tgaaccccaa aggcacaaaa aatttttagtt tactttcatt 240
 tggagaggaa gctgagggaag aagaggagga agtaaatacga gttagtcaga gcatgaaggg 300
 caaaaagcaaa agtagtcattg acttgcttaa ggatgatcca catctcagtt ctgttccagt 360
 tgtagaaagt gaaaaagggtg atgcagcaga tttagttgat gatggagaag atgaaagtgc 420
 agagcatgat gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 480
 aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag aagtggagaa 540
 gaaatcagtc agccgcagtg aagagctcag aaaagaagca agacaattaa aacgggaact 600
 cttagcagca gaacaaaaaa aagtagaaaa tgcagcaaaa caagcagaaa aaagaagtga 660
 agaggaagaa gccctccag atggtgctgt tgccgaatac agaagagaaa agcaaaagta 720
 tgaagctctg aggaagcaac agtcaaagaa ggaacttcc cggaagatc agacccttgc 780
 actgctgaac cagtttaaat cttaactcac tcaagcaatt gctgaaacgc ctgaaaatga 840
 cattcctgaa acagaagtag aagatgatga aggatggatg tcacatgtac ttcagtttga 900
 ggataaaagc agaaaagtga aagatgcaag catgcaagac tcagatacat ttgaaatcta 960
 tgatcctcgg aatccagtga ataaaagaag gaggaagaa agcaaaaagc tgatgagaga 1020
 gaaaaaagaa agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1080
 acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt gaaaagaagt 1140
 atttttgaac ctgttgtctg gttttgaaaa acaattatct tgttttgcaa attgtggaat 1200
 gatgtaagca a 1211

<210> 571
 <211> 354
 <212> PRT
 <213> Homo Sapiens

<400> 571
 Pro Ser Leu Glu Arg Leu Gln Gly Tyr Thr Val Tyr Asn Met Leu Arg
 1 5 10 15
 Leu Ser Glu Val Asp Ile Asp Asp Asp Glu Arg Pro His Asn Pro His
 20 25 30
 Lys Ile Lys Ser Cys Glu Val Leu Phe Asn Pro Phe Asp Asp Ile Ile
 35 40 45
 Pro Arg Glu Ile Lys Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val
 50 55 60
 Lys Lys Leu Lys Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe
 65 70 75 80
 Gly Glu Glu Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln
 85 90 95
 Ser Met Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp

100 105 110
 Pro His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala
 115 120 125
 Ala Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp Glu
 130 135 140
 Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile Ala Lys
 145 150 155 160
 Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala Gly Glu Gly
 165 170 175
 Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu Leu Arg Lys Glu
 180 185 190
 Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala Glu Gln Lys Lys Val
 195 200 205
 Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg Ser Glu Glu Glu Ala
 210 215 220
 Pro Pro Asp Gly Ala Val Ala Glu Tyr Arg Arg Glu Lys Gln Lys Tyr
 225 230 235 240
 Glu Ala Leu Arg Lys Gln Gln Ser Lys Lys Gly Thr Ser Arg Glu Asp
 245 250 255
 Gln Thr Leu Ala Leu Leu Asn Gln Phe Lys Ser Lys Leu Thr Gln Ala
 260 265 270
 Ile Ala Glu Thr Pro Glu Asn Asp Ile Pro Glu Thr Glu Val Glu Asp
 275 280 285
 Asp Glu Gly Trp Met Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg
 290 295 300
 Lys Val Lys Asp Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr
 305 310 315 320
 Asp Pro Arg Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys
 325 330 335
 Leu Met Arg Glu Lys Lys Glu Arg Arg Ile Leu Pro Val Asn Glu Gly
 340 345 350
 Lys Asn

<210> 572
 <211> 604
 <212> DNA
 <213> Homo Sapiens

<400> 572
 ccttcggcaa aaaatttttg tcccaacttt ttgttccatt ccaaaagggc ttaccttcat 60
 tcccttttagc aacaggggcc ccaagaagct cccgttcatt cacccttacc ttggccccc 120
 ggttggaacc ccaaaggctc ccttacccca aagtgggtgg ttgaataaat cttctcagtt 180
 ccctggctcc caaggcccat tgaagaagat tgtacaaggc gtgcctcaag taccctcaggt 240
 ggaaacagaa gcacctgcct cacttcaagc cgtggctgca cccggagcag agcccgttgc 300
 cgagcctggc gctgtcggag ctgtcgggtc agcatgcgga ctactggag aacatcgacg 360
 agagcgcggt ggccgagagc agagaggagc ggaatggcgcg cgcgggcggc gagggcagcg 420
 acgacgacac cttcacctga gcccgaccg cttcagggac ggagacagga ccgggcgagc 480
 cctggggcgcg cgcccgctcc tgcaactttct cccctccccc acccggcacc tgggtggcacc 540
 gggccaggcc caggcggtg ctgcagcctg gctggacaga gccaataaaa cggatccacc 600
 agcc 604

<210> 573
 <211> 195
 <212> PRT

<213> Homo Sapiens

<400> 573

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Leu Arg Gln Lys Ile Leu Val Pro Thr Phe Cys Ser Ile Pro Lys Gly
 1           5           10           15
Leu Thr Phe Ile Pro Phe Ser Asn Arg Ala Pro Lys Lys Leu Pro Phe
          20           25           30
Ile His Pro Tyr Leu Gly Pro Gln Val Gly Pro Pro Lys Ala Pro Leu
          35           40           45
Pro Gln Ser Gly Trp Leu Asn Lys Ser Ser Gln Phe Pro Gly Ser Gln
          50           55           60
Gly Pro Leu Lys Lys Ile Val Gln Gly Val Pro Gln Val Pro Arg Val
65           70           75           80
Glu Thr Glu Ala Pro Ala Ser Leu Gln Ala Val Ala Ala Pro Gly Ala
          85           90           95
Glu Pro Val Ala Glu Pro Gly Ala Val Gly Ala Val Gly Ala Ala Cys
          100          105          110
Gly Leu Thr Gly Glu His Arg Arg Glu Arg Gly Gly Arg Glu Gln Arg
          115          120          125
Gly Ala Asp Gly Arg Arg Gly Arg Arg Gly Gln Arg Arg Arg His Leu
          130          135          140
His Leu Ser Pro His Arg Phe Arg Asp Gly Asp Arg Thr Gly Arg Ala
          145          150          155          160
Leu Gly Arg Arg Pro Leu Leu His Phe Leu Pro Ser Pro Thr Arg His
          165          170          175
Leu Val Ala Pro Gly Gln Ala Gln Ala Gly Ala Ala Ala Trp Leu Asp
          180          185          190
Arg Ala Gln
          195

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<210> 574

<211> 742

<212> DNA

<213> Homo Sapiens

<400> 574

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cccaccaggg cccctcgat gcagagacag aggtcgggtgc tgaccgctgc acgtcgactg      60
cctaccagga gcagaggccc caggtggagc aagttggcaa agtcgctcct ctctcccag      120
ggctgccggc aatggggggg cctggccccg gccctgtga ggaccccgcg ggtgctgggg      180
gagcaggtgc agggggctcc gagcccctgg tgactgtcac cgtgcagtgc gccttcacag      240
tgccctgag ggcaggaaga ggagccgacc tgtccagcct gcgggcactg ctgggccaag      300
ccttccttca ccaggcccag cttgggcaat tcagttacct agccccaggt gaggacgggc      360
actgggtccc catccccgag gaggagtcgc tgacaggggc ctggcaggac gcagctgcct      420
gccccagggg gctgcagctg cagtgcaggg gagccggggg tcggccgggtc ctttaccagg      480
tggtggccca gcacagatac tccgcccagg ggccagagga cctgggcttc cgacaggggg      540
acacggtgga cgtcctgtgt gaagtggacc aggcattggt ggagggccac tgtgacggcc      600
gcatcgcat cttcccgaag tgcttcgtgg tccccgccgg ccctcgatg tcaggagccc      660
ccggccgcct gcccgcattc cagcaggag atcagcccta atgatgctgt gtccatgatg      720
cttttaataa aaacaacccc ca                                     742

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<210> 575

<211> 232

<212> PRT

<213> Homo Sapiens

<400> 575

His Gln Gly Pro Leu Asp Ala Glu Thr Glu Val Gly Ala Asp Arg Cys
 1 5 10 15
 Thr Ser Thr Ala Tyr Gln Glu Gln Arg Pro Gln Val Glu Gln Val Gly
 20 25 30
 Lys Val Ala Pro Leu Ser Pro Gly Leu Pro Ala Met Gly Gly Pro Gly
 35 40 45
 Pro Gly Pro Cys Glu Asp Pro Ala Gly Ala Gly Gly Ala Gly Ala Gly
 50 55 60
 Gly Ser Glu Pro Leu Val Thr Val Thr Val Gln Cys Ala Phe Thr Val
 65 70 75 80
 Ala Leu Arg Ala Gly Arg Gly Ala Asp Leu Ser Ser Leu Arg Ala Leu
 85 90 95
 Leu Gly Gln Ala Phe Leu His Gln Ala Gln Leu Gly Gln Phe Ser Tyr
 100 105 110
 Leu Ala Pro Gly Glu Asp Gly His Trp Val Pro Ile Pro Glu Glu Glu
 115 120 125
 Ser Leu Gln Arg Ala Trp Gln Asp Ala Ala Ala Cys Pro Arg Gly Leu
 130 135 140
 Gln Leu Gln Cys Arg Gly Ala Gly Gly Arg Pro Val Leu Tyr Gln Val
 145 150 155 160
 Val Ala Gln His Arg Tyr Ser Ala Gln Gly Pro Glu Asp Leu Gly Phe
 165 170 175
 Arg Gln Gly Asp Thr Val Asp Val Leu Cys Glu Val Asp Gln Ala Trp
 180 185 190
 Leu Glu Gly His Cys Asp Gly Arg Ile Gly Ile Phe Pro Lys Cys Phe
 195 200 205
 Val Val Pro Ala Gly Pro Arg Met Ser Gly Ala Pro Gly Arg Leu Pro
 210 215 220
 Arg Ser Gln Gln Gly Asp Gln Pro
 225 230

<210> 576

<211> 1087

<212> DNA

<213> Homo Sapiens

<400> 576

aagatgatgc ctagttaaatt acagaagaac aaacagagac tgcgaaacga tcctetcaat 60
 caaaataagg gtaaaccaga cttgaataca acattgccaa ttagacaaac agcatcaatt 120
 ttcaaaacac cggtaaccaa agtcacaaat catcctagta ataaagtga atcagaccca 180
 caacgaatga atgaacagcc acgtcagctt ttctgggaga agaggctaca aggacttagt 240
 gcatcagatg taacagaaca aattataaaa accatggaac taccctaaagg tcttcaagga 300
 gttggtccag gtagcaatga tgagaccctt ttatctgctg ttgccagtgc tttgcacaca 360
 agctctgctc caatcacagg gcaagtctcc gctgctgtgg aaaagaaccc tgctgtttgg 420
 cttaacacat ctcaaccct ctgcaaagct tttattgtca cagatgaaga catcaggaaa 480
 caggaagagc gagtacagca agtacgcaag aaattggaag aagcactgat ggcagacatc 540
 ttgtcgcgag ctgctgatac agaagagatg gatattgaaa tggacagtgg agatgaagcc 600
 taagaatatg atcaggtaac tttcgaccga ctttcccaa gagaaaattc ctagaaattg 660
 aacaaaaatg tttccactgg cttttgcctg taagaaaaaa aatgtaccgc agcacataga 720
 gctttttaat agcactaacc aatgcctttt tagatgtatt tttgatgtat atatctatta 780
 ttcaaaaaat catgtttatt ttgagtccta ggacttaaaa ttagtctttt gtaatatcaa 840
 gcaggaccct aagatgaagc tgagcttttg atgccaggtg caatttactg gaaatgtagc 900
 acttacgtaa aacatttgtt tccccacag ttttaataag aacagatcag gaattctaaa 960
 taaatttccc agttaagat tattgtgact tcaactgtata taaacatatt tttatacttt 1020

attgaaaggg gacacctgta cattcttcca tcgtcactgt aaagacaaat aaatgattat 1080
attcaca 1087

<210> 577
<211> 200
<212> PRT
<213> Homo Sapiens

<400> 577
Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn
1 5 10 15
Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu
20 25 30
Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val
35 40 45
Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn
50 55 60
Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser
65 70 75 80
Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys
85 90 95
Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser
100 105 110
Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln
115 120 125
Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser
130 135 140
Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys
145 150 155 160
Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu
165 170 175
Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile
180 185 190
Glu Met Asp Ser Gly Asp Glu Ala
195 200

<210> 578
<211> 2569
<212> DNA
<213> Homo Sapiens

<400> 578
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tctgaaattt tgtgagttcc cacagaagac tataatgcct ggatttaaaa caactgtata 120
tgtttctcat ataaatgacc ttccagactt ttatgttcaa ctaatagaag atgaagctga 180
aattagtcac ctttcagaga gattaaacag tgtaaaaca aggccgaat attatgtagg 240
tccacctttg caaagaggag atatgatatg tgctgttttc ccagaagata atttatggta 300
tcgtgctgtg atcaaggagc aacaacccaa tgaccttctc tctgtgcagt ttatagatta 360
tggcaatggt tctgtggttc atactaaca aataggtagg cttgaccttg ttaatgcaat 420
attgccgggg ttgtgcattc attgtcctt gcagggattt gaggttctcg acaataaaaa 480
ttctaagaaa atgatgcatt acttttccca acggaccagc gaggctgcaa taagatgtga 540
atttggtaaa tttcaagaca gatgggaagt tattcttgct gatgaacatg ggatcatagc 600
agatgatatg attagcaggt atgctctcag tgaaaaatct caagtagaac tttctacca 660
agtaattaaa agtgccagtt caaagtctgt taacaaatca gacattgaca cttcagtatt 720
tcttaactgg tataatccag aaaaaaaat gataagagct tatgccactg tgatagatgg 780

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acctgagtag ttttggtgtc agtttgctga tacggagaaa cttcagtgtt tagaagtaga      840
agtagacact gctggagAAC aggtagcaga caggagaaat tgtatcccat gtccttatat      900
tgtagatcct tgtatagtaa gatacagaga agatggacat tattataggg cacttatcac      960
taatatattgt gaagattatc ttgtatctgt caggcttgtg gactttggaa acattgaaga     1020
ctgtgtggac ccaaaagcac tctgggccat tccttctgaa cttctgtcgg ttcccatgca     1080
agcctttcca tgttgctctc cagggtttaa catttcagaa ggattatgtt ctcaagaggg     1140
aaatgactat ttctatgaaa taataacaga agatgtgttg gaaataacaa tactagaaat     1200
cagaagggat gtttgtgata tcccttttagc aattgttgac ttgaaaagca aaggtaaaag     1260
tattaatgag aaaatggaga aatattctaa gactggtatt aaaagtgtct ttccttatga     1320
aaatattgac tcagagataa agcagactct tgggtcctac aatcttgatg taggacttaa     1380
gaaattaagt aataaagctg tacaaaataa aatatatatg gaacaacaga cagatgagct     1440
tgctgaaata actgaaaaag atgtaaacat tattggaacc aaaccaagta acttccgtga     1500
ccctaaaact gataacattt gtgaaggggt tgaaaacccc tgcaaagata aaattgatac     1560
tgaggaactg gaaggtgaat tagagtgcga tctggttgac aaagcagagt ttgatgataa     1620
atactgatt acaggattta acacattact accacatgct aatgaaacaa aggagatact     1680
agaactgaat tcacttgagg tgccgctttc tcctgatgat gaatcaaaag aattcttaga     1740
actggaatct attgagttac agaattctct ggtggtggat gaagaaaaag gggagctaag     1800
cccgttgcca ccgaatgtgc cactctccca agagtgtgtc acaaaaggcg ccatggagct     1860
atttacaactg cagcttcctc tcagctgtga agctgagaaa cagccagaac tagaactacc     1920
tacagcccag ctgccttttag atgacaagat ggatcctttg tctttaggag ttagtcagaa     1980
agcacaggaa tccatgtgta ctgaggacat gagaaagtca agttgtgtag aatcttttga     2040
tgaccagcgc aggatgtcat tgcactaca tggagcagat tgtgatccta aaacacagaa     2100
tgaaatgaat atatgtgaag aagaatttgt agagtataaa aacaggggatg ccatttcggc     2160
attgatgcct ttttctctga ggaagaaagc agtgatggaa gcaagcacia taatggttta     2220
ccagatcata tttcagntca attacagaac acctacactn tgaaagcctt tactgttgga     2280
tctaaatgtg ttgtgtggtc aagtntaaga aacanatggg ctaaatgtga gattttagaa     2340
acagctgaag aaggnacaag ggttttgaac ctttcaaag gtatggagga gatagtgaac     2400
cctgagaatg tctgggaatg nanaccctaa ttggataaga gtccacctga gaaaaggggt     2460
ttggaggtga tggagattta accgtggatn tatagctgtg gccaatcagt cagaagctgc     2520
ccntgaacaa gtggcatctt acgcagacca acagagtatt tgagaaaat      2569

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<210> 579

<211> 752

<212> PRT

<213> Homo Sapiens

<400> 579

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Arg Val Lys Ala Thr Leu Ser Glu Arg Lys Ile Gly Asp Ser Cys Asp
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Lys Asp Leu Pro Leu Lys Phe Cys Glu Phe Pro Gln Lys Thr Ile Met
      20              25              30
Pro Gly Phe Lys Thr Thr Val Tyr Val Ser His Ile Asn Asp Leu Ser
      35              40              45
Asp Phe Tyr Val Gln Leu Ile Glu Asp Glu Ala Glu Ile Ser His Leu
      50              55              60
Ser Glu Arg Leu Asn Ser Val Lys Thr Arg Pro Glu Tyr Tyr Val Gly
      65              70              75              80
Pro Pro Leu Gln Arg Gly Asp Met Ile Cys Ala Val Phe Pro Glu Asp
      85              90              95
Asn Leu Trp Tyr Arg Ala Val Ile Lys Glu Gln Gln Pro Asn Asp Leu
      100             105             110
Leu Ser Val Gln Phe Ile Asp Tyr Gly Asn Val Ser Val Val His Thr
      115             120             125
Asn Lys Ile Gly Arg Leu Asp Leu Val Asn Ala Ile Leu Pro Gly Leu
      130             135             140

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Cys Ile His Cys Ser Leu Gln Gly Phe Glu Val Pro Asp Asn Lys Asn
 145 150 155 160
 Ser Lys Lys Met Met His Tyr Phe Ser Gln Arg Thr Ser Glu Ala Ala
 165 170 175
 Ile Arg Cys Glu Phe Val Lys Phe Gln Asp Arg Trp Glu Val Ile Leu
 180 185 190
 Ala Asp Glu His Gly Ile Ile Ala Asp Asp Met Ile Ser Arg Tyr Ala
 195 200 205
 Leu Ser Glu Lys Ser Gln Val Glu Leu Ser Thr Gln Val Ile Lys Ser
 210 215 220
 Ala Ser Ser Lys Ser Val Asn Lys Ser Asp Ile Asp Thr Ser Val Phe
 225 230 235 240
 Leu Asn Trp Tyr Asn Pro Glu Lys Lys Met Ile Arg Ala Tyr Ala Thr
 245 250 255
 Val Ile Asp Gly Pro Glu Tyr Phe Trp Cys Gln Phe Ala Asp Thr Glu
 260 265 270
 Lys Leu Gln Cys Leu Glu Val Glu Val Gln Thr Ala Gly Glu Gln Val
 275 280 285
 Ala Asp Arg Arg Asn Cys Ile Pro Cys Pro Tyr Ile Gly Asp Pro Cys
 290 295 300
 Ile Val Arg Tyr Arg Glu Asp Gly His Tyr Tyr Arg Ala Leu Ile Thr
 305 310 315 320
 Asn Ile Cys Glu Asp Tyr Leu Val Ser Val Arg Leu Val Asp Phe Gly
 325 330 335
 Asn Ile Glu Asp Cys Val Asp Pro Lys Ala Leu Trp Ala Ile Pro Ser
 340 345 350
 Glu Leu Leu Ser Val Pro Met Gln Ala Phe Pro Cys Cys Leu Ser Gly
 355 360 365
 Phe Asn Ile Ser Glu Gly Leu Cys Ser Gln Glu Gly Asn Asp Tyr Phe
 370 375 380
 Tyr Glu Ile Ile Thr Glu Asp Val Leu Glu Ile Thr Ile Leu Glu Ile
 385 390 395 400
 Arg Arg Asp Val Cys Asp Ile Pro Leu Ala Ile Val Asp Leu Lys Ser
 405 410 415
 Lys Gly Lys Ser Ile Asn Glu Lys Met Glu Lys Tyr Ser Lys Thr Gly
 420 425 430
 Ile Lys Ser Ala Leu Pro Tyr Glu Asn Ile Asp Ser Glu Ile Lys Gln
 435 440 445
 Thr Leu Gly Ser Tyr Asn Leu Asp Val Gly Leu Lys Lys Leu Ser Asn
 450 455 460
 Lys Ala Val Gln Asn Lys Ile Tyr Met Glu Gln Gln Thr Asp Glu Leu
 465 470 475 480
 Ala Glu Ile Thr Glu Lys Asp Val Asn Ile Ile Gly Thr Lys Pro Ser
 485 490 495
 Asn Phe Arg Asp Pro Lys Thr Asp Asn Ile Cys Glu Gly Phe Glu Asn
 500 505 510
 Pro Cys Lys Asp Lys Ile Asp Thr Glu Glu Leu Glu Gly Glu Leu Glu
 515 520 525
 Cys His Leu Val Asp Lys Ala Glu Phe Asp Asp Lys Tyr Leu Ile Thr
 530 535 540
 Gly Phe Asn Thr Leu Leu Pro His Ala Asn Glu Thr Lys Glu Ile Leu
 545 550 555 560
 Glu Leu Asn Ser Leu Glu Val Pro Leu Ser Pro Asp Asp Glu Ser Lys
 565 570 575
 Glu Phe Leu Glu Leu Glu Ser Ile Glu Leu Gln Asn Ser Leu Val Val

580	585	590
Asp Glu Glu Lys Gly Glu Leu Ser Pro Val Pro Pro Asn Val Pro Leu		
595	600	605
Ser Gln Glu Cys Val Thr Lys Gly Ala Met Glu Leu Phe Thr Leu Gln		
610	615	620
Leu Pro Leu Ser Cys Glu Ala Glu Lys Gln Pro Glu Leu Glu Leu Pro		
625	630	635
Thr Ala Gln Leu Pro Leu Asp Asp Lys Met Asp Pro Leu Ser Leu Gly		
645	650	655
Val Ser Gln Lys Ala Gln Glu Ser Met Cys Thr Glu Asp Met Arg Lys		
660	665	670
Ser Ser Cys Val Glu Ser Phe Asp Asp Gln Arg Arg Met Ser Leu His		
675	680	685
Leu His Gly Ala Asp Cys Asp Pro Lys Thr Gln Asn Glu Met Asn Ile		
690	695	700
Cys Glu Glu Glu Phe Val Glu Tyr Lys Asn Arg Asp Ala Ile Ser Ala		
705	710	715
Leu Met Pro Phe Ser Leu Arg Lys Lys Ala Val Met Glu Ala Ser Thr		
725	730	735
Ile Met Val Tyr Gln Ile Ile Phe Gln Asn Tyr Arg Thr Pro Thr Leu		
740	745	750

<210> 580

<211> 2077

<212> DNA

<213> Homo Sapiens

<400> 580

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gaggtgactc	gagcagtgat	gaggataaa	aataacatga	aactcctgtg	gaagtagaac	180
tcatgactca	ggttgaccaa	gaggatatca	ctcttcagag	tggcagagat	gaactaaatg	240
aggagctcat	tcaggaagaa	agctctgaag	acgaaggaga	atatgaagag	gttagaaaag	300
atcaggattc	tggttggtgaa	atgaaggatg	aagggggaaga	gacttaaatt	atcctgatac	360
taccattgac	ttgtctcacc	ttcaacccca	aaggtccatc	cagaaattgg	cttcaaaaga	420
ggaatcttct	aattctagt	acagtaaattc	acagagccgg	agacatttgt	cagccaagga	480
aagaaggga	atgaaaaaga	aaaaacttcc	aagtgactca	ggagatttag	aagcgttaga	540
gggaaaggat	aaagaaaaag	aaagtactgt	acacattgaa	actcatcaga	acacaagcaa	600
aaatgttgcg	gctgtgcagc	caatgaaacg	aggacaaaag	agtaaaatga	aaaaaatgaa	660
agaaaaatac	aaagaccagg	atgaagaaga	ccgtgaactt	atcatgaagt	tgctggggtc	720
tgcaggttca	aacaaagaag	aaaaaggga	gaagggaag	aaaggaaaaa	caaaggacga	780
acctgtgaag	aaacagcccc	agaaacctag	aggtggacag	aggtgtctctg	acaacattaa	840
gaaagaaact	ccgttccttg	aggttataac	tcatgagtta	caagactttg	ctgtagatga	900
tccacatgat	gacaaggaag	agcaagatct	ggatcaacag	ggaaatgagg	aaaacctatt	960
tgattctttg	acaggccagc	cacatcctga	agatgtacta	ctgtttgcca	ttccaatatg	1020
tgccctttac	accaccatga	caaactacaa	atataaagtg	aaacttactc	ctggagtga	1080
gaaaaaggga	aaagctgcaa	aaacagcctt	gaatagtctc	atgcattcca	agaagcaaac	1140
agcaagagaa	aaagacttat	tccgcagcgt	aaaggacaca	gatttatcaa	gaaacattcc	1200
tggcaaaagt	aaaagtgtct	gcaccaatc	ttctgaacgt	aaaaaggaaa	tagctgaaat	1260
gaaattctaa	aatatttgag	aagagccaat	tttatagcct	tttggaaagt	caaagatgaa	1320
agcaccatgt	atcaggattt	ccgcattata	aaaatgaact	aaacattgcc	ttgctatatt	1380
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<210> 581
 <211> 312
 <212> PRT
 <213> Homo Sapiens

<400> 581

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			20					25					30		
Ser	Asn	Ser	Ser	Asp	Ser	Lys	Ser	Gln	Ser	Arg	Arg	His	Leu	Ser	Ala
			35				40					45			
Lys	Glu	Arg	Arg	Glu	Met	Lys	Lys	Lys	Lys	Leu	Pro	Ser	Asp	Ser	Gly
			50			55					60				
Asp	Leu	Glu	Ala	Leu	Glu	Gly	Lys	Asp	Lys	Glu	Lys	Glu	Ser	Thr	Val
65					70				75					80	
His	Ile	Glu	Thr	His	Gln	Asn	Thr	Ser	Lys	Asn	Val	Ala	Ala	Val	Gln
				85					90					95	
Pro	Met	Lys	Arg	Gly	Gln	Lys	Ser	Lys	Met	Lys	Lys	Met	Lys	Glu	Lys
			100					105					110		
Tyr	Lys	Asp	Gln	Asp	Glu	Glu	Asp	Arg	Glu	Leu	Ile	Met	Lys	Leu	Leu
			115				120					125			
Gly	Ser	Ala	Gly	Ser	Asn	Lys	Glu	Glu	Lys	Gly	Lys	Lys	Gly	Lys	Lys
			130				135					140			
Gly	Lys	Thr	Lys	Asp	Glu	Pro	Val	Lys	Lys	Gln	Pro	Gln	Lys	Pro	Arg
145					150					155					160
Gly	Gly	Gln	Arg	Val	Ser	Asp	Asn	Ile	Lys	Lys	Glu	Thr	Pro	Phe	Leu
				165					170					175	
Glu	Val	Ile	Thr	His	Glu	Leu	Gln	Asp	Phe	Ala	Val	Asp	Asp	Pro	His
			180					185					190		
Asp	Asp	Lys	Glu	Glu	Gln	Asp	Leu	Asp	Gln	Gln	Gly	Asn	Glu	Glu	Asn
			195				200					205			
Leu	Phe	Asp	Ser	Leu	Thr	Gly	Gln	Pro	His	Pro	Glu	Asp	Val	Leu	Leu
			210			215					220				
Phe	Ala	Ile	Pro	Ile	Cys	Ala	Pro	Tyr	Thr	Thr	Met	Thr	Asn	Tyr	Lys
225					230					235					240
Tyr	Lys	Val	Lys	Leu	Thr	Pro	Gly	Val	Gln	Lys	Lys	Gly	Lys	Ala	Ala
			245						250					255	
Lys	Thr	Ala	Leu	Asn	Ser	Phe	Met	His	Ser	Lys	Glu	Ala	Thr	Ala	Arg
			260					265					270		
Glu	Lys	Asp	Leu	Phe	Arg	Ser	Val	Lys	Asp	Thr	Asp	Leu	Ser	Arg	Asn
			275				280					285			
Ile	Pro	Gly	Lys	Val	Lys	Ser	Val	Cys	Thr	Gln	Ser	Ser	Glu	Arg	Lys
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<210> 582
 <211> 3309
 <212> DNA
 <213> Homo Sapiens

<400> 582

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<210> 583
 <211> 872
 <212> PRT
 <213> Homo Sapiens

<400> 583

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20          25          30
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35          40          45
Thr Pro Ser Val Ile Ser Phe Gly Ser Lys Asn Arg Thr Ile Gly Val
50          55          60
Ala Ala Lys Asn Gln Gln Ile Thr His Ala Asn Asn Thr Val Ser Asn
65          70          75          80
Phe Lys Arg Phe His Gly Arg Ala Phe Asn Asp Pro Phe Ile Gln Lys
85          90          95
Glu Lys Glu Asn Leu Ser Tyr Asp Leu Val Pro Leu Lys Asn Gly Gly
100         105         110
Val Gly Ile Lys Val Met Tyr Met Gly Glu Glu His Leu Phe Ser Val
115         120         125
Glu Gln Ile Thr Ala Met Leu Leu Thr Lys Leu Lys Glu Thr Ala Glu
130         135         140
Asn Ser Leu Lys Lys Pro Val Thr Asp Cys Val Ile Ser Val Pro Ser
145         150         155         160
Phe Phe Thr Asp Ala Glu Arg Arg Ser Val Leu Asp Ala Ala Gln Ile
165         170         175
Val Gly Leu Asn Cys Leu Arg Leu Met Asn Asp Met Thr Ala Val Ala
180         185         190
Leu Asn Tyr Gly Ile Tyr Lys Gln Asp Leu Pro Ser Leu Asp Glu Lys
195         200         205
Pro Arg Ile Val Val Phe Val Asp Met Gly His Ser Ala Phe Gln Val
210         215         220
Ser Ala Cys Ala Phe Asn Lys Gly Lys Leu Lys Val Leu Gly Thr Ala
225         230         235         240
Phe Asp Pro Phe Leu Gly Gly Lys Asn Phe Asp Glu Lys Leu Val Glu
245         250         255
His Phe Cys Ala Glu Phe Lys Thr Lys Tyr Lys Leu Asp Ala Lys Ser
260         265         270
Lys Ile Arg Ala Leu Leu Arg Leu Tyr Gln Glu Cys Glu Lys Leu Lys
275         280         285
Lys Leu Met Ser Ser Asn Ser Thr Asp Leu Pro Leu Asn Ile Glu Cys
290         295         300
Phe Met Asn Asp Lys Asp Val Ser Gly Lys Met Asn Arg Ser Gln Phe
305         310         315         320
Glu Glu Leu Cys Ala Glu Leu Leu Gln Lys Ile Glu Val Pro Leu Tyr

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Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala Gln Ala
 770 775 780
 Lys Lys Ser Leu Asp Gln Asp Pro Val Val Arg Ala Gln Glu Ile Lys
 785 790 795 800
 Thr Lys Ile Lys Glu Leu Asn Asn Thr Cys Glu Pro Val Val Thr Gln
 805 810 815
 Pro Lys Pro Lys Ile Glu Ser Pro Lys Leu Glu Arg Thr Pro Asn Gly
 820 825 830
 Pro Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu Asp Lys Asn Asn Phe
 835 840 845
 Gly Ala Glu Pro Pro His Gln Asn Gly Glu Cys Tyr Pro Asn Glu Lys
 850 855 860
 Asn Ser Val Asn Met Asp Leu Asp
 865 870

<210> 584

<211> 2918

<212> DNA

<213> Homo Sapiens

<400> 584

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<210> 585

<211> 687

<212> PRT

<213> Homo Sapiens

<400> 585

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Ala Ser Tyr Thr Trp Gln Phe Glu Ala Arg Lys Ala Gln Ile Leu Lys
  35          40          45
Cys Met Glu Cys Gly Ser Ser His Asp Thr Leu Gln Gln Leu Thr Ala
  50          55          60
His Met Met Val Thr Gly His Phe Leu Lys Val Thr Thr Ser Ala Ser
  65          70          75          80
Lys Lys Gly Lys Gln Leu Val Leu Asp Pro Val Val Glu Glu Lys Ile
  85          90          95
Gln Ser Ile Pro Leu Pro Pro Thr Thr His Thr Arg Leu Pro Ala Ser
 100          105          110
Ser Ile Lys Lys Gln Pro Asp Ser Pro Ala Gly Ser Thr Thr Ser Glu
 115          120          125
Glu Lys Lys Glu Pro Glu Lys Glu Lys Pro Pro Val Ala Gly Asp Ala
 130          135          140
Glu Lys Ile Lys Glu Glu Ser Glu Asp Ser Leu Glu Lys Phe Glu Pro
 145          150          155          160
Ser Thr Leu Tyr Pro Tyr Leu Arg Glu Glu Asp Leu Asp Asp Ser Pro
 165          170          175
Lys Gly Gly Leu Asp Ile Leu Lys Ser Leu Glu Asn Thr Val Ser Thr
 180          185          190
Ala Ile Ser Lys Ala Gln Asn Gly Ala Pro Ser Trp Gly Gly Tyr Pro
 195          200          205
Ser Ile His Ala Ala Tyr Gln Leu Pro Gly Thr Val Lys Pro Leu Pro
 210          215          220
Ala Ala Val Gln Ser Val Gln Val Gln Pro Ser Tyr Ala Gly Gly Val
 225          230          235          240
Lys Ser Leu Ser Ser Ala Glu His Asn Ala Leu Leu His Ser Pro Gly
 245          250          255
Ser Leu Thr Pro Pro Pro His Lys Ser Asn Val Ser Ala Met Glu Glu

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275	280	285
Pro Pro Glu Lys Glu Lys Ser Ser Leu Ala Lys Ala Ala Ser Pro Ile		
290	295	300
Ala Lys Glu Asn Lys Asp Phe Pro Lys Thr Glu Glu Val Ser Gly Lys		
305	310	315
Pro Gln Lys Lys Gly Pro Glu Ala Glu Thr Trp Glu Ala Lys Lys Glu		
325	330	335
Gly Pro Leu Asp Val His Thr Pro Asn Gly Thr Glu Pro Leu Lys Ala		
340	345	350
Lys Val Thr Asn Gly Cys Asn Asn Leu Gly Ile Ile Met Asp His Ser		
355	360	365
Pro Glu Pro Ser Phe Ile Asn Pro Leu Ser Ala Leu Gln Ser Ile Met		
370	375	380
Asn Thr His Leu Gly Lys Val Ser Lys Pro Val Ser Pro Ser Leu Asp		
385	390	395
Pro Leu Ala Met Leu Tyr Lys Ile Ser Asn Ser Met Leu Asp Lys Pro		
405	410	415
Val Tyr Pro Ala Thr Pro Val Lys Gln Ala Asp Ala Ile Asp Arg Tyr		
420	425	430
Tyr Tyr Glu Asn Ser Asp Gln Pro Ile Asp Leu Thr Lys Ser Lys Asn		
435	440	445
Lys Pro Leu Val Ser Ser Val Ala Asp Ser Val Ala Ser Pro Leu Arg		
450	455	460
Glu Ser Ala Leu Met Asp Ile Ser Asp Met Val Lys Asn Leu Thr Gly		
465	470	475
Arg Leu Thr Pro Lys Ser Ser Thr Pro Ser Thr Val Ser Glu Lys Ser		
485	490	495
Asp Ala Asp Gly Ser Ser Phe Glu Glu Ala Leu Asp Glu Leu Ser Pro		
500	505	510
Val His Lys Arg Lys Gly Arg Gln Ser Asn Trp Asn Pro Gln His Leu		
515	520	525
Leu Ile Leu Gln Ala Gln Phe Ala Ser Ser Leu Arg Glu Thr Thr Glu		
530	535	540
Gly Lys Tyr Ile Met Ser Asp Leu Gly Pro Gln Glu Arg Val His Ile		
545	550	555
Ser Lys Phe Thr Gly Leu Ser Met Thr Thr Ile Ser His Trp Leu Ala		
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Asn Val Lys Tyr Gln Leu Arg Arg Thr Gly Gly Thr Lys Phe Leu Lys		
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Asn Leu Asp Thr Gly His Pro Val Phe Phe Cys Asn Asp Cys Ala Ser		
595	600	605
Gln Phe Arg Thr Ala Ser Thr Tyr Ile Ser His Leu Glu Thr His Leu		
610	615	620
Gly Phe Ser Leu Lys Asp Leu Ser Lys Leu Pro Leu Asn Gln Ile Gln		
625	630	635
Glu Gln Gln Asn Val Ser Lys Val Leu Thr Asn Lys Thr Leu Gly Pro		
645	650	655
Leu Gly Ala Thr Glu Glu Asp Leu Gly Ser Thr Phe Gln Cys Lys Leu		
660	665	670
Cys Asn Arg Thr Phe Ala Lys Gln Ala Arg Ser Gln Thr Ala Pro		
675	680	685

<210> 586

<211> 1898

<212> DNA

<213> Homo Sapiens

<400> 586

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gcctggacga naagctgcgg actctgctct accaggagca cgtgcccacc tcctcagcct      240
cagctgggac cctctgggag gtgggcgaca ganacttcac cctggagccc ctgagagggg      300
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<210> 587

<211> 399

<212> PRT

<213> Homo Sapiens

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35      40      45
Pro Arg Val Gly Phe Val Asp Ser Thr Ile Lys Ser Leu Asp Lys Leu
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<212> DNA

<213> Homo Sapiens

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<213> Homo Sapiens

<400> 607

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ttataatttg aaaactgcat ctgaaagcaa actttattgt tcaattatc ttaatgatgg	240
tgttttatga ctaatacact gatttttcaa taaggaaacc catgttaaaa atatttttat	300
tttaaaaaata agcctgtgtt caagctctga tcatatttct tttattttga tttgggaaga	360
aaatactgtt tctgatagca tgaaatgcaa aatttttaga tttttaatct cnctaatttt	420
aagaactatt gagaaattga ttaatgacat gaagtgcaca aactaatta ctggccagct	480
gttggcattg tgtttcttac ttagttctcc caaggaaaac tcttaaaactg aatcttcagc	540
ngaataacct taaatatact ttgttagcca aacaaaactt ttttggttac atagttcttt	600
ggattttact gttcctaatt ttattctgaa actccatttt tcccagacc ataattacc	660
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<210> 608

<211> 994

<212> DNA

<213> Homo Sapiens

<400> 608

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accgttatc ccagttccaa gatgaatata gttagatga agtgatggca tctaaagaag	180
ttttgatatt tttgactatc ttacaatgtt gtcccacttc agatggtgct gcagcagcaa	240
ttttggccag tgaagcattt gtacagaagt atggcctgca atccaaagct gtggaaattt	300

tggcacaaga	aatgatgact	gatttgccaa	gctcgtttga	agaaaaaagc	attattaaaa	360
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ataatacata	tgaggagaaag	tggtgcataa	atcctagtgg	tggaactgatt	tcaaagggac	600
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atgtgtgaaa	gaaaaatncg	gngggaattt	ttgccttca	aggggaaana	atggccctgg	960
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<210> 609

<211> 843

<212> DNA

<213> Homo Sapiens

<400> 609

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tngcaaatan	ttaaccttnc	ttgaaaang	aaattntac	caanggacng	aaancntnt	180
aattngaant	naaattatan	ttngaaancg	gcnnngaaa	ccaancttna	tggtccaatt	240
atcctnaang	agggnnnttn	annactaatn	cccngatttt	ccaatangga	ancccnntt	300
aaaantnttt	tnatttttaa	aataaccncg	tncccaaccc	cngatcanat	tccttttnatt	360
tggtattggg	aaaaaaatnc	ngttccnnt	accnngaann	gcaaantttt	taaattttta	420
acccccctan	ttttaaaanc	tatngaaaan	tngattanng	acttgaattg	ccaaccctan	480
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tttaantant	ccttgggatt	taacgggtcc	ccaatttnat	ccngaaccce	nttttcccc	660
naaccatant	taccatttta	ccttggttaag	gcncagtngt	ttgcantncc	gcaaancagt	720
antnttcccc	nggcnccttc	ccccgancct	tgggaaaaac	gggatnggtc	cccccttaa	780
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aag						843

<210> 610

<211> 707

<212> DNA

<213> Homo Sapiens

<400> 610

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gttcagtgt	ttaatctgac	gcaggcttat	gcggaggana	atgttttcat	gttacttata	180
ctaaccattag	ttcttctata	gggtgataga	ttggtccaat	tggtgtgag	gagttcagtt	240
atatgttttg	gatttttttag	gtantgggtg	ttgagcttga	acgctttctt	aattgggtggc	300
tgcttttagg	cctactatgg	gtgttaaatt	tttactctc	tctacaagg	tttttccctag	360
tgtccaaaan	gctgttcctc	tttgactaa	cagttaaatt	tacaagggga	tttagagggt	420
tctgtgggca	aatttaaagt	tgaactaaga	ttctatcttg	gacaaccagc	tatcaccagg	480
ctcggtagg	ttgtgcctc	tacctataaa	tcttccact	attttgctac	atagacgggg	540
tgtgctcttt	tancgtttct	tangtanctc	gtctggtttc	gggggtctta	gctttggctc	600
tccttgcaaa	gttattttcta	agttnaattc	attatgcnc	angtatagg	gttagtcctt	660
gctcatatta	tgcttggtta	taattttcca	nctttccct	tgcggtta		707

<210> 611

<211> 663
 <212> DNA
 <213> Homo Sapiens

<400> 611
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 aaagtaatct canaaaaaaa aggttttttg aaattaaact tgacttttaa aaaatcatac 180
 ggacaaacaa ctttcaaaaca aaactggatt agtaggattt cttgcctgct taactaacat 240
 gacanaacttc ttgtcccagg cccttctcan aaaaacctca tgtggaaacc aagctanaga 300
 taanaattct tccctgatgc agttagggga aagggaaagg ctagaaactt ctttggcaag 360
 caattccaca cacagccatt tatgtgtgag tgctctgctt caagcacagt acgctctttg 420
 cagggacggc cagatgttca gagtgggagt ggtacttttc aaccagctaa aagtgcagaa 480
 gtcacttant cgtctgctc tcccactgc cagtgcctgc agccttgca caacttttaa 540
 ccaccccta tgggactgga atnttgagtt aaaaagccaa ngctgaactg gctgacgctg 600
 tantctocan tgaaaaggaa atgggatgaa atggaaaccg aaaaacccc ngtnacntga 660
 tga 663

<210> 612
 <211> 621
 <212> DNA
 <213> Homo Sapiens

<400> 612
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 aagtaatctc anaaaaaaa gggtttttga aattaaactt gacttttaaa aaatcatac 180
 gacaaacaac tttcaaaaca aactggatta gtaggatttc ttgcctgctt aactaacatg 240
 acaaacttct tgtcccaggc ccttctcana aaaaacctcat gtggaaacca agctar.anat 300
 aanaattctt ccctgatgca gttaggggaa agggaaaggc tagaaacttc tttggcaagc 360
 aattccacnc acagccattt atgtgtgagt gctctgcttc aagcacanta cgctctttgc 420
 agggacggcc anatgttcnn antgggagt gtagctttca accagctaaa antgcanaag 480
 tcatctantc gtctgctctt tcccactgcc agttgcttgc agccttgca catcttttaa 540
 ccacccctat nggactggaa tattgaatta taaaccngg ntgaactggc tgangctgtt 600
 tctcccttga aaaggaaatg g 621

<210> 613
 <211> 637
 <212> DNA
 <213> Homo Sapiens

<400> 613
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 tatctccct ntntatttnn gggggttaca antntnctt catttnaant atnccccaa 120
 tantntnctn aaaaaaaga gggttganga aattaaactt gacttttaaa anatcatgng 180
 gacaaacnac tttcaaaaca agctggatta gnaggatttc tngnctgctt aactaacatn 240
 aanacttct tgtcccaggc cctnctnaaa aaaacctctt gtggaaaccn agcnaaaaat 300
 aanantctc ccctgatgca ntggggggag anggagaggc taaaaaacttc tntggcaanc 360
 anttccacnc acngccattt ttntntnagt gcncctgtnc nancnnagta cgctctttgg 420
 gnggacggcn anntntnat agngggagt gtnctttcaa ccagctaata ntgaagaaat 480
 catctagtgc nctgctctn cccactgcc gtgcctgcnt ccttgcaacn tcttttaacc 540
 cccctangg acnggattat nnagttaana ccgaggntga gctggntgac gctntctcct 600
 ccatttgaaa angaaatgga taagatggaa ccgaaaa 637

<210> 614

<211> 673
 <212> DNA
 <213> Homo Sapiens

<400> 614
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 cttgaaggct acaagtggca aggaagattc tatttcaa atagccacag aaataaagga 180
 tggacaaaaa tctgggacag tgtcttctca gaaacaaccg gccttgaagg atacaagtga 240
 caaggatgat tctgtttcga acacagccac agaaataaaa gatgaacaaa aatctgggac 300
 agtgcttctc gctgttgaac agtgtttaaa caggagtctc tacagacctg atgctgttgc 360
 acagcctgtg acagagaatg agttttcttt ggaatctgag attatttcaa aactatacat 420
 cccaaagaga aagattatct ctccacgacg tataaaagat gtgcttcctc ctgttgaaga 480
 ggctgttgac aggtgtctct acctactgga ccgttttgca cagcctgtga caaagggata 540
 agtttgcttt ggaatctgag aatatttcag aaccatactt tacgaacaga aggactattc 600
 tcaacaatct gcagaaaatt tagatgctgc atgtggcatt gacaaaacag aaaatggana 660
 catgtttgaa gac 673

<210> 615
 <211> 714
 <212> DNA
 <213> Homo Sapiens

<400> 615
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 acagaatctt cctcgtcact tgtacccttc aagggttggtg gttcttgana anacactttc 180
 ctanatatct cctcactcct tttctctctg gttatattcg aaaaanaatc cttctcatca 240
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 ctgtccana tttttctcca tcttttattt ctgtggctat ntgcgaaaca gaatcttctc 540
 cgtcagttgt accttcnagg ntggttgttt ctgaaaaaan actgtcccac actgtatcca 600
 tctttttatt tntgttanct atatcnaagc aaaatctggt ttgtcccttg ttacntttg 660
 aaggtnngtn gtttctgaaa aataanctgt tccanatttt cccaccacc attt 714

<210> 616
 <211> 688
 <212> DNA
 <213> Homo Sapiens

<400> 616
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 ttctcanaan aactgttct anatttttct ccacctttt tttctctggc tatattcaaa 120
 acanaatctt cctcgtcacc tgtagccttc aaggctggtg gtttctgaaa anacactgtc 180
 ctanatgttt cctcactcct tctttctctg gttatatttg aaaaanaatc tttctcatca 240
 cttgtagcct tcaaggctgc ttttttccga naanacactt caagcctggt ggttgcctc 300
 aaaacactgt tctaaatttt tctccatcct ttttttctc ggctatatcc aaaacanaat 360
 cttcctcgtc actgttagcc ttcaaggctg gtggtttctg aaaananact gtcctanatg 420
 tttctccatc ctttctttct ctggttatat ttgaaaaana atctttctca tcaattgtan 480
 ccttcaagggt tcttttttct cganaaaaaa cttcaagcct ggtggttgc cngaaaaaac 540
 tgtcctaaaa tttttctcca tcttttctct ctctnggcta tactcnaaac aaaatcntcc 600
 tctgctccttg ttnccttcca anggtgggtg gtttctcgaa aaaaanactg tctanaatt 660
 tctctcctc ccttttttct tctgggtt 688

<210> 617
 <211> 721
 <212> DNA
 <213> Homo Sapiens

<400> 617
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 tcatgaaagt cgccagtggc agcaccgcca ccgcgcgcgc gggccccagc tgcgcgtga 120
 aggccggcaa gacagcgagc ggtgcgggcg aggtggtgcg ctgtctgtct gagcagagcg 180
 tggccatctc gcgctgcgcc gggggcgccg gggcgcgccct gcctgccctg ctggacgagc 240
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 gccgagggtt gccggtccgg gctccgctca gcacctcaa cggcgagatc agcgccctga 480
 cggccgangt gagatccaga tccgaccact anacatcct tataccgacg gggaaacnga 540
 agccatanaa ggcggtggcg cttgcaccac ttccgtccca tccttgccgg tacctggctt 600
 atgcnngggg ncctaaggac cttggaaaaa acgctcccc gtcgttgctt cctggggaaan 660
 ggggcgttnc gctgcgcttc ggaacggggg tccttccaac ccgcgggtct cattttcttct 720
 c 721

<210> 618
 <211> 461
 <212> DNA
 <213> Homo Sapiens

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 aaanacacca ancttnacca ttttttaaan tttctgcttt ncaaaaanta aaaacncnca 180
 attgnantcc cacccectaa attctctggt nactattagg tntncaaaaa gnaccncccn 240
 ctccnccca ttgcctcanc cncancccca ggctgnatnc atttaagggc ncattggccg 300
 ccaatcggnc tnntcncnc ncaaatccgg caaggcnctt nggggnaaac ccacaaanca 360
 cttattcccc ctngccccct gaattggtgg ggtccgcccg tccttggggg aggcncctcca 420
 ccaacncaaa atgcaatcnt cncagnaac ccntgcccgc t 461

<210> 619
 <211> 751
 <212> DNA
 <213> Homo Sapiens

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 cccagggcct ggcaggaacg tcacagtggc ctgcagcagg agccccgggt gccttatcgc 180
 ccatctacga cgggggtctc cacggcctgc agagtaagat agaagaccac ctggacgang 240
 ccatccacgt gctccgcagc cacnccgtgg gcacagccgg cgacatgcac acgctgctgc 300
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 caggcctggt tggaggcagc caccocgagg acggcctcgc aggcagcacc agcctcatgc 420
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 actgaaggac cgggaaaagg cncatggcaa ttacncccc ggaaccggtg cccttccggg 720
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<210> 620
 <211> 556
 <212> DNA
 <213> Homo Sapiens

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 gcaaaaaaag cttaaaaaaa ccaaaaacca aaggcagcat ccttgctaatt tttcatctac 180
 attaanaaaa aaaaaatctt gtaactaatg tttttatttn ccttaaaaaa aatatttcgc 240
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 gagtgatatn tttccatttc tccgcttttt atagttaagg cattttttnc tnccttgaca 360
 aagtgtatgt tttgttgctt gctttcaggt tttgtttact ggaaaaaaa aaaaatgccc 420
 tgtcanccca ngcaanaggg ccaanatgca attcagggat ccntgggaca ggtccaaaat 480
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 canggaacc tgaacc 556

<210> 621
 <211> 708
 <212> DNA
 <213> Homo Sapiens

<400> 621
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 caacaaaaac ttgtttaaat ngttccttna atttnnacta cttaaaanca taggtntaaa 180
 ggaaaaacnt ncaaactggt ccacttgggc ttnttaccag gcaaagnaac cctgcttncc 240
 aaaaactnat atattccaaa ttcncggcat ntggnaatnt tnccatggac nctgnatctt 300
 aacaaatgct atantnttta caaaactacn cccncaaaaa aaccccaagg aacctgcagg 360
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 cnccatgcaa aactttatgn aaaaccccca aactaggcta tttancnct nccatnaatg 480
 gnccccaaat catntnatnc tacggcataa acaacanctg ccctatttac ncggaacctg 540
 caaanctcac aagnaatgtg aattngcnc ngggantcaa tgttnccggg tnaattatct 600
 tggatnanaa ccnttttcta catnactatt gaaaaaacct gtggtttctt gctttttaac 660
 aaatnnggtg ttcctttgcc cccccccctt atttttcaag ggtggtgt 708

<210> 622
 <211> 675
 <212> DNA
 <213> Homo Sapiens

<400> 622
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 gattctcaaa acttaaattc aagaaggagc cctgtcccag ctcaaatagc tataactgta 180
 ccaagacnt ggaagaaacc aaaagatcgg acccgancca ctgaagagat gttagaggca 240
 gaattggagc ttanagctga agaggagctt tccattgaca aagtacttga atctgancaa 300
 gatntaatga gccagggggt tcatcctgaa agagaccct ctgacctana aaaagtga 360
 gctgtggaag aaantggaga anaagctgag ccagtnctg ntgggtgctga gagtgtctct 420
 gaggggtgaag gantagatgc tacttcaggc tccncagata gttctggtga tgggggttacn 480
 tntccatttn aaccngaact ctggaagcct actgatnctg aaggtnctgan gcnntntgac 540
 ngggagttct gctggacttc cagttcatgc ctgcttggtg tncctttccc gagggcctgc 600
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 tctgggatcc ttcga 675

<210> 623
 <211> 713
 <212> DNA
 <213> Homo Sapiens

<400> 623
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 acttttatcc agtacctttt tcctccatga tcacctttt tttcttttcc cctctccac 180
 tcgtgcacac gtgggggttt ctgcgagaat tggccttgct gcactgtgat tggcgaanac 240
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 ccttctctgt atctgantct aggtacttga gtaagatcgg cactctctgc ttgataacag 600
 cagtgtccac tctgaaggta naagaatcng gttattatag cttgctttaa caaacagcng 660
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<210> 624
 <211> 554
 <212> DNA
 <213> Homo Sapiens

<400> 624
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 tggtatctt cnaggatttg gttggtaaat gtgaccctcg agaanaagca gcgaaagaca 180
 tttntgccac caaagttgaa actgaagaag ctactgcttg ttttagacta actttnatcc 240
 aattaaagct gaattagcta aaaccaatgg agaattaatc tcnaccncnc acnanttcnc 300
 ccagaganaa natgaatccg attcattgat tcaagagctt gagacatctg ntaaganaat 360
 aatnccacan aatctggaga attnnagaat tgatnaatat nattgatcnn tcgaagatac 420
 tatcancgaa tttcagaacc tnangtctca tatggaaaac tcntttaaat gcnatgacaa 480
 ggctgatata ttttctttaa taataaaca taaattgatt tggatgaaa cagttgaagt 540
 acctaaggga cagc 554

<210> 625
 <211> 551
 <212> DNA
 <213> Homo Sapiens

<400> 625
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 tggggatggt taatgggtac aaaaacaaat aagatnaaaa gaatgattta atatctgata 180
 gcacaatana ntgactataa tcaataataa cttacttgta tttttttaa tgatctaaaa 240
 aatgtaattg gattatctgt aattcaaagg aaaaatgctt gaggggatgg atacctcatt 300
 ctccatgata cagntnttc acattgatgc ctgtgtcaaa acatctcaca taccctgtaa 360
 atatatacat gtactatgta ccacaaaatg tttacaaaat aagtganaca ttctaattaa 420
 agactgaaat ctttttctaa ataattgata tacatgtttt gtgatctgta cacacttatt 480
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<210> 626
 <211> 680

<212> DNA

<213> Homo Sapiens

<400> 626

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cgcanaaatg	caaagacgcc	tgagttatac	aacttgcaat	tattattttc	tanacagaag	180
tgccaactgt	tgtgctttcc	agtgtatcag	tggttgctac	attctccttc	ttgtcttcgg	240
gtttcatggc	aggaaacaga	agtacttcct	tgatgttggt	ggagtccgtg	agaaacatgg	300
cgactcgatc	aatgcccacg	ccccagccag	ctgtgggggg	cagcccatat	tccagggcag	360
tcagagaagt	ttcatctatg	aacatggcct	catcatcacc	tcagccttg	gccttggcct	420
gttcttcaaa	aanctgccgc	tgccgcatgg	gatcattcag	ctcagtatac	gcattgcata	480
tctcttttct	catgacaaac	agctcaaaac	gctcagtcag	acctctttaa	anccgtgcca	540
tttaaccnaa	gggccattat	ctgtgggtga	tcacagatga	atgtnggatt	gatgcaagtc	600
acttccanga	actccccaac	aancttgctc	aggaacctgg	ctgtgggtcca	angtgaaggg	660
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<210> 627

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 627

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gagaaagtgg	ctcaantnna	acnaattccc	tttgatgcct	cnnaattacn	cagttctccg	600
cagatggcag	cccagcacia	tatgggtgat	gatggttctg	gccaagtggg	aatttggcgt	660
gtncaaaaca	atggtaggat	ccaagttgac	cnnaactcct	atgggtgactc	ccatgggtgg	720
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<210> 628

<211> 675

<212> DNA

<213> Homo Sapiens

<400> 628

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gttaaancca	ccttaacata	aaccttatng	caattntaca	cntcttttga	acncaatcta	180
taaaaaaaaa	aataactncc	anggcattac	aacttttnct	ctggcatntt	aaaaaacaac	240
tctnactaat	ggctaatagca	ttataaaatt	ncctatctna	caaactctnc	ttaattatgc	300
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tatnggccca	taacaaaant	tccctncagg	ttattttaat	ntnttaacnt	aaaaaaacnc	420
cagntgaaaa	aaaattncaa	nccaaaacta	accnttaaaa	aataggcntt	nggttnaggt	480
taattttttt	tttttttttt	ttgnaaanaa	antcncnttt	gccagntctg	gattgtgggt	540
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<210> 629
 <211> 677
 <212> DNA
 <213> Homo Sapiens

<400> 629
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 gtanagtggg gagagccaca gaattcccct tagctgggac agtttcaaca agggtgactg 540
 cttcatcatt gacctggga ccgaaattta tcanttggtg tggttcctcn tgcaacaaat 600
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<210> 630
 <211> 665
 <212> DNA
 <213> Homo Sapiens

<400> 630
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 ggcggtgcacc accacgcgca gctaattttt ttgtattttt agtaaaggcg aggtttcgcc 180
 atgttggcca ggctggtctc gaaatcctga cccagtgat ctgcctacct cactctctca 240
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 cttcattagc atctttgcca atccaaataa atatctgttc ccaagcatct agtaacatga 600
 catcatcttc agctaaatca tcctgggtga actctccctg gaatctcttc aataacaaat 660
 ctccc 665

<210> 631
 <211> 698
 <212> DNA
 <213> Homo Sapiens

<400> 631
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 tgatgttact ggtcaatggc agtaatcctg aaggtgaaga tcctgagagg gaacctgtan 180
 aaaatgaaga ttatagagaa aagtcttcag atgatgatga aatggattct tccttgggtc 240
 ctacagagcc tcccgataac caggaaaagg aacgactaaa tacatccatt ccacaaaaaa 300
 ggaaaatgag aaatctgtta gttaccattg agaatgatac tcctctagag gaactctcaa 360
 aatatgtaga catcantatt attgccctta ctcgaaatcg gaggacaagg agatggtaca 420
 cttgtccact gtgtgggaaa cagtttaatg aaagtctta cctcatttcc caccagagga 480
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 caaacctcaa taaacatgag cgaattcnta caggagagaa accttattcc tgttctcagt 600
 gtggaaaaaa cttccgtcng aattctcatc ggagtcgtcc tgaaggaatc catntaacgg 660

agaagatatt aagtgtccan aatgtgggaa aacctccc

698

<210> 632
 <211> 466
 <212> DNA
 <213> Homo Sapiens

<400> 632
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 ttaaacaggt attcttagag gggtatatga attgctatca gaagctgttg gctaacaagc 180
 cagtaatttg gttctttcac canaacacag ttccagataa gcatctttgc actatttctc 240
 aantatgaat ccccatgtgg ggggaaaacg gatatacttt caatagacac aagtcactct 300
 ttgccttcca agtaagcana ctccagattc atcttcaaag tgttgggaaa ngggatctgt 360
 gacctgtnc a ttatcatata acttcaaaaa ggaaagctcc ttantccaaa aagcctanat 420
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<210> 633
 <211> 734
 <212> DNA
 <213> Homo Sapiens

<400> 633
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 gtttatataa actctacatt ctcttaaaagg ttttcgtttt gttttcactg gagattttta 120
 gcctccaagt gaacttaaca tattgcctat gcatctgatt ctttatanac ttttanattt 180
 taaaactaaa tttganaaac catgcatact gtatacctta ttttaataatc caaanaattg 240
 tttgcacttt caaaaaagtt acaaaaaggc tgaacacaag ttaaataacc tatatgatgt 300
 aaattttcca tttctgaata ctttttcagt attatatatt gcttgctgtc taataagtta 360
 gattgtcaga nacgcttcag taaattatct ctactttaaa attatatctg aatccccctt 420
 ctctganatg aacttgccaa tattaacat tgtgccatat gcagtattan cccaaaagct 480
 taaataagaa ccaaacttgt agactgaata ttttaacctt aaaattatat acctatatat 540
 ncacctatgg tatgtgtcat attaaattta acatttcaag taacatatat atagcaaaaca 600
 ttcagccaaa tactctttca tgaaaagata ctgtccctaa aataaaaagt tantgaaaag 660
 cttattttaga ccnaatgtct aaatataant nctaagccta tgaaacttga anctaaagtc 720
 tgtgtntcta tttta 734

<210> 634
 <211> 822
 <212> DNA
 <213> Homo Sapiens

<400> 634
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 tgtaaatatt gtacttttca aactccagat cttaaataatg ttacttttca tgtggattcg 180
 gaacatccca atgtagtgt aaattcatcc tatgtttgtg tcgaatgcaa ttttcttacc 240
 aaaaggatg atgcactttc tgagcataat ctgaaatata acccaggaga agagaatttt 300
 aagtgacta tgggtgaaacg taataaccag acaatctttg aacaacaat aaatgatctg 360
 acttttgatg gtatgtttgt taaagaggag aatgcagagc aagcagaatc tacagaagtt 420
 tcttcttcgg gaatatctat cagtaaaact cctatcatga aaatgatgaa aaataaagtg 480
 gaaaaataac ggattgcagt tcatcataac tcagttgagg acgttcctga agagaaagag 540
 aatgaaatca aaccagaccg tgaagaaatt gtagaaaatc caagttcttc agcttctgaa 600
 tctaatacaa gtacttccat tgtaaacaga atacatccaa gtactgccag caaggtagtg 660
 acccagcagc agttcctccc tggattgggc ccagggtgata actgtgtnt ctgctccgcc 720

agaattctaa ttgtattccc naagtcttaa tccctgttna tancatcccc cctacaatgc 780
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<210> 635

<211> 819

<212> DNA

<213> Homo Sapiens

<400> 635

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 gaatatgagg acaagctcta gtgggtcatta aacccccctca gaaagtctaa gattcagaat 180
 gtctccatca tattagaaga aaaatgtact gtattaaaat ttaaattgca tttttacaag 240
 ttgtttttta attagtgttc tatttacatt gcanaacttc caccaactgc agtagtttaa 300
 ctttggcaca acattaagtt ccatttcttt tgggtattgg atcctgcttt ttgagtgtgt 360
 atgccccaaa acgttttcaa tgtcatcaaa gattgggcaa attcacagta aatcagacat 420
 cttgagttga agaattgatt ctcttcaac gttttaggca gatttcagtc atctgattta 480
 gacagcttcc gtttcacatg tcgtggaagt cccaagtgtc actatcatct gtttcttctt 540
 catctcttc ctgggtcatca ataacttcat ctctctctc attttctca aataattcta 600
 tacctaattc tgatcttctc tgtctttctg caaaccactc tctgacctgc tcatanccca 660
 tatgtgattt gttaacaaat tcatcaaggt cttgctcatt aaaaaacttg tgcttcagggt 720
 tataatcctt aanttttgcg gttccagttt taaattttat gaatnaatgg tccccgggc 780
 cccagttgtt aattcctttt ggctcctcca aggcgcccc 819

<210> 636

<211> 704

<212> DNA

<213> Homo Sapiens

<400> 636

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 aaaggaaaaa-aatattttcc-aaantccatg-tgaaattgtc-tcccattttt-tggcttttgg 180
 gggggttcag tttgggttgc ttgtctgttt ccgggttggg gggaaagtgt gttgggtggg 240
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 naattcctgg tctggggcac caacgtccaa gggggccaca tcnatnatgg gcaggcggga 360
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 nccatcgaca gtgacgctgt aggtgaancg gctgttgcgc tggcgcgga tctcgatctc 480
 gttggaaccc tggaggancca gggccttctt gaggttgcca gtctgctggt ccatgtaggc 540
 cacgctgttc ttgcantggt angtgatgtt ctgggagcct cggtggacat caggcgcagg 600
 aaggtcacct ggatgccaca tcngcanggt cggaaccctg gccgccatac cccaactggg 660
 aatccatcng tcatgctctc cccgaaacaa aacatcctct tggt 704

<210> 637

<211> 693

<212> DNA

<213> Homo Sapiens

<400> 637

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 agccaccttc aaatgaatct tcaaattgga aaatactgct tcaccacctg ttggggataa 180
 nttgcaaatg gaataattta gtatggtttg tagctatttt gatnaccacc tcgcctgnat 240
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 cctctaaatc cccactgttg ctgttctgta tattgtncct tcgacatggc tacttttatt 360

tcacatttac taaaaccaac attgtggtat ttcttttcca ttatcttctt cactggttct 420
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 agctctatgg attccacctc accaaaacca ccaaagtact cccttatttt ctcttcaggt 540
 gtatctggan aaaggccacc ancnaaaatt ttttaaccgg ctcttttgtt tccatggctt 600
 tgggcctttt angatcaatc accttccccca ttcaatttat gttctttttg gatccatgaa 660
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<210> 638

<211> 619

<212> DNA

<213> Homo Sapiens

<400> 638

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 tgattgatcc taaaagggcc aaagccatga aaacaaaaga gccggttaaa aaatttttgt 180
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 gcaacagtgg ggtatctanag gaggatttgc angaagagct cgtggaagan gtggtggccc 480
 cactcaaac tgggaaccang gatatanatna ctattggaat cnaggctatg gcaactatgg 540
 atatnacagc ccagggttacc gtggttntgg aagatatgac tncactgggtt acnacaacta 600
 ctatggatat ggtgattat 619

<210> 639

<211> 694

<212> DNA

<213> Homo Sapiens

<400> 639

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 ttagtgagc- gggagagagc- gggagtgtgc- gccgcgcgag- agtgggaggc- gaagggggca 120
 ngccagggan aggcgcagga gcctttgcag ccacgcgcgc gccttccttg tcttggtgc 180
 ttcgcgaggt acagcgggcg gcggcgancg gcggggatta ctttgctgct agtttcggtt 240
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 cttanctggg acactnccca gaaagatctg aaggactact tttccnaatt ttgggtgaaa 600
 ttgttaaaact gccctcttga aatttttnatn ctatccnngg ggcnatcaaa ggggtttttg 660
 gcttttttcc tattttaaac aaatcccga aaat 694

<210> 640

<211> 728

<212> DNA

<213> Homo Sapiens

<400> 640

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 tcacagatca ggtgatgcag aatcctcgag ttctggcagc tttacaggag cgacttgaca 180
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tagaattcca	ctttgaaccc	cacgactact	ttaccaactc	agtcctgaca	aaaaccttac	720
cagatgaa						728

<210> 641

<211> 732

<212> DNA

<213> Homo Sapiens

<400> 641

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ctgtgttcac	aagttccctg	aagcttaggt	tttgagagaa	tattgttgag	tcactaggca	180
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cacaattcag	ggccactctg	caccaacaga	gataagcacc	caggtggaag	cccccttcc	420
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gcgggactat	ccgctcacgg	aaaaagtgtc	caatttcaaa	atcagaagct	aatgtgaatt	540
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aaaaggactc	attgggtact	gtttcgtaat	tgttctaaca	gtgcctcaac	cttatgcttc	660
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<210> 642

<211> 582

<212> DNA

<213> Homo Sapiens

<400> 642

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naaggcgetg	cctgatttcc	tcaagctcct	ccttctctct	cttcttatct	cgttcacctg	180
cttccatttc	cttttctcta	tcacgcaacc	ttttctgaaa	agcacttcc	ctgtaatat	240
tggggctcatc	tctatcatca	tcatagtctt	ctaanaattc	ttttagtcgt	ttagcttctt	300
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gganttttct	ttcaagtttt	cttcgttcgt	atgcatcttc	ttcatcttct	tctcggtccc	480
gttttttgtc	tttttctctt	tctcgtctcc	gttctctct	cnetctctct	ctcgtctccc	540
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<210> 643

<211> 784

<212> DNA

<213> Homo Sapiens

<400> 643

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ataatgagga	tgcaacagat	aaagttaata	aagttggtga	gatccatgtg	aagacattag	120
aagaaattct	tcttgaaaga	gccagtcaga	aacgtggaga	attgcaaact	aaactcaaga	180

cagaaggacc	ttcaaaaact	gatgattcta	cttcagggag	caagaagctc	ctccactatc	240
cgtatcaaaa	ccttctctga	ggtcctggct	gaaaaaaaac	atcggcagca	gggaagcaga	300
gagacnaaaa	agcnaaaagg	gatacaactt	gcatacaagct	aaagattgat	agtgaatta	360
aaaaaacagt	agttttgcc	cccattgttg	ccagcagagg	acaatcagag	gagcctgcag	420
gtaaaacaaa	gtctatgcag	ggaggtgcac	atcaagacgc	tggaaganat	taaactggag	480
anggcactga	gggtgcagca	gagctctgag	agcagcacca	gctccccgtc	tcaacacgag	540
gccactccag	ggggcnaggc	ggctgctgcg	aatcacnnnn	agaaccggga	tgaaagaaga	600
gaagancctt	ccgggaagg	aatgaagttg	attctcagag	cngtattaga	acngaagcta	660
aagangctcc	gggtgagaac	nccggggttg	acctccctaa	aattccagtc	cagagatgtg	720
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<210> 644

<211> 749

<212> DNA

<213> Homo Sapiens

<400> 644

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tattttttta	aaaagcaaaa	naataaagaa	tatatcaaaa	agggacctgn	aatctgtaag	180
gtgattccaa	aaacnaaata	antagaaaat	ccatggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggtatcat	acaacattca	gtcagctgaa	natggattgg	tanaggtgtg	300
tctatacata	aacttcagtc	atttttgctt	gtgcanaatc	atcccaatct	tcccaanact	360
gaatgggcag	tcctgtggct	ttcttctctt	tccatattcc	caacaaggct	acgtgaagtt	420
caactcttga	tgagccgctt	acaacagcag	ttccttaggg	agccaacatg	acaggtgggt	480
canatttccc	tatgagaaac	aaaactggcc	acctacagca	aaatatcaaa	atgggtaagt	540
ccttccttcc	tcttctctct	gattatatac	aacatatctc	ctttcaagac	tattatttcc	600
atcatgctta	ttccttcaca	aatctaaacc	ttgaggtgat	atgaaggaaa	ccancntcaa	660
aaaaaagaaa	actcaattcc	gaaatgaana	aaactgggcn	nggtatncaa	tacnccccan	720
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<210> 645

<211> 751

<212> DNA

<213> Homo Sapiens

<400> 645

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acaaaattat	tttttaaaaa	agcaaaagaa	taaagaatat	atacaaaagg	gacctggaat	180
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agggtgtgtc	atacataaac	ttcagtcatt	tttgcttgty	cagaatcatc	ccaatcttcc	360
caanactgaa	tgggcagtc	tgtggcttcc	ttccttttcc	atattcccaa	caaggctacg	420
tgaagttaa	ctcttgatga	gccgcttaca	acagcagttc	cttaggancc	caacatgaca	480
ggtgggtcag	atttccctat	gagaaacaaa	actggncacc	tacagcaaaa	tntcaaaatg	540
ggtaaagtc	tccttctctc	tcctctctgat	tatntacaac	atatctcctt	tcaagantat	600
tatttccatc	atgcttattc	cttcccaaat	ctaaaccttg	aagggtgattt	gaagggaaac	660
cnccatccnn	aaaaagaaaa	accttctccc	aaattgaaaa	aaaactnggc	agggtataca	720
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<210> 646

<211> 760

<212> DNA

<213> Homo Sapiens

<400> 646

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tattttttta	aaaagcaaaa	gaataaagaa	tatatataaa	agggacctgg	aatctgtaag	180
gtgattccaa	aaacnaaata	agtagaaaat	ccatggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggctatcat	acaacattca	gtcagctgaa	natggattgg	tagagggtgtg	300
tctatacata	aacttcagtc	atttttgctt	gtgcanaatc	atcccaatct	tcccaanact	360
gaatgggcag	tctgtggct	ttcttccttt	tccatattcc	caacaaggct	acgtgaagtt	420
caactcttga	tgagccgctt	acaacagcag	ttccttagga	gccaacatga	cagggtgggtc	480
aaatttcctt	atganaaaca	aaactggcca	cctacagcaa	aatatcaaaa	tgggtaantc	540
cttccttcct	cttcctcctg	attatataca	acatatctcc	tttcaagact	attattccat	600
catgcttatt	ccttcacaaa	tctaaacctt	gaagtgatat	gaangaaacc	ncctccaga	660
aaagaaaact	cnantcanaa	atgaaaaaaa	ctggcaggta	tncaatacac	cccaaaacnt	720
ctcaatntcc	tggcacanta	caatccattg	ttctgctaca			760

<210> 647

<211> 1041

<212> DNA

<213> Homo Sapiens

<400> 647

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tgataaaaaa	cgagtgaaa	ttccttgcta	ttgggaaaat	cagccaacag	gatgtcaaaa	180
'attaaactgc	gctttccatc	acaatagagg	acgatatgtt	gatggccttt	tcctacctcc	240
gagcaaaaact	gtgttgccca	ctgtgcctga	gtcaccagaa	gaggaagtga	aggctagcca	300
acttttcagtt	cagcagaaca	aattgtctgt	ccagtccaat	ccttcccttc	agctgcggag	360
cgttatgaaa	gtgaaaagtt	ccgaaaatgt	tctagcccc	acgcatccac	cagttgtaat	420
taatgctgca	gatgatgatg	aagatgatga	tgatcagttt	tctgaggag	gtgatgaaac	480
caaaacacct	accctgcaac	caactcctga	agttcacat	ggattacgag	tgacttctgt	540
ccggaacact	gcagtcaata	taaagcaagg	tgaatgtttg	aattttggaa	taaaaactct	600
tgaggaaatt	aagtcaaaga	aaatgaagga	aaaaatctaag	aagcaagggtg	agggttcttc	660
aggagtttcc	aagtctttta	ctccacctg	agcccgttcc	aagtcctgaa	aaagaaaatg	720
tcaggactgt	ggtgaaggac	agtaactctc	tccaacaaac	aanggagaaa	gaanccttgg	780
gtagattgag	tctactgan	agacggggga	aacgaaaant	tcagcaagcg	gtgacaagtg	840
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actaacattg	acaaaaccac	caaagaaagc	tcaagnttcc	aagtcctcta	agggaaccgan	960
taagcatgtc	aaccggatca	anataatgng	gntgcaacag	ttaaagntta	aaaaattggg	1020
gaaattcagt	taaaacattt	g				1041

<210> 648

<211> 810

<212> DNA

<213> Homo Sapiens

<400> 648

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ttatttttta	aaaaagcaaa	agaataaana	atatatacaa	aagggacctg	naatctgtaa	180
gctgattcca	aaaacnaaat	aantanaaaa	tccatgggtga	aacctgaaca	ttctacctct	240
gctttggana	agggtatca	tacaacattc	antcagctga	aaatggattg	gtaaagggtg	300
gtctatacat	aaacttcant	catttttgct	tgtgcaaaat	catcccaatc	ttcccaaaac	360
tgaatgggca	gtcctgtggc	tttcttcctt	ttccatattc	ccaacaaggc	tacntgaant	420

tcaactcttg	atnagccgct	tacaacagca	gttccttagg	agccaacatg	acaggtgggt	480
caaatttccc	tatgaanaaa	caaaactggc	cacctacagc	aaaatatcaa	aatgggtaag	540
tccttccttc	ctcttctccc	tgattatata	caacatatct	cctttcaaga	ctattatttc	600
catcatgctt	attccttcac	aaatctaaac	cttgagggtga	tatgaaggaa	accancatca	660
agaaaagaaa	accaattcan	aaatgaanaa	aactggcagg	tntacaatac	accccananc	720
atctcaatat	ccctggcaca	gttacaattc	agtgttctgc	tacagcccat	aaaataaata	780
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<210> 649

<211> 656

<212> DNA

<213> Homo Sapiens

<400> 649

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ttatttttta	aaaaancaaa	aaaataaaaa	atatntacaa	aaggggacctg	aaatctgtaa	180
nctnatncca	aaaacaaaaat	aattaaaaaa	tccatggtna	aacctnaacn	tnctacctct	240
gcttnggaaa	agggctatca	tacaacntnc	antcanctna	aaatggatng	gtaaaggtn	300
ntctatacat	aaacttcant	cattttngct	tgtgcaaaat	cancccaatc	tncccaaaac	360
tnaatgggca	ntcctgtggc	ttntctnctt	tnccatatnc	ccaacaaggc	tacttnaatt	420
tcaactcttn	ataancgct	tacaacagca	ntnccttagn	anccaacatn	acaggtgggt	480
caaattcccc	tataaaaaac	aaaactggcc	ncctacanca	aaatatcaaa	atgggtaatt	540
ccttcctncc	tctnccnctt	nattatatac	aacattttct	ctttcaaaac	tattattncc	600
atcatgcttn	ttcctncaca	aatctaaacc	ttgangtgat	ttgaaggaac	cacctc	656

<210> 650

<211> 645

<212> DNA

<213> Homo Sapiens

<400> 650

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ncaaanatt	tttttaaaaa	acaaaaaaa	taaaaaatnt	ttccaaangg	gacctgaaan	180
ctntaaccta	atcccaaaaa	caaaataatt	aaaaannccn	nggtnaancc	tnaacntnct	240
ncnctnctt	tgnaaaaggg	ctatcanaca	acntncattc	ncctaaaaat	gnatnggtaa	300
aggtttttct	anacataaac	ttcattcatt	ttggcttntn	caaaancacc	ccaanctncc	360
caaaactnaa	tgggcnnctt	ntggcttntc	ccctttccca	tnncccaac	aaggctactt	420
naattncaac	ncttnataac	ccccttaca	caccattncc	ttagnaccaa	cataacaggt	480
gggtcaaatt	ncccnataaa	aaacaaanct	ggcccctncc	ccaaaatncc	caaagtggta	540
ttcctnctn	ccctcccccc	ngnatatata	caacatntcc	cctttcanaa	atatattccc	600
ccacgcttat	tcncccaaaa	nntaancctt	gaagttattt	aagga		645

<210> 651

<211> 780

<212> DNA

<213> Homo Sapiens

<400> 651

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cacgccatat	gtatgcagaa	cacttaacag	aattatgcta	tgttgtctgt	ttttgtttgt	180
atttcttgtc	cttgctgaag	attgacttga	aatcttaaac	taagttctcc	ctctttatag	240
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aagttggtga	gatccatgtg	aagacattag	aagaaattct	tcttgaaaga	gccagtcaga	480
aacgtggaga	attgcaaaact	aaactcaaga	cagaaggacc	ttcaaaaact	gatgattcta	540
cttcaggagc	aagaagctcc	tccactatcc	gtatcaaaac	cttctctgag	gtcctggctg	600
aaaaaaaaaca	tcngcagcag	ggaactgaag	agacaaaaaa	gccnaaagga	tacaacttgc	660
atcaagctaa	agattgatag	tgaatttaaa	aaaaacagta	atthttngcca	cccattgttg	720
ccngcagaag	acaatcanaa	gaacctgcag	gtaaaacaaa	ntctatgcag	ggaggtgccc	780

<210> 652

<211> 518

<212> DNA

<213> Homo Sapiens

<400> 652

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acaaaattat	tttttaaaaa	ancaaaaaaa	taaaaaatnt	ttncaaangg	gacctgaaat	180
ctntaanctn	atnccaaaaa	caaaataatt	naaaaaatcca	nggtgaaacc	tnaactnct	240
nccnctgctt	tggaaaaggg	ctntcataca	acnttcattc	ncctaaaaat	ggattggtaa	300
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caaaaactnaa	tgggcantcc	tntggcttcc	tncctttccc	anatncccaa	caaggctact	420
tnaatttcaa	cncttnataa	nccgcttaca	acancatttc	cttaggancc	aacatnacgg	480
tgggtcaaat	cccctataaa	aaacaaaact	ggccnctt			518

<210> 653

<211> 490

<212> DNA

<213> Homo Sapiens

<400> 653

gttaataaag	ttgggtgagat	ccatgtgaag	acattagaag	aaattcttct	tgaaagagcc	60
agtcagaaac	gtggagaatt	gcaaaactaaa	ctcaagacag	aaggaccttc	aaaaactgat	120
gattctactt	caggagcaag	aagctcctcc	actatccgta	tcaaaacctt	ctctgagggtc	180
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gcacatcaag	acgctggaag	aaattaaact	ggagaaggca	ctgagggtgc	agcagagctc	420
tgagagcagc	accagctccc	cgtctcaaca	cnaggccact	ccaagggcaa	ggcggctgct	480
gcnaatcccc						490

<210> 654

<211> 359

<212> DNA

<213> Homo Sapiens

<400> 654

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tccaattatn	ncgaacncca	aaccttnaan	natnccaatt	ncttaaatnt	taaaccaaat	120
tnntttttta	aaaagccaaa	naattaagaa	ttttttccaa	agggaaacng	aatccnttag	180
ggtaatccca	aaaccaaatt	agttaaaaat	ccctggntaa	accnaacnt	tcnccnccn	240
ccttggaaaa	agggnnnccn	ncnaccttcc	atnccnntaa	aaatgaatgg	ntaaagnntt	300
ttcnncctt	aacntccatc	ctttttgnct	nttccaaanc	ctccccance	tccccaaaa	359

<210> 655

<211> 611
 <212> DNA
 <213> Homo Sapiens

<400> 655
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 cancagagga caatcanagg agcctgcagg taaaannaag tctatgcagg aggtgcacat 180
 caagacgctg gaagaaatta aactggagaa ggcactgagg gtgcagcana gctctgagag 240
 cagcaccagc tccccgtctc aacacnaagc cactccatgg gcnangcggc tgctgcgant 300
 cncnnaaga ncagggatga angaagagaa gaaccttcag gaaggaaatg aatttgattc 360
 tcagancatt attataactg aagctnnana ngcttcnggt gagaccacng ganttgacat 420
 cactaaaatt ccagtcaaga gatgtgagac catgagagag aagcacatgc aaaaaacanc 480
 nngagagggg aaaatcagtc ttgacacctc ttccggggaga tgtagcatct tgcggnaccc 540
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 ggcttccac a 611

<210> 656
 <211> 634
 <212> DNA
 <213> Homo Sapiens

<400> 656
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 tatttttttaa aaancnaaa naataaagaa tatntncaaa agggacctgg aatctgttag 180
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 caactcttga nnanccgctt acaacagcag ttcccttagga nccccatgac aggtgggtcn 480
 aatttcccta tnaaaaacaa aactgggccc tacagcaaaa tatccaaatg ggtnagtctt 540
 tcttctctct tccccgtant atatacacat atctccttcc aanaatanta tttccccatg 600
 cttattcctt ccnaatcta aaccttgaag tgat 634

<210> 657
 <211> 958
 <212> DNA
 <213> Homo Sapiens

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 aggcagtgtc catcaagata ctgctgaaaa gaatgcatct tccccagaga aagccaaggg 180
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 ccaggtcacc aatcagttg acttccactt ccgcacagat gagcgaatca aacaacatcc 420
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 cctgttacc tccaaatctt ctgtgaccaa gatttgagga gaccacagc actcctgtac 720
 tgcaaacaa acaccgtgca cgggctgtga cctgcaaaaa gtacagcaga gctggaggct 780
 gaggagctnc gagaaattgc aaccantaca anttccaaag cacgtngaac cttgattccc 840

agaataactt ganggggtggg cccaaccttg cccaagaaaa ccaccngtga aancaancca 900
acggagccct antnggcttt gatttgggaa tttgggaaan gaatncaagg gagngag 958

<210> 658

<211> 816

<212> DNA

<213> Homo Sapiens

<400> 658
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gcctgctgcy tggctgctgt gaggtctccc atgaatccac gcagtcttct tctcactgg 180
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cctaggtttg aagttaaaaa caggtcccaa ttgcccgggc ggtatccgcc agctcacagc 720
tgaatttaan catggaaatc caatggaaaa attggganat acnggcacat tcanaaggct 780
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<210> 659

<211> 726

<212> DNA

<213> Homo Sapiens

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cttgatgat gaaggagata ctcaaaacat agattcatgg tttgaggaga aggccaat 180
ggagaataag ttactgggga agaatggaac tggagggcct tttcagggca aaactcctt 240
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agccaagaga tgtgccactc ctgtaatcat cgatgaaatt ctaccctcta agaaaatgaa 540
agtttctaac ancacaaaga agccagagga agaaggcagt gctcatcaag atactgctga 600
aaagaatgca tcttcccaa gagaaagcca agggtagaca tactgtgcct tgtatgccac 660
ctgcanagca gaagttna aaangtactg angagcaang aatctggaga agagtatgaa 720
aatgc 726

<210> 660

<211> 824

<212> DNA

<213> Homo Sapiens

<400> 660
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<210> 661

<211> 399

<212> DNA

<213> Homo Sapiens

<400> 661

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<210> 662

<211> 826

<212> DNA

<213> Homo Sapiens

<400> 662

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<210> 663

<211> 770

<212> DNA

<213> Homo Sapiens

<400> 663

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gttggtgagg	ttttctaccc	tcacagcaaa	gggatcctta	actataaatt	cacggtatgc	240

anagaanagg	acagaatctg	atttactgat	tgttcctcat	ttaaaccatg	acttaatctc	300
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ggtgagagtc	gtaaggggca	atagcaatag	agattacact	gtgctgacac	agagactaaa	420
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<210> 664

<211> 593

<212> DNA

<213> Homo Sapiens

<400> 664

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<210> 665

<211> 1024

<212> DNA

<213> Homo Sapiens

<400> 665

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<210> 666

<211> 734

<212> DNA

<213> Homo Sapiens

<400> 666

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<210> 667

<211> 592

<212> DNA

<213> Homo Sapiens

<400> 667

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ggtggaanaa gcccaanaa tacacgtgag gcagttggct gagatgcacg ctacagtcag      540
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<210> 668

<211> 373

<212> DNA

<213> Homo Sapiens

<400> 668

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gtttttgtnt atagtaaacc anaanatgtg tntggaccct gttatggnc aagcatctcaa      180
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acaaagtaaa aatttttaaa cttgactcta actagtctct ttttgtttta cattctcaaa      300
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<210> 669

<211> 661

<212> DNA

<213> Homo Sapiens

<400> 669

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<210> 670

<211> 401

<212> DNA

<213> Homo Sapiens

<400> 670

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<210> 671

<211> 1347

<212> DNA

<213> Homo Sapiens

<400> 671

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<210> 672
 <211> 3441
 <212> DNA
 <213> Homo Sapiens

<400> 672

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<211> 1016

<212> DNA

<213> Homo Sapiens

<400> 673

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<210> 674

<211> 1135

<212> DNA

<213> Homo Sapiens

<400> 674

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 <211> 1067
 <212> DNA
 <213> Homo Sapiens

<400> 675	
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<210> 676
 <211> 784
 <212> DNA
 <213> Homo Sapiens

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<210> 677
 <211> 1362
 <212> DNA
 <213> Homo Sapiens

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<210> 678
 <211> 1771
 <212> DNA
 <213> Homo Sapiens

<400> 678
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<210> 679

<211> 1367

<212> DNA

<213> Homo Sapiens

<400> 679

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<210> 680

<211> 2545

<212> DNA

<213> Homo Sapiens

<400> 680

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<210> 681

<211> 1745

<212> DNA

<213> Homo Sapiens

<400> 681

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<210> 682

<211> 1745

<212> DNA

<213> Homo Sapiens

<400> 682

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<210> 683

<211> 3127

<212> DNA

<213> Homo Sapiens

<400> 683						
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attaccc						3127

<210> 684
 <211> 803
 <212> PRT
 <213> Homo Sapiens

<400> 684
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 Lys Ala Thr Ile Pro Glu Val Lys Asn Ser Glu Asn Ser Ser Ser Arg
 35 40 45
 Gln Val Ser Ala Asn Asn Gln Phe Ser Ile Thr Lys Asn Arg Asp Gly
 50 55 60
 Arg Glu Asn Arg Arg Arg Asn Ser Lys Ile Gly Asp Asp Asn Glu Asn
 65 70 75 80
 Leu Thr Phe Lys Leu Glu Val Asn Glu Leu Ser Gly Lys Leu Asp Asn
 85 90 95
 Thr Asn Glu Tyr Asn Ser Asn Asp Gly Lys Lys Leu Pro Gln Gly Glu
 100 105 110
 Ser Arg Ser Tyr Glu Val Met Gly Ser Met Glu Glu Thr Leu Cys Asn
 115 120 125
 Ile Asp Asp Arg Asp Gly Asn Arg Asn Val His Leu Glu Phe Thr Glu
 130 135 140
 Arg Glu Ser Arg Lys Asp Gly Glu Asp Glu Phe Val Lys Glu Met Arg
 145 150 155 160
 Glu Glu Arg Lys Phe Gln Lys Leu Lys Asn Lys Glu Glu Val Leu Lys
 165 170 175
 Ala Ser Arg Glu Glu Lys Val Leu Met Asp Glu Gly Ala Val Leu Thr
 180 185 190
 Leu Ala Ala Asp Leu Ser Ser Ala Thr Leu Asp Ile Ser Lys Gln Trp
 195 200 205
 Ser Asn Val Phe Asn Ile Leu Arg Glu Asn Asp Phe Glu Pro Lys Phe
 210 215 220
 Leu Cys Glu Val Lys Leu Ala Phe Lys Cys Asp Gly Glu Ile Lys Thr
 225 230 235 240
 Phe Ser Asp Leu Gln Ser Leu Arg Lys Phe Ala Ser Gln Lys Ser Ser
 245 250 255
 Met Xaa Xaa Leu Leu Xaa Asp Val Leu Pro Gln Lys Glu Glu Ile Asn
 260 265 270
 Gln Gly Gly Arg Lys Tyr Gly Ile Gln Glu Lys Arg Asp Lys Thr Leu
 275 280 285
 Ile Asp Ser Xaa His Arg Ala Gly Glu Ile Thr Ser Asp Gly Leu Ser
 290 295 300
 Phe Leu Phe Leu Lys Glu Val Lys Val Ala Lys Pro Glu Glu Met Lys
 305 310 315 320
 Asn Leu Glu Thr Gln Glu Glu Glu Phe Ser Glu Leu Glu Glu Leu Asp
 325 330 335
 Glu Glu Ala Ser Gly Met Glu Asp Asp Glu Asp Thr Ser Gly Leu Glu
 340 345 350
 Glu Glu Glu Glu Glu Glu Ala Ser Gly Leu Glu Glu Asp Xaa Ser Ser
 355 360 365
 Xaa Leu Glu Glu Glu Glu Glu Gln Thr Ser Glu Gln Asp Ser Thr Phe
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 Xaa Gly His Thr Leu Val Asp Ala Lys His Glu Val Glu Ile Thr Ser

<210> 685

<211> 947
 <212> PRT
 <213> Homo Sapiens

<400> 685
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 Gln Tyr Leu Gln Lys Val Val Leu Lys Asp Leu Trp Lys His Ser Phe
 35 40 45
 Ser Trp Pro Phe Gln Arg Pro Val Asp Ala Val Lys Leu Lys Leu Pro
 50 55 60
 Asp Tyr Tyr Thr Ile Ile Lys Asn Pro Met Asp Leu Asn Thr Ile Lys
 65 70 75 80
 Lys Arg Leu Glu Asn Lys Tyr Tyr Ala Lys Ala Ser Glu Cys Ile Glu
 85 90 95
 Asp Phe Asn Thr Met Phe Ser Asn Cys Tyr Leu Tyr Asn Lys Pro Gly
 100 105 110
 Asp Asp Ile Val Leu Met Ala Gln Ala Leu Glu Lys Leu Phe Met Gln
 115 120 125
 Lys Leu Ser Gln Met Pro Gln Glu Glu Gln Val Val Gly Val Lys Glu
 130 135 140
 Arg Ile Lys Lys Gly Thr Gln Gln Asn Ile Ala Val Ser Ser Ala Lys
 145 150 155 160
 Glu Lys Ser Ser Pro Ser Ala Thr Glu Lys Val Phe Lys Gln Gln Glu
 165 170 175
 Ile Pro Ser Val Phe Pro Lys Thr Ser Ile Ser Pro Leu Asn Val Val
 180 185 190
 Gln Gly Ala Ser Val Asn Ser Ser Ser Gln Thr Ala Ala Gln Val Thr
 195 200 205
 Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr Pro Ala Thr Ser Ala
 210 215 220
 Val Lys Ala Ser Ser Glu Phe Ser Pro Thr Phe Thr Glu Lys Ser Val
 225 230 235 240
 Ala Leu Pro Pro Ile Lys Glu Asn Met Pro Lys Asn Val Leu Pro Asp
 245 250 255
 Ser Gln Gln Gln Tyr Asn Val Val Glu Thr Val Lys Val Thr Glu Gln
 260 265 270
 Leu Arg His Cys Ser Glu Ile Leu Lys Glu Met Leu Ala Lys Lys His
 275 280 285
 Phe Ser Tyr Ala Trp Pro Phe Tyr Asn Pro Val Asp Val Asn Ala Leu
 290 295 300
 Gly Leu His Asn Tyr Tyr Asp Val Val Lys Asn Pro Met Asp Leu Gly
 305 310 315 320
 Thr Ile Lys Glu Lys Met Asp Asn Gln Glu Tyr Lys Asp Ala Tyr Ser
 325 330 335
 Phe Ala Ala Asp Val Arg Leu Met Phe Met Asn Cys Tyr Lys Tyr Asn
 340 345 350
 Pro Pro Asp His Glu Val Val Thr Met Ala Arg Met Leu Gln Asp Val
 355 360 365
 Phe Glu Thr His Phe Ser Lys Ile Pro Ile Glu Pro Val Glu Ser Met
 370 375 380
 Pro Leu Cys Tyr Ile Lys Thr Asp Ile Thr Glu Thr Thr Gly Arg Glu
 385 390 395 400

Asn Thr Asn Glu Ala Ser Ser Glu Gly Asn Ser Ser Asp Asp Ser Glu
 405 410 415
 Asp Glu Arg Val Lys Arg Leu Ala Lys Leu Gln Glu Gln Leu Lys Ala
 420 425 430
 Val His Gln Gln Leu Gln Val Leu Ser Gln Val Pro Phe Arg Lys Leu
 435 440 445
 Asn Lys Lys Lys Glu Lys Ser Lys Lys Glu Lys Lys Lys Glu Lys Val
 450 455 460
 Asn Asn Ser Asn Glu Asn Pro Arg Lys Met Cys Glu Gln Met Arg Leu
 465 470 475 480
 Lys Glu Lys Ser Lys Arg Asn Gln Pro Lys Lys Arg Lys Gln Gln Phe
 485 490 495
 Ile Gly Leu Lys Ser Glu Asp Glu Asp Asn Ala Lys Pro Met Asn Tyr
 500 505 510
 Asp Glu Lys Arg Gln Leu Ser Leu Asn Ile Asn Lys Leu Pro Gly Asp
 515 520 525
 Lys Leu Gly Arg Val Val His Ile Ile Gln Ser Arg Glu Pro Ser Leu
 530 535 540
 Ser Asn Ser Asn Pro Asp Glu Ile Glu Ile Asp Phe Glu Thr Leu Lys
 545 550 555 560
 Ala Ser Thr Leu Arg Glu Leu Glu Lys Tyr Val Ser Ala Cys Leu Arg
 565 570 575
 Lys Arg Pro Leu Lys Pro Pro Ala Lys Lys Ile Met Met Ser Lys Glu
 580 585 590
 Glu Leu His Ser Gln Lys Lys Gln Glu Leu Glu Lys Arg Leu Leu Asp
 595 600 605
 Val Asn Asn Gln Leu Asn Ser Arg Lys Arg Gln Thr Lys Ser Asp Lys
 610 615 620
 Thr Gln Pro Ser Lys Ala Val Glu Asn Val Ser Arg Leu Ser Glu Ser
 625 630 635 640
 Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Glu Ser Ser Ser Ser Asp
 645 650 655
 Leu Ser Ser Ser Asp Ser Ser Asp Ser Glu Ser Glu Met Phe Pro Lys
 660 665 670
 Phe Thr Glu Val Lys Pro Asn Asp Ser Pro Ser Lys Glu His Val Lys
 675 680 685
 Lys Met Lys Asn Glu Cys Ile Leu Pro Glu Gly Arg Thr Gly Val Thr
 690 695 700
 Gln Ile Gly Tyr Cys Val Gln Asp Thr Thr Ser Ala Asn Thr Thr Leu
 705 710 715 720
 Val His Gln Thr Thr Pro Ser His Val Met Pro Pro Asn His His Gln
 725 730 735
 Leu Ala Phe Asn Tyr Gln Glu Leu Glu His Leu Gln Thr Val Lys Asn
 740 745 750
 Ile Ser Pro Leu Gln Ile Leu Pro Pro Ser Gly Asp Ser Glu Gln Leu
 755 760 765
 Ser Asn Gly Ile Thr Val Met His Pro Ser Gly Asp Ser Asp Thr Thr
 770 775 780
 Met Leu Glu Ser Glu Cys Gln Ala Pro Val Gln Lys Asp Ile Lys Ile
 785 790 795 800
 Lys Asn Ala Asp Ser Trp Lys Ser Leu Gly Lys Pro Val Lys Pro Ser
 805 810 815
 Gly Val Met Lys Ser Ser Asp Glu Leu Phe Asn Gln Phe Arg Lys Ala
 820 825 830
 Ala Ile Glu Lys Glu Val Lys Ala Arg Thr Gln Glu Leu Ile Arg Lys

835 840 845
 His Leu Glu Gln Asn Thr Lys Glu Leu Lys Ala Ser Gln Glu Asn Gln
 850 855 860
 Arg Asp Leu Gly Asn Gly Leu Thr Val Glu Ser Phe Ser Asn Lys Ile
 865 870 875 880
 Gln Asn Lys Cys Ser Gly Glu Glu Gln Lys Glu His Pro Gln Ser Ser
 885 890 895
 Glu Ala Gln Asp Lys Ser Lys Leu Trp Leu Leu Lys Asp Arg Asp Leu
 900 905 910
 Ala Arg Pro Lys Glu Gln Glu Arg Arg Arg Arg Glu Ala Met Val Gly
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<210> 686
 <211> 3106
 <212> DNA
 <213> Homo Sapiens

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actttgatta	aaactcagtt	tttaaatata	ccatccactt	aaaatgaatg	gtaaaagatc	3000
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<210> 687

<211> 1759

<212> DNA

<213> Homo Sapiens

<400> 687

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caggccaggc	ttcaagacca	tcctgggcaa	catagccaga	ctaccatcta	taccaggggt	1380
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1759

<210> 688
 <211> 207
 <212> PRT
 <213> Homo Sapiens

<400> 688
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 Met Glu Lys Leu Pro Thr Lys Lys Arg Gly Arg Lys Pro Ala Gly Leu
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 Ile Ser Ala Ser Arg Lys Val Pro Asn Leu Ser Val Ser Lys Leu Ile
 35 40 45
 Thr Glu Ala Leu Ser Val Ser Gln Glu Arg Val Gly Met Ser Leu Val
 50 55 60
 Ala Leu Lys Lys Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys Asn
 65 70 75 80
 Asn Ser Arg Ile Lys Leu Ser Leu Lys Ser Leu Val Asn Lys Gly Ile
 85 90 95
 Leu Val Gln Thr Arg Gly Thr Gly Ala Ser Gly Ser Phe Lys Leu Ser
 100 105 110
 Lys Lys Val Ile Pro Lys Ser Thr Arg Ser Lys Ala Lys Lys Ser Val
 115 120 125
 Ser Ala Lys Thr Lys Lys Leu Val Leu Ser Arg Asp Ser Lys Ser Pro
 130 135 140
 Lys Thr Ala Lys Thr Asn Lys Arg Ala Lys Lys Pro Arg Ala Thr Thr
 145 150 155 160
 Pro Lys Thr Val Arg Ser Gly Arg Lys Ala Lys Gly Ala Lys Gly Lys
 165 170 175
 Gln Gln Gln Lys Ser Pro Val Lys Ala Arg Ala Ser Lys Ser Lys Leu
 180 185 190
 Thr Gln His His Glu Val Asn Val Arg Lys Ala Thr Ser Lys Lys
 195 200 205

<210> 689
 <211> 1464
 <212> DNA
 <213> Homo Sapiens

<400> 689
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 aaggaagaat ttcctctgaa gcaccggaac ttgctactac cagcaccatg ccctaccaat 180
 atccagcact gaccccgag cagaagaagg agctgtctga catcgctcac cgcacgtgg 240
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 agtccattgg caccgagaac accgaggaga accggcgctt ctaccgccag ctgctgtgta 360
 cagctgacga ccgcgtgaac ccctgcattg ggggtgtcat cctcttccat gagacactct 420
 accagaaggc ggatgatggg cgtcccttcc cccaagttat caaatccaag ggcggtgttg 480
 tgggcatcaa ggtagacaag ggcgtgggtcc ccctggcagg gacaaatggc gagactacca 540
 cccaaggggt ggatgggctg tctgagcgct gtgcccagta caagaaggac ggagctgact 600
 tcgccaagtg gcgttgtgtg ctgaagattg gggaacacac cccctcagcc ctgcctatca 660
 tggaaaatgc caatgttctg gcccgttatg ccagtatctg ccagcagaat ggcattgtgc 720
 ccacgtgga gcctgagatc ctccctgatg gggaccatga cttgaagcgc tgccagtatg 780
 tgaccgagaa ggtgctggct gctgtctaca aggctctgag tgaccaccac atctacctgg 840

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atgccattaa caagtgcccc ctgctgaagc cctggggcct gaccttctcc tacggccgag 1080
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aagaggaggc cgctctctcg gggctccagg ctggcttgcc cgcgctcttt cttccctcgt 1380
gacagtgggt tgtgggtgct tctgtgaatg ctaagtccat caccctttcc ggcacactgc 1440
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<210> 690

<211> 363

<212> PRT

<213> Homo Sapiens

<400> 690

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Pro Tyr Gln Tyr Pro Ala Leu Thr Pro Glu Gln Lys Lys Glu Leu Ser
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Asp Ile Ala His Arg Ile Val Ala Pro Gly Lys Gly Ile Leu Ala Ala
          20           25           30
Asp Glu Ser Thr Gly Ser Ile Ala Lys Arg Leu Gln Ser Ile Gly Thr
          35           40           45
Glu Asn Thr Glu Glu Asn Arg Phe Tyr Arg Gln Leu Leu Leu Thr
          50           55           60
Ala Asp Asp Arg Val Asn Pro Cys Ile Gly Gly Val Ile Leu Phe His
          65           70           75           80
Glu Thr Leu Tyr Gln Lys Ala Asp Asp Gly Arg Pro Phe Pro Gln Val
          85           90           95
Ile Lys Ser Lys Gly Gly Val Val Gly Ile Lys Val Asp Lys Gly Val
          100          105          110
Val Pro Leu Ala Gly Thr Asn Gly Glu Thr Thr Thr Gln Gly Leu Asp
          115          120          125
Gly Leu Ser Glu Arg Cys Ala Gln Tyr Lys Lys Asp Gly Ala Asp Phe
          130          135          140
Ala Lys Trp Arg Cys Val Leu Lys Ile Gly Glu His Thr Pro Ser Ala
          145          150          155          160
Leu Ala Ile Met Glu Asn Ala Asn Val Leu Ala Arg Tyr Ala Ser Ile
          165          170          175
Cys Gln Gln Asn Gly Ile Val Pro Ile Val Glu Pro Glu Ile Leu Pro
          180          185          190
Asp Gly Asp His Asp Leu Lys Arg Cys Gln Tyr Val Thr Glu Lys Val
          195          200          205
Leu Ala Ala Val Tyr Lys Ala Leu Ser Asp His His Ile Tyr Leu Glu
          210          215          220
Gly Thr Leu Leu Lys Pro Asn Met Val Thr Pro Gly His Ala Cys Thr
          225          230          235          240
Gln Lys Phe Ser His Glu Glu Ile Ala Met Ala Thr Val Thr Ala Leu
          245          250          255
Arg Arg Thr Val Pro Pro Ala Val Thr Gly Ile Thr Phe Leu Ser Gly
          260          265          270
Gly Gln Ser Glu Glu Glu Ala Ser Ile Asn Leu Asn Ala Ile Asn Lys
          275          280          285
Cys Pro Leu Leu Lys Pro Trp Ala Leu Thr Phe Ser Tyr Gly Arg Ala

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290 295 300
 Leu Gln Ala Ser Ala Leu Lys Ala Trp Gly Gly Lys Lys Glu Asn Leu
 305 310 315 320
 Lys Ala Ala Gln Glu Glu Tyr Val Lys Arg Ala Leu Ala Asn Ser Leu
 325 330 335
 Ala Cys Gln Gly Lys Tyr Thr Pro Ser Gly Gln Ala Gly Ala Ala Ala
 340 345 350
 Ser Glu Ser Leu Phe Val Ser Asn His Ala Tyr
 355 360

<210> 691
 <211> 1216
 <212> DNA
 <213> Homo Sapiens

<400> 691
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 cacaacatct cagatgcttt tgaccagaag ttctcaaagg tgcctacca ggtcaaaggc 240
 tatgacaacc tctttgctat ggagattgac cccagcctgg gcgtggcgga cgtgcctgac 300
 gagttcttcg aggaggacaa catgctgagc atgggcaaga agatgatgca ggaggccatg 360
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 atcagccctt tcatctcaca gatgtgcaac atgctggggc tgggggacat gaacgcagac 600
 cagctggcct ccaagctgga ggagacgctg cccgtcatcc gctcagtcag cgaacagttc 660
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 gagacagaga ggtgatcca ggagctgccc aagtgcgaaga ttgacacaca caatataatt 780
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 aagctgcccg tgttacccca tgaggtgccc ggggcagaca aggtcaacac cttctcggcc 960
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 ctgccatttc aactcacc cccaccctcc ccacccctc ggggcagagt ttgcacaaag 1080
 tcccccccat aatacagggg gagccacttg ggcaggaggc agggaggggg ccatccccc 1140
 tgggtgggct ggtggggagc tgtagttgcc ccctacctct cccacctctt gctcttcaat 1200
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<210> 692
 <211> 1958
 <212> DNA
 <213> Homo Sapiens

<400> 692
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 cgtggccacc tatgcggggc agttcaacca ggactatctc tcgggaatgg cggccaacat 360
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 tccctatggg atgtatccac cccagagg aaacccaccc tcaggatgc cctcatatcc 540
 gccataacca gggggccctg tgccgggcca gccatgcca cccccggac agcagccccc 600
 aggggcctac cctgggcagc caccagtgc ctaccctggt cagcctccag tgccactccc 660

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tcaccgtcct agagcttagg cctgtcttcc acccctctg acccgtatag tgtgccacag 1860
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ttgctgctaa aatagatggt tcatttttct gaaaaaaaa 1958

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<210> 693

<211> 505

<212> PRT

<213> Homo Sapiens

<400> 693

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Met Ser Tyr Pro Gly Tyr Pro Pro Pro Pro Gly Gly Tyr Pro Pro Ala
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Ala Pro Gly Gly Gly Pro Trp Gly Gly Ala Ala Tyr Pro Pro Pro Pro
          20          25          30
Ser Met Pro Pro Ile Gly Leu Asp Asn Val Ala Thr Tyr Ala Gly Gln
  35          40          45
Phe Asn Gln Asp Tyr Leu Ser Gly Met Ala Ala Asn Met Ser Gly Thr
  50          55          60
Phe Gly Gly Ala Asn Met Pro Asn Leu Tyr Pro Gly Ala Pro Gly Ala
  65          70          75          80
Gly Tyr Pro Pro Val Pro Pro Gly Gly Phe Gly Gln Pro Pro Ser Ala
          85          90          95
Gln Gln Pro Val Pro Pro Tyr Gly Met Tyr Pro Pro Pro Gly Gly Asn
          100          105          110
Pro Pro Ser Arg Met Pro Ser Tyr Pro Pro Tyr Pro Gly Ala Pro Val
          115          120          125
Pro Gly Gln Pro Met Pro Pro Gly Gln Gln Pro Pro Gly Ala Tyr
          130          135          140
Pro Gly Gln Pro Pro Val Thr Tyr Pro Gly Gln Pro Pro Val Pro Leu
          145          150          155          160
Pro Gly Gln Gln Gln Pro Val Pro Ser Tyr Pro Gly Tyr Pro Gly Ser
          165          170          175
Gly Thr Val Thr Pro Ala Val Pro Pro Thr Gln Phe Gly Ser Arg Gly
          180          185          190
Thr Ile Thr Asp Ala Pro Gly Phe Asp Pro Leu Arg Asp Ala Glu Val
          195          200          205

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Leu Arg Lys Ala Met Lys Gly Phe Gly Thr Asp Glu Gln Ala Ile Ile
 210 215 220
 Asp Cys Leu Gly Ser Arg Ser Asn Lys Gln Arg Gln Gln Ile Leu Leu
 225 230 235 240
 Ser Phe Lys Thr Ala Tyr Gly Lys Asp Leu Ile Lys Asp Leu Lys Ser
 245 250 255
 Glu Leu Ser Gly Asn Phe Glu Lys Thr Ile Leu Ala Leu Met Lys Thr
 260 265 270
 Pro Val Leu Phe Asp Ile Tyr Glu Ile Lys Glu Ala Ile Lys Gly Val
 275 280 285
 Gly Thr Asp Glu Ala Cys Leu Ile Glu Ile Leu Ala Ser Arg Ser Asn
 290 295 300
 Glu His Ile Arg Glu Leu Asn Arg Ala Tyr Lys Ala Glu Phe Lys Lys
 305 310 315 320
 Thr Leu Glu Glu Ala Ile Arg Ser Asp Thr Ser Gly His Phe Gln Arg
 325 330 335
 Leu Leu Ile Ser Leu Ser Gln Gly Asn Arg Asp Glu Ser Thr Asn Val
 340 345 350
 Asp Met Ser Leu Ala Gln Arg Asp Ala Gln Glu Leu Tyr Ala Ala Gly
 355 360 365
 Glu Asn Arg Leu Gly Thr Asp Glu Ser Lys Phe Asn Ala Val Leu Cys
 370 375 380
 Ser Arg Ser Arg Ala His Leu Val Ala Val Phe Asn Glu Tyr Gln Arg
 385 390 395 400
 Met Thr Gly Arg Asp Ile Glu Lys Ser Ile Cys Arg Glu Met Ser Gly
 405 410 415
 Asp Leu Glu Glu Gly Met Leu Ala Val Val Lys Cys Leu Lys Asn Thr
 420 425 430
 Pro Ala Phe Phe Ala Glu Arg Leu Asn Lys Ala Met Arg Gly Ala Gly
 435 440 445
 Thr Lys Asp Arg Thr Leu Ile Arg Ile Met Val Ser Arg Ser Glu Thr
 450 455 460
 Asp Leu Leu Asp Ile Arg Ser Glu Tyr Lys Arg Met Tyr Gly Lys Ser
 465 470 475 480
 Leu Tyr His Asp Ile Ser Gly Asp Thr Ser Gly Asp Tyr Arg Lys Ile
 485 490 495
 Leu Leu Lys Ile Cys Gly Gly Asn Asp
 500 505

<210> 694

<211> 1141

<212> DNA

<213> Homo Sapiens

<400> 694

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cctgatgggt	ggaaggaacc	agctttttcc	aaagaggaca	atcccagagg	acttttggag	180
gagagcagtt	tcgcaacttt	gttcccaaaa	tacagggaag	cttacttgaa	agagtgttgg	240
ccattggtgc	agaaagcctt	aaatgaacat	catgttaatg	caaccctgga	cctgatcgaa	300
ggcagcatga	ctgtttgtac	tacaaagaag	acttttgcac	catatatcat	cattagggcc	360
agagatctga	taaaactgtt	agcaaggagt	gtttcatttg	aacaggcagt	acgaattctt	420
caggatgatg	ttgcatgtga	catcattaaa	atagggttctt	tagtaaggaa	taaagagaga	480
tttgtaaaac	gaagacaacg	gcttattggt	cccaaaggat	ctacattgaa	ggcattggaa	540
ctcttaacta	attgttacat	tatggttcag	ggaaacacag	tttcagccat	tggacctttt	600

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agtggccttaa aagagggttag aaaagtagtc cttgatacta tgaagaatat tcatccaatt      660
tataacatta aaagcttaat gattaagaga gagttggcaa aagattctga attacgatca      720
caaagttggg agagattttt gccacagttc aaacacaaaa atgtgaataa acgcaaggaa      780
ccaaagaaaa aaactgttaa gaaagatata cgccattccc accaccacaa ccagaaagtc      840
agatcgataa agaattggct agtgggtgaat actttttgaa ggcaaatcag aagaagcggc      900
agaaaatgaa gcaataaagg ctaaacaagc agaagccatc agtaagagac aagaggaaaag      960
aaacaaagca ttattccac ctaaggaaaa accaattgtg aaacctagg aagcttctac     1020
tgaaactaaa attgatgtgg ccagcatcaa ggaaaagggtt aagaaagcaa agaataagaa     1080
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a                                                                                   1141

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<210> 695

<211> 288

<212> PRT

<213> Homo Sapiens

<400> 695

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Glu Phe Arg Asn Gln Lys Pro Lys Pro Glu Asn Gln Asp Glu Ser Glu
      20              25              30
Leu Leu Thr Val Pro Asp Gly Trp Lys Glu Pro Ala Phe Ser Lys Glu
      35              40              45
Asp Asn Pro Arg Gly Leu Leu Glu Glu Ser Ser Phe Ala Thr Leu Phe
      50              55              60
Pro Lys Tyr Arg Glu Ala Tyr Leu Lys Glu Cys Trp Pro Leu Val Gln
      65              70              75              80
Lys Ala Leu Asn Glu His His Val Asn Ala Thr Leu Asp Leu Ile Glu
      85              90              95
Gly Ser Met Thr Val Cys Thr Thr Lys Lys Thr Phe Asp Pro Tyr Ile
      100             105             110
Ile Ile Arg Ala Arg Asp Leu Ile Lys Leu Leu Ala Arg Ser Val Ser
      115             120             125
Phe Glu Gln Ala Val Arg Ile Leu Gln Asp Asp Val Ala Cys Asp Ile
      130             135             140
Ile Lys Ile Gly Ser Leu Val Arg Asn Lys Glu Arg Phe Val Lys Arg
      145             150             155             160
Arg Gln Arg Leu Ile Gly Pro Lys Gly Ser Thr Leu Lys Ala Leu Glu
      165             170             175
Leu Leu Thr Asn Cys Tyr Ile Met Val Gln Gly Asn Thr Val Ser Ala
      180             185             190
Ile Gly Pro Phe Ser Gly Leu Lys Glu Val Arg Lys Val Val Leu Asp
      195             200             205
Thr Met Lys Asn Ile His Pro Ile Tyr Asn Ile Lys Ser Leu Met Ile
      210             215             220
Lys Arg Glu Leu Ala Lys Asp Ser Glu Leu Arg Ser Gln Ser Trp Glu
      225             230             235             240
Arg Phe Leu Pro Gln Phe Lys His Lys Asn Val Asn Lys Arg Lys Glu
      245             250             255
Pro Lys Lys Lys Thr Val Lys Lys Asp Ile Arg His Ser His His His
      260             265             270
Asn Gln Lys Val Arg Ser Ile Lys Asn Trp Leu Val Val Asn Thr Phe
      275             280             285

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<210> 696

<211> 1008
 <212> DNA
 <213> Homo Sapiens

<400> 696

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aacgtggcag	aggaaaagcc	caagttaaag	caacaaatga	atccgaagac	gaaatccac	180
agctgggtacc	aataggaaaag	aagactccag	ctaataaaaa	agtagagatt	caaaaacatg	240
ccacagggaa	gaagtctcca	gcaaagagtc	ctaataccag	cacacctcgt	gggaagaaaa	300
agaaaggctt	tgccagcatc	tgagacccca	aaagctgcag	agtctgagac	cccagggaaa	360
agcccagaga	agaagcctaa	aatcaaagaa	gaggcagtga	aggaaaaaag	tccttcgctg	420
gggaaaaaag	atgagagaca	gactcccaaa	aaagccagag	gccaaagttt	tcaccattcc	480
tagtaaatct	gtgagaaaaag	cttcccacac	ccccaaaaaa	tggcccaaaa	aaccctaaag	540
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<210> 697
 <211> 685
 <212> DNA
 <213> Homo Sapiens

<400> 697

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agacagccaa	gtaaaaacgg	ctcccaagac	aatctacaag	cactgggagg	atggggtgca	180
gcacaaaaat	gttcacacca	tttgacagag	ggaacagcct	ggccctgct	gttcaggat	240
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 <211> 1205
 <212> DNA
 <213> Homo Sapiens

<400> 698

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<211> 1427

<212> DNA

<213> Homo Sapiens

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<210> 700

<211> 1967

<212> DNA

<213> Homo Sapiens

<400> 700

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<210> 701

<211> 3423

<212> DNA

<213> Homo Sapiens

<400> 701

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<211> 1106

<212> DNA

<213> Homo Sapiens

<400> 702

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<210> 703

<211> 1095

<212> DNA

<213> Homo Sapiens

<400> 703

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<210> 704

<211> 1968

<212> DNA

<213> Homo Sapiens

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<212> DNA

<213> Homo Sapiens

<400> 705

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<210> 708

<211> 1123

<212> PRT

<213> Homo Sapiens

<400> 708

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Pro His Gly Asp Tyr Arg Gly Gly Glu Gly Pro Gly His Asp Phe Arg
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Gly Gly Asp Phe Ser Ser Ser Asp Phe Gln Ser Arg Asp Ser Ser Gln
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Leu Asp Phe Arg Gly Arg Asp Ile His Ser Gly Asp Phe Arg Asp Arg
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Glu Gly Pro Pro Met Asp Tyr Arg Gly Gly Asp Gly Thr Ser Met Asp
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Tyr Arg Gly Arg Glu Ala Pro His Met Asn Tyr Arg Asp Arg Asp Ala
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<400> 709

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<211> 1177

<212> PRT

<213> Homo Sapiens

<400> 710

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Gly Asp Phe Arg Asp Arg Glu Gly Pro Pro Met Asp Tyr Arg Gly Gly
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Asp Gly Thr Ser Met Asp Tyr Arg Gly Arg Glu Ala Pro His Met Asn
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Tyr Arg Asp Arg Asp Ala His Ala Val Asp Phe Arg Gly Arg Asp Ala
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Pro Pro Ser Asp Phe Arg Gly Arg Gly Thr Tyr Asp Leu Asp Phe Arg
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65     70     75     80
His Glu Thr Leu Tyr Gln Lys Ala Asp Asp Gly Arg Pro Phe Pro Gln
85     90     95
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Asp Gly Leu Ser Glu Arg Cys Ala Gln Tyr Lys Lys Asp Gly Ala Asp
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Ala Leu Ala Ile Met Glu Asn Ala Asn Val Leu Ala Arg Tyr Ala Ser
165    170    175
Ile Cys Gln Gln Asn Gly Ile Val Pro Ile Val Glu Pro Glu Ile Leu
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Pro Asp Gly Asp His Asp Leu Lys Arg Cys Gln Tyr Val Thr Glu Lys
195    200    205
Val Leu Ala Ala Val Tyr Lys Ala Leu Ser Asp His His Ile Tyr Leu
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35          40          45
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50          55          60
Thr Gln Phe Asp Val Lys Asn Asp Arg Tyr Ile Val Asn Gly Ser His
65          70          75          80
Glu Ala Asn Lys Leu Gln Asp Met Leu Asp Gly Phe Ile Lys Lys Phe
85          90          95
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Gly Met Leu Asp Thr His His Lys Leu Cys Thr Phe Ile Leu Lys Asn
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gtacagcact gttatttttc aaagatgtgt tgctatcctg aaaattctgt aggttctgtg 2160
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```

<210> 804

<211> 609

<212> PRT

<213> Homo Sapiens

<400> 804

```

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
  1             5             10             15
Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
  20             25             30
His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
  35             40             45
Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
  50             55             60
Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
  65             70             75             80
Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
  85             90             95
Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
 100            105            110
Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
 115            120            125
His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
 130            135            140
Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
 145            150            155            160
Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
 165            170            175
Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
 180            185            190
Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu

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195          200          205
Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
210          215          220
Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225          230          235          240
Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
245          250          255
Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
260          265          270
Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
275          280          285
Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
290          295          300
Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
305          310          315          320
Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
325          330          335
Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
340          345          350
Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
355          360          365
Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
370          375          380
Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
385          390          395          400
Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
405          410          415
Glu Leu Phe Lys Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
420          425          430
Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
435          440          445
Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
450          455          460
Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
465          470          475          480
Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
485          490          495
Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
500          505          510
Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
515          520          525
Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
530          535          540
Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
545          550          555          560
Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
565          570          575
Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
580          585          590
Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
595          600          605
Leu

```

<210> 805

<211> 1356

<212> DNA

<213> Homo Sapiens

<400> 805

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acaacaccca aggagtggag gtcagagtgt cacttttttg ttttcttttt gaaagatcat    60
tcgagaaaca cgtcactgat ctcccctgcg accatgtctt ccattaagat tgagtgtgtt    120
ttgccagaga actgccgggtg tggtagagtct ccagtatggg aggaagtgtc caactctctg    180
ctctttgtag acattcctgc aaaaaagggt tgcgggtggg attcattcac caagcaagta    240
cagcgagtga ccatggatgc cccagtcagc tccgtggctc ttcgccagtc gggaggctat    300
gttgccacca ttggaacaaa gttctgtgct ttgaactgga aagaacaatc agcagttgtc    360
ttggccacgg tggataacga caagaaaaac aatcgcttca atgatgggaa ggtggatccc    420
gccgggaggt actttgctgg caccatggct gaggaacag ctccagcagt tcttgagcgg    480
caccaggggg ccctgtactc cctctttcct gatcaccacg tgaaaaagta ctttgaccag    540
gtggacattt ccaatggttt ggattggctg ctagaccaca aaatcttcta ttacattgac    600
agcctgtcct actccgtgga tgcctttgac tatgacctgc agacaggaca gatctccaac    660
cgcagaagtg tttacaagct agaaaaggaa gaacaaatcc cagatggaat gtgtattgat    720
gctgagggga agctctgggt ggcctgttac aatggaggaa gagtgattcg ttagatcct    780
gtgacaggga aaagacttca aactgtgaag ttgcctgttg ataaaaaac ttcatgctgc    840
tttggaggga agaattactc tgaatgtat gtgacctgcg cccgggatgg gatggacccc    900
gagggtcttt tgaggcaacc tgaagctggt ggaattttca agataactgg tctgggggtc    960
aaaggaattg ctccctactc ctatgcggga tgaggacagg tcttctttcc tgccagaggg   1020
agctctgaag acaactagag aattctgggc ctgaaatttc aatctagtta gaaagaaaaa   1080
tgaggcaatg attttattaa cagcgttaag ttttaattta caacttttaa aaggcagagc   1140
atttttaaca aggggtgaca ggtggttttg ataacacact tataaggctt tctgtaaaag   1200
gtactataga agggcgaaga atcgttcaac tgtcaatcag cctcttgatt ctttgtaa   1260
tgccagggtg ggtgggtaca tatctcttct tgattctgca tttcatactt aactatatta   1320
aagcttcaag gaacaataaa tagtaacctg gtaatg    1356

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<210> 806

<211> 299

<212> PRT

<213> Homo Sapiens

<400> 806

```

Met Ser Ser Ile Lys Ile Glu Cys Val Leu Pro Glu Asn Cys Arg Cys
 1          5          10          15
Gly Glu Ser Pro Val Trp Glu Glu Val Ser Asn Ser Leu Leu Phe Val
 20          25          30
Asp Ile Pro Ala Lys Lys Val Cys Arg Trp Asp Ser Phe Thr Lys Gln
 35          40          45
Val Gln Arg Val Thr Met Asp Ala Pro Val Ser Ser Val Ala Leu Arg
 50          55          60
Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu
 65          70          75          80
Asn Trp Lys Glu Gln Ser Ala Val Val Leu Ala Thr Val Asp Asn Asp
 85          90          95
Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg
100          105          110
Tyr Phe Ala Gly Thr Met Ala Glu Glu Thr Ala Pro Ala Val Leu Glu
115          120          125
Arg His Gln Gly Ala Leu Tyr Ser Leu Phe Pro Asp His His Val Lys
130          135          140
Lys Tyr Phe Asp Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
145          150          155          160

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<210> 807
<211> 1980
<212> DNA
<213> Homo Sapiens
```

-404-

actgaaaaat ttgagagcat gaagagctta ttatcaagcg aagtaaatga gaaggtgaaa 1860
 aaaattggag agacagaaag agagtatgaa aaatcactta ctgaaatcag acagttaagg 1920
 agagagcttg agaattgtaa gcgcctaaact tcctcagcat gtcaagccag aggagcatga 1980

<210> 808
 <211> 659
 <212> PRT
 <213> Homo Sapiens

<400> 808
 Met Pro Ser Ser Leu Leu Leu Ala Thr Arg Asn Gln Ile Leu Ser Met
 1 5 10 15
 Met Asn Cys Trp Phe Ser Cys Ala Pro Lys Asn Arg His Ala Ala Asp
 20 25 30
 Trp Asn Lys Tyr Asp Asp Arg Leu Met Lys Ala Ala Glu Arg Gly Asp
 35 40 45
 Val Glu Lys Val Ser Ser Ile Leu Ala Lys Lys Gly Ile Asn Pro Gly
 50 55 60
 Lys Leu Asp Val Glu Gly Arg Ser Ala Phe His Val Val Ala Ser Lys
 65 70 75 80
 Gly Asn Leu Glu Cys Leu Asn Ala Ile Leu Ile His Gly Val Asp Ile
 85 90 95
 Thr Thr Ser Asp Thr Ala Gly Arg Asn Ala Leu His Leu Ala Ala Lys
 100 105 110
 Tyr Gly His Ala Leu Cys Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro
 115 120 125
 Thr Glu His Ala Asp Leu Gln Gly Arg Thr Ala Leu His Asp Ala Ala
 130 135 140
 Met Ala Asp Cys Pro Ser Ser Ile Gln Leu Leu Cys Asp His Gly Ala
 145 150 155 160
 Ser Val Asn Ala Lys Asp Val Asp Gly Arg Thr Pro Leu Val Leu Ala
 165 170 175
 Thr Gln Met Cys Arg Pro Ala Ile Cys Gln Leu Leu Ile Asp Arg Gly
 180 185 190
 Ala Glu Ile Asn Ser Arg Asp Lys Gln Asn Arg Thr Ala Leu Met Leu
 195 200 205
 Gly Cys Glu Tyr Gly Cys Lys Asp Ala Val Glu Val Leu Leu Lys Asn
 210 215 220
 Gly Ala Asp Val Ser Leu Leu Asp Ala Leu Gly His Asp Ser Ser Tyr
 225 230 235 240
 Tyr Ala Arg Ile Gly Asp Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr
 245 250 255
 Ala Ser Glu Asn Thr Asn Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro
 260 265 270
 Ser Leu Gln Gln Arg Asn Leu Pro Tyr Met Leu Asp Glu Val Asn Val
 275 280 285
 Lys Ser Ser Gln Arg Glu His Arg Asn Ile Gln Glu Leu Glu Ile Glu
 290 295 300
 Asn Glu Asp Leu Lys Asp Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg
 305 310 315 320
 Ile Leu Leu Asp Lys Val Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu
 325 330 335
 Val Met Val Ala Asp Asp Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser
 340 345 350
 Leu Leu Val Ala Lys Glu Lys Gln His Glu Glu Ser Leu Arg Thr Ile

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      355              360              365
Glu Ser Leu Lys Asn Arg Phe Lys Tyr Phe Glu Cys Thr Ser Pro Gly
 370              375              380
Val Pro Ala His Met Gln Ser Arg Ser Met Leu Arg Pro Leu Glu Leu
 385              390              395              400
Ser Leu Pro Asn Gln Thr Ser Tyr Ser Glu Asn Asp Leu Leu Lys Lys
      405              410              415
Glu Leu Glu Ala Met Arg Thr Phe Cys Glu Ser Ala Lys Gln Asp Arg
      420              425              430
Leu Lys Leu Gln Asn Gly Val Ala His Lys Val Ala Glu Cys Lys Ala
      435              440              445
Leu Gly Leu Glu Cys Glu Arg Ile Lys Glu Asp Ser Asp Glu Gln Ile
      450              455              460
Lys Gln Leu Glu Asp Ala Leu Lys Asp Val Gln Lys Arg Met Tyr Glu
 465              470              475              480
Ser Glu Gly Lys Val Lys Gln Met Gln Thr His Phe Leu Ala Leu Lys
      485              490              495
Glu His Leu Thr Ser Glu Ala Ala Ile Gly Asn His Arg Leu Met Glu
      500              505              510
Glu Leu Lys Asp Gln Leu Lys Asp Met Lys Ala Lys Tyr Glu Gly Ala
      515              520              525
Ser Ala Glu Val Gly Lys Leu Arg Asn Gln Ile Lys Gln Asn Glu Leu
      530              535              540
Leu Val Glu Gln Phe Arg Arg Asp Glu Gly Lys Leu Val Glu Glu Asn
 545              550              555              560
Lys Arg Leu Gln Lys Glu Leu Ser Met Cys Glu Thr Glu Arg Asp Lys
      565              570              575
Lys Gly Arg Arg Val Ala Glu Val Glu Gly Gln Val Lys Glu Leu Leu
      580              585              590
Ala Lys Leu Thr Leu Ser Val Pro Thr Glu Lys Phe Glu Ser Met Lys
      595              600              605
Ser Leu Leu Ser Ser Glu Val Asn Glu Lys Val Lys Lys Ile Gly Glu
 610              615              620
Thr Glu Arg Glu Tyr Glu Lys Ser Leu Thr Glu Ile Arg Gln Leu Arg
 625              630              635              640
Arg Glu Leu Glu Asn Cys Lys Arg Gln Thr Ser Ser Ala Cys Gln Ala
      645              650              655
Arg Gly Ala

```

<210> 809

<211> 1725

<212> DNA

<213> Homo Sapiens

<400> 809

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tttctttgtt aagtcgttcc ctctacaaag gacttcctag tgggtgtgaa aggcagcggg      60
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gctgtcccct tttctgggac tattcaagga ggtctccagg acggacttca gatcactgtc      180
aatgggaccg ttctcagctc cagtggaaac aggtttgctg tgaactttca gactggcttc      240
agtggaaatg acattgcctt ccacttcaac cctcggtttg aagatggagg gtacgtggtg      300
tgcaacacga ggcagaacgg aagctggggg cccgaggaga ggaagacaca catgcctttc      360
cagaagggga tgccctttga cctctgcttc ctggtgcaga gctcagattt caaggtgatg      420
gtgaacggga tcctcttcgt gcagtacttc caccgcgtgc cctccaccg tgtggacacc      480
atctccgtca atggctctgt gcagctgtcc tacatcagct tccagaacct ccgcacagtc      540

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cctgttcagc ctgccttctc cacggtgccg ttctcccage ctgtctgttt cccacccagg 600
cccagggggc gcagacaaaa acctcccggc gtgtggcctg ccaacccggc tcccattacc 660
cagacagtca tccacacagt gcagagcgcc cctggacaga tgttctctac tcccgccatc 720
ccacctatga tgtaccccca ccccgccctat cccgatgcctt tcatcaccac cattctggga 780
gggctgtacc catccaagtc catcctcctg tcaggcactg tcctgccag tgctcagagg 840
ttccacatca acctgtgctc tggaaccac atcgcttcc acctgaacct cgttttgat 900
gagaatgctg tggccgcaa caccagatc gacaactcct gggggtctga ggagcgaagt 960
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accagctgtc tgctcctggt gggaggtggc ctctcagcc cctcctctct gacctttaac 1560
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gcttcccact ggctccacc acctgaccag agtgttctct tcagaggact ggctccttcc 1680
ccagtgtcct taaaataaag aaatgaaaat gcttgttggc acatt 1725

```

<210> 810

<211> 355

<212> PRT

<213> Homo Sapiens

<400> 810

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Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro
1          5          10          15
Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr
20          25          30
Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn
35          40          45
Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
50          55          60
Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
65          70          75          80
Ser Trp Gly Pro Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
85          90          95
Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
100          105          110
Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
115          120          125
His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
130          135          140
Ile Ser Phe Gln Asn Pro Arg Thr Val Pro Val Gln Pro Ala Phe Ser
145          150          155          160
Thr Val Pro Phe Ser Gln Pro Val Cys Phe Pro Pro Arg Pro Arg Gly
165          170          175
Arg Arg Gln Lys Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
180          185          190
Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
195          200          205
Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
210          215          220

```

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
 225 230 235 240
 Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
 245 250 255
 Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
 260 265 270
 Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
 275 280 285
 Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
 290 295 300
 Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
 305 310 315 320
 Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
 325 330 335
 Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
 340 345 350
 Val Gln Thr
 355

<210> 811
 <211> 1022
 <212> DNA
 <213> Homo Sapiens

<400> 811
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 aagaagaggc ctggggcctg gtgggtgcac aggctcctac tactgaggag caggaggctg 180
 ctgtctcctc ctctctcct ctggctctgg gcacctgga gaaagtgcct gctgctgagt 240
 cagcagatcc tccccagagt cctcagggag cctctgcctt acccactacc atcagcttca 300
 cttgctggag gcaacccaat gaggggtcca gcagccaaga agaggaggag gccagcacct 360
 cgctgacgc agagtccctg ttccgagaag cactcagtaa caagggtgat gagttggctc 420
 attttctgct ccgcaagtat cgagccaagg agctggtcac aaaggcagaa atgctggaga 480
 gagtcatcaa aaattacaag cgctgctttc ctgtgatctt cggcaaagcc tccgagtccc 540
 tgaagatgat ctttggcatt gacgtgaagg aagtggacct cgccagcaac acctacacct 600
 ttgtcacctg cctgggcctt tcctatgatg gcctgctggg taataatcag atctttccca 660
 agacaggcct cctgataatc gtccctggga caattgcaat ggagggcgac agcgccctcg 720
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 tctatgggga gccagggaaa ctgctcacc aagattgggt gcaggaaaac tacctggagt 840
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 tggctgaaac cagctatgtg aaagtcctgg agcatgtggt cagggtcaat gcaagagttc 960
 gcattgccta cccatccctg cgtgaagcag ctttgtaga ggaggaagag ggagtctgag 1020
 ca 1022

<210> 812
 <211> 317
 <212> PRT
 <213> Homo Sapiens

<400> 812
 Met Ser Leu Glu Gln Lys Ser Gln His Cys Lys Pro Glu Glu Gly Val
 1 5 10 15
 Glu Ala Gln Glu Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Thr
 20 25 30
 Thr Glu Glu Gln Glu Ala Ala Val Ser Ser Ser Ser Pro Leu Val Leu

35	40	45
Gly Thr Leu Glu Lys Val Pro Ala Ala Glu Ser Ala Asp Pro Pro Gln		
50	55	60
Ser Pro Gln Gly Ala Ser Ala Leu Pro Thr Thr Ile Ser Phe Thr Cys		
65	70	75
Trp Arg Gln Pro Asn Glu Gly Ser Ser Ser Gln Glu Glu Glu Ala		
85	90	95
Ser Thr Ser Pro Asp Ala Glu Ser Leu Phe Arg Glu Ala Leu Ser Asn		
100	105	110
Lys Val Asp Glu Leu Ala His Phe Leu Leu Arg Lys Tyr Arg Ala Lys		
115	120	125
Glu Leu Val Thr Lys Ala Glu Met Leu Glu Arg Val Ile Lys Asn Tyr		
130	135	140
Lys Arg Cys Phe Pro Val Ile Phe Gly Lys Ala Ser Glu Ser Leu Lys		
145	150	155
Met Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Ala Ser Asn Thr		
165	170	175
Tyr Thr Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly		
180	185	190
Asn Asn Gln Ile Phe Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly		
195	200	205
Thr Ile Ala Met Glu Gly Asp Ser Ala Ser Glu Glu Glu Ile Trp Glu		
210	215	220
Glu Leu Gly Val Met Gly Val Tyr Asp Gly Arg Glu His Thr Val Tyr		
225	230	235
Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Trp Val Gln Glu Asn Tyr		
245	250	255
Leu Glu Tyr Arg Gln Val Pro Gly Ser Asn Pro Ala Arg Tyr Glu Phe		
260	265	270
Leu Trp Gly Pro Arg Ala Leu Ala Glu Thr Ser Tyr Val Lys Val Leu		
275	280	285
Glu His Val Val Arg Val Asn Ala Arg Val Arg Ile Ala Tyr Pro Ser		
290	295	300
Leu Arg Glu Ala Ala Leu Leu Glu Glu Glu Glu Gly Val		
305	310	315

<210> 813
 <211> 5175
 <212> DNA
 <213> Homo Sapiens

<400> 813	
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agactgactt cactatagaa occacagttg tatcaatggg tggggaaaga tagtggcaac	120
aggcaaagga gaaacagctc tgacatacaa agaaaatgag tatgctaaag ccaagtgggc	180
ttaaggcccc caccaagatc ctgaagcctg gaagcacagc tctgaagaca cctacggctg	240
ttgtagctcc agtagaaaa accatatcca gtgaaaaagc atcaagcact ccatcatctg	300
agactcagga ggaatttggt gatgactttc gagggtggga gcgagtttg gtgaatggaa	360
ataagcctgg atttatccag tttcttggag aaacccagtt tgcaccaggc cagtgggctg	420
gaattgtttt agatgaacct ataggcaaga acgatggttc ggtggcagga gttcgggtatt	480
tccagtgtga acctttaag ggcataattt cccgaccttc aaagttaaca aggaaggtgc	540
aagcagaaga tgaagctaag ggcctgcaga caacgcccgc ctcccagact acttcaccgc	600
tgtgcacttc tacggccagc atgggtgtct cctccccctc cacccttca aacatccctc	660
agaaaccatc acagccagca gcaaaggaac cttcagctac gcctccgac agcaacctta	720
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<210> 814

<211> 1392

<212> PRT

<213> Homo Sapiens

<400> 814

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Val Glu Lys Thr Ile Ser Ser Glu Lys Ala Ser Ser Thr Pro Ser Ser
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Glu Thr Gln Glu Glu Phe Val Asp Asp Phe Arg Val Gly Glu Arg Val
50      55      60
Trp Val Asn Gly Asn Lys Pro Gly Phe Ile Gln Phe Leu Gly Glu Thr
65      70      75      80
Gln Phe Ala Pro Gly Gln Trp Ala Gly Ile Val Leu Asp Glu Pro Ile
85      90      95
Gly Lys Asn Asp Gly Ser Val Ala Gly Val Arg Tyr Phe Gln Cys Glu
100     105     110
Pro Leu Lys Gly Ile Phe Thr Arg Pro Ser Lys Leu Thr Arg Lys Val
115     120     125
Gln Ala Glu Asp Glu Ala Asn Gly Leu Gln Thr Thr Pro Ala Ser Arg
130     135     140
Ala Thr Ser Pro Leu Cys Thr Ser Thr Ala Ser Met Val Ser Ser Ser
145     150     155     160
Pro Ser Thr Pro Ser Asn Ile Pro Gln Lys Pro Ser Gln Pro Ala Ala
165     170     175
Lys Glu Pro Ser Ala Thr Pro Pro Ile Ser Asn Leu Thr Lys Thr Ala
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Ser Glu Ser Ile Ser Asn Leu Ser Glu Ala Gly Ser Ile Lys Lys Gly
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Val Ala Gly Thr Arg Tyr Phe Gln Cys Gln Pro Lys Tyr Gly Leu Phe		255
	260	265
Ala Pro Val His Lys Val Thr Lys Ile Gly Phe Pro Ser Thr Thr Pro		270
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Ala Lys Ala Lys Ala Asn Ala Val Arg Arg Val Met Ala Thr Thr Ser		285
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Ala Ser Leu Lys Arg Ser Pro Ser Ala Ser Ser Leu Ser Ser Met Ser		300
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Ser Val Ala Ser Ser Val Ser Ser Arg Pro Ser Arg Thr Gly Leu Leu		320
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Thr Glu Thr Ser Ser Arg Tyr Ala Arg Lys Ile Ser Gly Thr Thr Ala		335
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Leu Gln Glu Ala Leu Lys Glu Lys Gln Gln His Ile Glu Gln Leu Leu		350
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Gln His Val Leu Glu Leu Glu Ala Lys Met Asp Gln Leu Arg Thr Met		400
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Val Glu Ala Ala Asp Arg Glu Lys Val Glu Leu Leu Asn Gln Leu Glu		415
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Glu Glu Lys Arg Lys Val Glu Asp Leu Gln Phe Arg Val Glu Glu Glu		430
	435	440
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	485	490
Asp Met Ser Leu Ser Leu Leu Gln Glu Ile Ser Ser Leu Gln Glu Lys		495
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Leu Glu Val Thr Arg Thr Asp His Gln Arg Glu Ile Thr Ser Leu Lys		510
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Glu His Phe Gly Ala Arg Glu Glu Thr His Gln Lys Glu Ile Lys Ala		525
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Leu Tyr Thr Ala Thr Glu Lys Leu Ser Lys Glu Asn Glu Ser Leu Lys		540
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Ser Lys Leu Glu His Ala Asn Lys Glu Asn Ser Asp Val Ile Ala Leu		560
	565	570
Trp Lys Ser Lys Leu Glu Thr Ala Ile Ala Ser His Gln Gln Ala Met		575
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Glu Glu Leu Lys Val Ser Phe Ser Lys Gly Leu Gly Thr Glu Thr Ala		590
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Glu Phe Ala Glu Leu Lys Thr Gln Ile Glu Lys Met Arg Leu Asp Tyr		605
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Gln His Glu Ile Glu Asn Leu Gln Asn Gln Gln Asp Ser Glu Arg Ala		620
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 Lys Ala Glu Asp Gln His Leu Val Glu Met Glu Asp Thr Leu Asn Lys
 675 680 685
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 Lys Ala Thr Glu Glu Lys Leu Leu Asp Leu Asp Ala Leu Arg Lys Ala
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 Ser Ser Glu Gly Lys Ser Glu Met Lys Lys Leu Arg Gln Gln Leu Glu
 740 745 750
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 Glu Thr Leu Glu Lys Glu Leu Gln Ile Leu Lys Glu Lys Phe Ala Glu
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 820 825 830
 Asn Lys Leu His Gln Lys Glu Glu Gln Phe Asn Met Leu Ser Ser Asp
 835 840 845
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 850 855 860
 Glu Lys Asp Glu Arg Glu Glu Gln Leu Ile Lys Ala Lys Glu Lys Leu
 865 870 875 880
 Glu Asn Asp Ile Ala Glu Ile Met Lys Met Ser Gly Asp Asn Ser Ser
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 Gln Leu Thr Lys Met Asn Asp Glu Leu Arg Leu Lys Glu Arg Asp Val
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Glu Glu Leu Gln Leu Lys Leu Thr Lys Ala Asn Glu Asn Ala Ser Phe
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 945 950 955 960
 Lys Leu Ser Asp Leu Glu Lys Lys Met Glu Thr Ser His Asn Gln Cys
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 980 985 990
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 1140 1145 1150
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 1250 1255 1260
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 Asn Ser Val Ile Val Asp Leu Gln Arg Lys Asn Gln Asp Leu Lys Met
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 Lys Val Glu Met Met Ser Glu Ala Ala Leu Asn Gly Asn Gly Asp Asp
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 Pro Arg Leu Phe Cys Asp Ile Cys Asp Cys Phe Asp Leu His Asp Thr
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 <212> PRT
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 35 40 45
 Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe Pro Gly Leu
 50 55 60
 Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val Trp Glu Gly
 65 70 75 80
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 85 90 95
 Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val
 100 105 110
 Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys
 115 120 125
 Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp Tyr Lys Ser
 130 135 140
 Cys Ala His Asp Trp Val Tyr Glu
 145 150